Iran's 26th International Congress of

MICROBIOLOGY

بیست و ششمین
کنگره بین المللی

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Abstracts Book

In the Name of God

In a world that new information is rapidly becoming available every day, maintaining up-to-date in the sciences in particular Bio-Medicine is of great importance. After the COVID-19 pandemic, the world has realized the importance of Biomedical Sciences more and more. Today, the significance of interdisciplinary approaches and the integration of diverse scientific perspectives—particularly to human diseases—has become more evident and requires being prepared for the complex challenges of today's world. In the meantime, the important role of microbiology in improving the quality of human life from the field of health to industry, agriculture, etc, is undeniable. Addressing microbial sciences and technologies, investing in this field, providing more facilities and appropriate conditions to specialists with high knowledge and skills, and training expert researchers and scholars will pave the way for the country's further development and promote national self-reliance.

The Iranian Society of Microbiology is proud to have been a pioneer in this important matter for many years. As the oldest scientific society, it has always been at the forefront of microbiology and has fulfilled its mission effectively by addressing the needs and capacities of this field, holding a congress, and bringing together top experts and researchers.

The 26th Iranian Microbiology Congress, as an important scientific event, provided an opportunity to exchange valuable information and experiences in the field of microbiology. As in previous years, this congress, with the presence of outstanding lecturers, professors, and experts from all over the world and presentation the most up-to-date content and data in this field, presentaion scientific articles and posters, organization useful workshops, has provided a suitable platform for scholars. The enthusiastic engagement of young researchers alongside senior scientists promises a bright future for the advancement of microbiology in Iran and helps to clarify the path of young people who are eager for science. The remarkable features of this congress included the high number of submitted papers, the diverse range of specialized sessions, workshops, and scientific panels, all of which contributed to elevating the scientific level of the event and creating a dynamic and constructive atmosphere.

I would like to sincerely thank all professors, researchers, members of the scientific and executive committees, and our academic and industrial supporters whose dedicated efforts made this event possible. It is hoped that the scientific outcomes and collaborations developed during this congress will pave the way for expanding the borders of knowledge, developing international collaborations, and promoting public health.

With the Best Regards
Professor Mohammad Mehdi Feizabadi
Scientific Secretary of Congress

In the Name of God

The 26th International Congress of Microbiology of Iran, held from August 26 to 28, 2025, at Tehran University of Medical Sciences, was recognized as a reputable scientific event that provided a unique opportunity for researchers, specialists, and students active in the field of microbiology. The congress was convened with the aim of exchanging knowledge, reviewing the latest achievements and scientific findings, and creating a suitable platform for both national and international scientific collaborations.

Through the participation of distinguished speakers, attendees were introduced to the most recent scientific methods and techniques, and engaged in discussions on the challenges and opportunities in various fields of microbiology. In addition to the keynote lectures, specialized workshops and panel discussions created an interactive environment that further enriched the scientific exchange among participants.

I would like to extend my sincere gratitude to all the esteemed professors, dear students, valued colleagues, the respected board members of the Iranian Society for Microbiology, the executive team, scientific centers and institutes (particularly the Pasteur Institute of Iran and the Razi Vaccine and Serum Research Institute), as well as the companies that generously supported this congress. Their encouraging presence and contributions greatly enriched the scientific and research quality of this event and supported us in fulfilling this significant undertaking.

It is hoped that this congress, along with its future continuations, will open new horizons toward further advancements in the field of medical microbiology. We trust that the collaboration established during this event will serve as foundation for sustained scientific progress and international cooperation.

Dr. Parviz Afrough
Executive Secretary of the Congress

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Abstract Background: Microorganisms are found in all environments and are transmitted to individuals through various devices, which is essential to identify its prevalence, especially in ATMs and its antibiotic resistance. Purpose: The aim of this study wa

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BACKGROUND AND OBJECTIVES: Background: Microorganisms are found in all environments and are transmitted to individuals through various devices, which is essential to identify its prevalence, especially in ATMs and its antibiotic resistance. Purpose: The aim of this study was to investigate the bacterial contamination and antibiogram of the keyboard of banking ATMs in Mashhad during the years 1402-1403

MATERIALS AND METHODS: Methods: This study was performed on 82 banks. After registering the ATM information, a sample of the keyboard was also taken. Chi-square and Fisher's exact test were used to compare the data. Results: 93.2% of ATM keyboards in Mashhad banks contain pathogenic bacteria. The most common cultures were Pneumoniae (39%) and Staphylococcus epidermis (37.8%), respectively. There was no statistically significant difference between keyboard cover and apparent contamination. Also, in the study of antibiotic resistance, it was found that the highest sensitivity (95.5%) was for the antibiotic imipenem and on the other hand, the lowest sensitivity (30.1%) was for the antibiotic ampicillin

RESULTS AND DISCUSSION: Conclusion: The prevalence of ATM keyboard contamination is high and on the other hand the antibiotic resistance is high and to remove such bacteria from ATM keyboards, preventive measures should be taken, including cleaning it at certain times with alcohol and other substances Disinfectant.

Keywords: Microorganism, Antibiogram, Bacteria, ATMs

A carotenoid pigment from Arthrobacter citreus with in vitro anticancer activity against Three cancer cell lines

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BACKGROUND AND OBJECTIVES: The global crisis stemming from rising mortality rates due to antimicrobial resistance and cancers has intensified researchers' efforts to identify novel, potent solutions from natural products for pharmaceutical applications. Bacterial pigments are recognized as significant secondary metabolites owing to their diverse pharmacological activities against both microbial resistance and various cancers.

MATERIALS AND METHODS: Antimicrobial activity was evaluated using the microbroth dilution method. The standard bacterial strains employed were Pseudomonas aeruginosa ATCC 27853, Staphylococcus aureus ATCC 25923, Escherichia coli ATCC 25922, and Klebsiella pneumoniae ATCC 13883. For evaluating anticancer activity, A549 (human lung cancer), HT-29 (human colorectal adenocarcinoma), MDA-MB-231 (triple-negative breast cancer), and HFF (Human foreskin fibroblasts) cell lines were utilized with Dulbecco's Modified Eagle Medium (DMEM) supplemented with 10% Fetal Bovine Serum (FBS). Pigment powders were dissolved in dimethyl sulfoxide (DMSO), and a range of pigment concentrations were prepared in DMEM for the MTT assay.

RESULTS AND DISCUSSION: The pigment under investigation exhibited a more prominent inhibitory effect against Gram-positive bacterial species compared to Gram-negative species. The calculated IC50 values were as follows: A549 (1009.53 µg/mL), HT-29 (343.95 µg/mL), MDA-MB-231 (107.86 µg/mL), and HFF (1043.77 µg/mL). Based on the results of the anticancer effect of the extracted pigment on various cell lines, this pigment represents a promising candidate for further studies, particularly concerning its potential anticancer effects, especially against breast cancer.

Keywords: microbial pigment , antibacterial , anticancer activity, Arthrobacter citreus

A Case Report of Chronic Inflammatory Demyelinating Polyneuropathy following COVID-19 Vaccination

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BACKGROUND AND OBJECTIVES: Chronic Inflammatory Demyelinating Polyneuropathy (CIDP) is a peripheral polyneuropathy. Chronic damage to neuronal myelin by the immune system results in inflammation and demyelination of the peripheral nervous system. Several side effects have been reported with Coronavirus disease 2019 (COVID-19) vaccines. There are some reports of vaccineinduced- CIDP. In this study, we described the occurrence of CIDP in a patient with a history of receiving the first dose of a COVID-19 vaccine, Sputnik V.

MATERIALS AND METHODS: We presented a patient receiving the COVID-19 vaccine Sputnik V two weeks before progressive flaccid tetraparesis and dysautonomia. He was first diagnosed with Guillain- Barre Syndrome (GBS). Two episodes of worsening the weakness occurred within 8 weeks from the onset of the disease, and the treatment was repeated as GBS-Treatment-related Fluctuations (TRF) and relapse. Also, a few relapses happened eight weeks after the disease's onset. Hence, he was diagnosed with "acute-onset CIDP". The patient received several intravenous immunoglobulin (IVIG) courses as maintenance therapy. No further deterioration was reported during the follow-up.

RESULTS AND DISCUSSION: Post-vaccination GBS is a known phenomenon. However, there are several reports of vaccine-induced-CIDP. This is the first reported case of acute-onset CIDP associated with the Sputnik V vaccine in Iran. Subsequent studies are required to determine the definite relationship between COVID-19 vaccination and CIDP.

Keywords: chronic inflammatory demyelinating polyneuropathy, COVID-19, Guillain-barre syndrome, peripheral neuropathy, vaccine

A Chimeric Subunit Vaccine Against Salmonella Typhi Delivered via Silica-Alginate Hybrid Nanoparticles Elicits Robust Mucosal and humoral Immunity

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BACKGROUND AND OBJECTIVES: Typhoid fever, caused by antimicrobial-resistant Salmonella Typhi, poses a global health burden, with 11–20 million annual cases. Current vaccines face limitations in durability and coverage, necessitating novel strategies.

MATERIALS AND METHODS: We designed a multi-epitope chimeric antigen (SOF) combining S. Typhi virulence factors (SteD, STIV, FliC-D1) with optimized linkers for structural stability. The SOF protein was expressed in E. coli, purified, and loaded into silica-alginate hybrid nanoparticles (NPs) engineered for pH-responsive release. NPs were characterized via SEM, DLS, and in vitro release assays. Immunogenicity was evaluated in BALB/c mice (n=10/group) via intraperitoneal/oral routes, with IgG/IgA titers measured by ELISA. Protective efficacy was assessed by challenging mice with lethal S. Typhi doses (10–100 LD50).

RESULTS AND DISCUSSION: The SOF protein (68 kDa) exhibited high adsorption efficiency (0.85 mg/mg NPs) and sustained release (e.g., 55% in SBF at 12 h). NPs showed uniform morphology (96.7 ± 12 nm by SEM) and colloidal stability (PDI 0.27). Vaccinated mice elicited significant IgG/IgA responses (*p*0.01 vs. controls), with 100% survival post-challenge at 50 LD50. Oral delivery induced robust mucosal immunity, critical for enteric pathogens. This study demonstrates a proof-of-concept for a nanoparticle-delivered chimeric vaccine against typhoid fever. The vaccine combines rational antigen design with advanced nanocarriers to enhance immunogenicity and protection. The platform holds promise for combating antimicrobial-resistant S. Typhi and other enteric diseases.

Keywords: Salmonella Typhi, Hybrid Nanoparticles, immunogenicity, Chimeric Vaccine

A Comprehensive Narrative Review of Bedaquiline and Delamanid: Novel Strategies Against Multidrug-Resistant and Extensively Drug-Resistant Mycobacterium tuberculosis

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BACKGROUND AND OBJECTIVES: The effective treatment of extensively drug-resistant (XDR) and multidrug-resistant (MDR) tuberculosis (TB) remains a significant therapeutic challenge worldwide. Bedaquiline (BDQ) and delamanid (DLM), two antimycobacterial drugs that have recently received approval, have become critical parts of novel treatment programs. This narrative review presents a summary of their pharmacodynamic properties, factors related to resistance, potential interactions whit other drug, and safety profiles.

MATERIALS AND METHODS: Studies that examined the clinical utility, resistance mechanisms, and antimicrobial efficacy of BDQ and DLM were searched in Scopus, PubMed, and Embase databases up to August 2024 for relevant references and were included in this review.

RESULTS AND DISCUSSION: BDQ indicated powerful antimicrobial activity against MDR/XDR Mycobacterium tuberculosis, along with other nontuberculous mycobacteria (NTM species, including slow-growing and fast-growing strains). The main cause of BDQ resistance in M. tuberculosis is mutations in the three genes mmpR (Rv0678), atpE, and pepQ. BDQ may have synergistic effects when combined with pretomanid/linezolid, pyrazinamide, and DLM. BDQ has few side effects. The QTc interval may be prolonged if BDQ is used. DLM also showed strong antibacterial effectiveness against MDR/XDR M. tuberculosis and NTM. Mutations in the fbiA, fbiB, fbiC, fgd1, and ddn genes are the main cause of resistance to DLM. DLM has a synergistic effect with moxifloxacin and BDQ. One of the few side effects that some people experience after using DLM is QTc prolongation.

Keywords: Mycobacterium tuberculosis, Drug resistance, delamanid, bedaquiline.

A Lytic Podoviridae Phage Active Against VRE Bloodstream Isolates

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BACKGROUND AND OBJECTIVES: Enterococci, part of the normal gut flora, have become significant nosocomial pathogens due to their ability to acquire virulence traits and antimicrobial resistance. Biofilm production enhances virulence, protects against immune responses, reduces antibiotic efficacy, and facilitates gene exchange. These factors complicate treatment, underscoring the need for alternatives. Phage therapy, using lytic bacteriophages, offers a promising strategy against multidrug-resistant Enterococcus faecalis bloodstream infections.

MATERIALS AND METHODS: Clinical isolates of Enterococcus faecalis were confirmed by PCR targeting the vanA and vanB resistance genes. Their antibiotic susceptibility profiles were assessed using minimum inhibitory concentration (MIC) testing. Bacteriophages were isolated from hospital wastewater and tested for lytic activity using spot and double-layer plaque assays. Transmission electron microscopy (TEM) was employed to obtain phage images for morphological characterization. The adsorption rate, host range, and stability of the isolated bacteriophage were evaluated. The latent period and burst size were determined using a one-step growth curve. Subsequently, the antimicrobial efficacy of the phage against Enterococcus faecalis was assessed.

RESULTS AND DISCUSSION: Based on TEM images, the phage was morphologically identified as belonging to the Podoviridae family. It exhibited a latent period of 20 minutes and a calculated burst size of 7.5 plaque-forming units (PFU) per infected cell. The phage demonstrated a broad host range, with optimal stability at 37°C and pH 7. It also showed tolerance to varying concentrations of NaCl. The isolated phage exhibited lytic activity against vancomycin-resistant Enterococcus faecalis strains, supporting its potential as an alternative strategy for controlling bloodstream infections.

Keywords: VRE, Enterococcus faecalis , Bacteriophages, Phage therapy, bloodstream infections, biofilm

A MgO Nanoparticle-Based Strategy to Combat Nosocomial Pathogens: Focus on MDR isolates of S. aureus and K. pneumoniae

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BACKGROUND AND OBJECTIVES: In the era of modern medicine, the crisis of the microbial resistance—driven by specific bacterial mechanisms that neutralize the effects of antibacterial agents—is expanding. Despite the assumption of sterile and safe healthcare environments, this phenomenon continues to leads to nosocomial infections and increased mortality rates. Among the most candidates, magnesium oxide (MgO) nanoparticles show notable physicochemical properties, such as high surface area, low toxicity, and perfect biocompatibility, making them highly effective in inhibiting bacterial growth. This study aims to evaluate the antibacterial activity of MgO NPs against Multidrug-resistance strains isolated from various ICU units of a tertiary care hospital, aiming to support the development of nanomaterial-based therapeutic strategies.

MATERIALS AND METHODS: MgO NPs were synthesized via Chemical Deposition, and their physical properties were examined through DLS and SEM tests. MDR strains of Staphylococcus aureus and Klebsiella pneumoniae were isolated and purified from various ICU wards. Using Antibiogram test for antibiotic susceptibility of the isolates. the antibacterial activity of the MgO NPs was evaluated using MIC and MBC test.

RESULTS AND DISCUSSION: The Minimum Inhibitory Concentration (MIC) and Minimum Bactericidal Concentration (MBC) of the MgO NPs were found to be 2 mg/mL for the K. pneumoniae, and 1 mg/mL for the S.aureus. The size of the synthesized nanoparticles, according to SEM observations, was below 100 nm. MgO NPs, due to their antimicrobial capabilities, high biocompatibility, and low toxicity, could be alternatives for combating these pathogenic multidrug-resistance strains and may play a significant role in controlling and limiting the spread of nosocomial infections.

Keywords: Antibacterial, Multidrug-resistance, Magnesium oxide nanoparticles

Anti-Cancer and Antibacterial Effects of the Native Probiotic Lactobacillus reuteri on HeLa Cervical Cancer Cells: Evaluation of Apoptosis and Expression of Key Genes

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BACKGROUND AND OBJECTIVES: Background: Cervical cancer remains one of the leading causes of cancer-related mortality among women worldwide. The application of probiotics as biotherapeutic agents in oncology has gained significant attention due to their ability to induce apoptosis and modulate the host immune response. This study aimed to investigate the cytotoxic and pro-apoptotic effects of the native probiotic Lactobacillus reuteri on HeLa cervical cancer cells, as well as its antibacterial activity against Escherichia coli and Staphylococcus aureus.

MATERIALS AND METHODS: Methods: A native strain of L. reuteri was cultured in MRS broth, and its cell-free supernatant (CFS) was prepared. HeLa cells were treated with various concentrations of the CFS, and cell viability was assessed using the MTT assay, with IC50 values calculated. Apoptosis was evaluated through DAPI staining, and the expression of Casp3 and Bcl-2 genes was quantified using Real-Time PCR. Antibacterial activity was tested via MIC and MBC assays.

RESULTS AND DISCUSSION: Results: Treatment of HeLa cells with L. reuteri CFS led to a dose-dependent reduction in cell viability. DAPI staining confirmed the induction of apoptosis. Gene expression analysis showed upregulation of Caspase-3 and downregulation of Bcl-2. Additionally, strong antibacterial effects were observed against both Gram-positive and Gram-negative bacteria. Conclusion: The native Lactobacillus reuteri strain exhibited potent anti-cancer and antibacterial properties. Its ability to induce apoptosis and regulate key genes involved in programmed cell death highlights its potential as a complementary agent in the treatment of cervical cancer.

Keywords: Lactobacillus reuteri, cervical cancer, HeLa cells, apoptosis, Casp3, Bcl-2

Antibiotic resistance in bioaerosols isolated from poultry farms in Zanjan Province

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BACKGROUND AND OBJECTIVES: The distribution of bioaerosols, particularly antibiotic-resistant microbes, in poultry farms poses a health risk to both workers and birds. The overuse of antibiotics in animal feed and medication has significantly exacerbated the problem of antimicrobial resistance. This study focused on determining the antibiotic resistance profiles of isolated bioaerosols in poultry farms.

MATERIALS AND METHODS: In a cross-sectional study, three poultry farms in Zanjan province were selected. Air samples were collected using an active air sampling method with a Flite 3-SKC pump for 5 minutes. Bacterial and fungal growth was assessed on Nutrient Agar and Sabouraud Dextrose Agar plates after incubation at 37ºC and 25ºC, respectively. The growth isolates were identified through microscopic analysis and biochemical tests. The antibiotic resistance profiles for airborne bacteria were evaluated using the disk diffusion method with ten selected antibiotics.

RESULTS AND DISCUSSION: The bacterial population ranged from 2820 to 4283 cfu/m³, which was three times higher than the fungal population. The most common isolates were gram-positive bacteria, including Staphylococcus aureus (45%) and Rhodococcus sp. (23%). Among the fungi, the highest populations were of Aspergillus (41%) and Penicillium (33%). The antibiotic resistance profile indicated the highest sensitivity to Vancomycin and Gentamicin, whereas the highest resistance was observed for Chloramphenicol. On average, more than 30% of isolates from the three poultry farms exhibited antibiotic resistance, highlighting the significant role of bioaerosols in the transmission of antibiotic resistance genes in the environment.

Keywords: Antibiotic resistance, Bioaerosols, poultry farm, Air

Antibiotic resistance pattern in Citrobacter freundii strains isolated from poultry meat in Shahrekord city

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BACKGROUND AND OBJECTIVES: Citrobacter freundi is an emerging food pathogen of public health importance. The present study aimed to investigate the prevalence and phenotypic and genotypic antibiotic resistance of Citrobacter isolates isolated from poultry meat in Shahrekord city. In this cross-sectional-descriptive study, 300 chicken, quail and turkey meat samples were examined for Citrobacter freundi contamination in Shahrekord city in 2024

MATERIALS AND METHODS: The samples were examined by biochemical and molecular methods. The disk diffusion method was used to determine the sensitivity of bacteria to antibiotics, and antibiotic resistance genes were examined using specific primers. Using biochemical methods, 24 isolates (8%) of Citrobacter freundi were isolated, which were also confirmed by molecular methods

RESULTS AND DISCUSSION: The contamination was reported to be 12% in quail meat, 7% in chicken meat, and 5% in turkey meat. After confirmation of the bacteria using microbiological and molecular tests and antibiogram, the highest resistance was reported to cotrimoxazole (70.83%). All strains were sensitive to the antibiotics gentamicin, ceftriaxone, ciprofloxacin, kanamycin and cefotaxime. The presence of antibiotic resistance in Citrobacter freundii isolates in the present study and similar studies mentioned indicates the use of antibiotics in the treatment of livestock and poultry, which will vary depending on the type of region and the method of antibiotic administration

Keywords: Citrobacter freundii, antibiotic resistance, poultry meat

Antibiotic-Resistant Enterococci in Equine Gut Microbiome: A Hidden Threat to Environmental and Human Health

Azar Motamedi Boroojeni [1], Zahra Naziri [1], Arash Shagerdi [1], Seyed Hesamoddin Hosseini [1] © Ⓟ

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BACKGROUND AND OBJECTIVES: The widespread use of antibiotic in veterinary medicine has led to the development of antibiotic-resistant bacteria which poses challenges in treating bacterial infections in both animals and humans including Enterococcus species. Given their role in the intestinal microbiome and potential to cause hospital-acquired infections, monitoring resistance in enterococci isolated from animals in close contact with humans is critical. The aim of the present study was to investigate the prevalence of antibiotic resistance among enterococci isolated from the healthy horse's intestinal microbiome.

MATERIALS AND METHODS: Disc diffusion method was used to evaluate the susceptibility of One hundred enterococcus isolates against different classes of antibiotics. The bacteria had been isolated from fecal samples of healthy horses (33 E. faecium, 11 E. faecalis, and 56 other species). The prevalence of tetM resistance gene was also determined using PCR.

RESULTS AND DISCUSSION: The most prevalent resistance was observed against Imipenem (67%), Rifampin (61%), Tetracycline (27%) and Erythromycin (24%), respectively. Only one and two of the isolates were resistant to Chloramphenicol and Nitrofurantoin, respectively. 57% of the isolates showed multi drug resistance. Among the isolates 59% had tetM resistance gene that among them 39% belonged to E. faecium, 11.9% to E. faecalis and 49.2% to other species.

Keywords: Enterococcus, antibiotic resistance, horse, zoonotic potential

A Novel Biosensor for One-Step Identification of E. coli Strains in Food and Water Samples

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BACKGROUND AND OBJECTIVES: The presence of E. coli in drinking water or food clearly signifies exposure to human or animal fecal matter and indicates potential contamination by more dangerous gastrointestinal pathogens (e.g., Salmonella, Shigella, and Campylobacter) Rapid detection of microbial contaminants using novel methods like biosensors has garnered significant interest among microbiology researchers. Nucleic acid probe-based biosensors conjugated with gold nanoparticles offer a highly cost-effective solution due to their speed and low operational cost. In this project, we have developed such a biosensor for rapid detection of diverse E. coli strains.

MATERIALS AND METHODS: E. coli strains were obtained from the Microbial Culture Collection of the Faculty of Veterinary Medicine (University of Tehran). Using bioinformatics tools (NCBI database), we analyzed the mRNA sequence encoding the Murein heteropolymer across E. coli strains and identified conserved regions exclusive to E. coli. Four nucleic acid probes complementary to different segments of these conserved regions were synthesized and conjugated to gold nanoparticles. Test samples (with/without E. coli) were prepared, and gold-conjugated probes were added to the samples. Samples underwent 20-minute annealing at 60°C to optimize probe-target binding. Finally, optical absorption within the 400 – 700 nm range was measured using a spectrophotometer device.

RESULTS AND DISCUSSION: Samples containing E. coli showed peak optical absorption at 524 nm. In contrast, E. coli-free samples exhibited a visible color shift from red to black with turbidity, discernible without instrumentation. This biosensor demonstrates great potential for rapid visual detection of diverse E. coli strains in food and water samples.

Keywords: Biosensor, E. coli, Gold nanoparticle, Murein

A Report on GLASS Implementation in Iran

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BACKGROUND AND OBJECTIVES: Antimicrobial resistance(AMR) is a major global health threat, and containing it is now among the top priorities that countries must incorporate into their national health policies. Iran as a country committed to addressing this critical issue, has since 2016 adopted the framework introduced by World Health Organization known as "Global Antimicrobial Resistance and Use Surveillance System"(GLASS) to establish its national AMR surveillance program, enabling systematic data collection and analysis of data on antibiotic resistance in priority bacterial pathogens isolated from human infections. This presentation provides the latest data obtained from sentinel sites participating in national program.

MATERIALS AND METHODS: Laboratory data on selected priority pathogens, together with accompanying clinical and epidemiological information, were collected from 14 sentinel sites across various provinces of the country. The data were assessed for completeness and quality, and subsequently analyzed using statistical methods recommended by reference guidelines (CLSI,WHO)

RESULTS AND DISCUSSION: The analysis revealed a high rate of resistance among priority bacteria to antibiotics of concern belonging to the WHO AWaRe "Watch" and "Reserve" groups, such as Carbapenems and Third-generation cephalosporins, as well as a significant rate of multidrug resistance among these pathogens, which further complicates therapeutic interventions. Comparison of national AMR surveillance data with globally reported rates underscores the need for establishing a multifaceted program that engages all relevant stakeholder to address this threat. Such a program should integrate strengthened laboratory capacity, standardized data collection and reporting, and promotion of rational antimicrobial use through appropriate stewardship programs as key components for tackling antimicrobial resistance.

Keywords: Antimicrobial resistance, GLASS, Surveillance

A Review of Aflatoxin Contamination and Risk Characterization in Food (Iran: 2019–2024)

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BACKGROUND AND OBJECTIVES: Aflatoxins, particularly Aflatoxin B1 and M1, are potent secondary metabolites produced by Aspergillus species. These compounds are commonly detected in milk, cheese, nuts, spices, and cereals, and are linked to hepatocellular carcinoma and immunosuppression. To assess the contamination of aflatoxins in major food products in Iran from 2019 to 2024 and to characterize related health risks.

MATERIALS AND METHODS: We reviewed articles published between 2019 and 2024 using databases including Pubmed, and Science Direct. Inclusion criteria were original studies reporting numerical aflatoxin data in food items. Data on contamination rates, concentration ranges, regulatory exceedance, and health risk metrics (e.g., Margin of Exposure) were extracted and summarized.

RESULTS AND DISCUSSION: Aflatoxin M1 was detected in 55–77% of milk samples from different cities, with 10–25% exceeding European Union safety limits. Cheese products also showed significant contamination. In nuts, especially imported hazelnuts and pistachios, Aflatoxin B1 concentrations reached up to 8.13 µg/kg, with some samples exceeding the regulatory limit, particularly in imported hazelnuts. Spices demonstrated alarming Aflatoxin B1 levels, particularly in samples from Tabriz. According to Margin of Exposure, a key indicator widely recognized in risk assessment, aflatoxin contamination in Iranian food products remains a serious public health threat. Regular screening, more stringent regulations, and enhanced agricultural and storage practices are critical to reducing population-level exposure, especially among vulnerable groups such as children.

Keywords: Aflatoxin B1, Aflatoxin M1, Food contamination, Risk assessment, Aspergillus species.

A Review of Machine Learning Approaches for Predicting Survival Genes in Extremophiles

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BACKGROUND AND OBJECTIVES: Extremophilic microorganisms, such as Deinococcus radiodurans, exhibit extraordinary resilience to harsh environmental conditions such as ionizing radiation and oxidative stress. Understanding the genetic basis of this survival is crucial for advancements in microbiology, synthetic biology, and astrobiology.

MATERIALS AND METHODS: This review explores the application of machine learning techniques in predicting survival-associated genes in D. radiodurans, highlighting how algorithms like Random Forests and Support Vector Machines facilitate rapid gene function annotation and candidate gene identification.

RESULTS AND DISCUSSION: Despite challenges related to limited labeled data and biological complexity, integrating multi-omics datasets and advanced computational models offers promising avenues to enhance prediction accuracy. The convergence of machine learning and microbial genomics not only accelerates gene discovery but also enables the design of engineered extremophiles tailored for space exploration and biotechnological applications.

Keywords: Deinococcus radiodurans, Radiation Resistance, Extremophiles, Machine Learning

A Review of Sepsis Diagnostic Criteria and Bloodstream Infections Using Artificial Intelligence

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BACKGROUND AND OBJECTIVES: Sepsis and microbial infections are among the most critical emergencies in hospitalized patients and are associated with high global mortality rates. Rapid and accurate treatment of these conditions remains a major challenge for infectious disease specialists. On the other hand, the role of Artificial Intelligence (AI) in infection diagnosis is rapidly expanding. This review aims to explore the application of AI in the diagnosis of sepsis and various types of infections directly from patients' blood samples.

MATERIALS AND METHODS: A targeted search was conducted in Persian across six AI platforms, including ChatGPT, Deepseek, Gork, Liner, Monica, and Citrus Search, as well as in international scientific databases such as PubMed and Google Scholar. The full topic title and keywords including "sepsis," "bacterial and viral infections," "artificial intelligence," and "neutrophil indices" were used for search queries and resource selection.

RESULTS AND DISCUSSION: Artificial intelligence (AI) is increasingly utilized in the early detection of sepsis and bloodstream infections, enhancing diagnostic sensitivity, specificity, and pathogen identification. Companies such as Karius, Day Zero Diagnostics, Inflammatix, MeMed, and Cytovale employ technologies including immune profiling, metagenomics, proteomics, and biomarker analysis (e.g., Procalcitonin, PSP, CRP). AI tools process hematological data, digital imaging, and lab results for rapid assessment. Karius and Day Zero lead in AI-based diagnostics, while Beckman Coulter and Roche integrate AI into lab systems. Micronoma and Freenome target microbial and metabolic blood signatures. These innovations support faster, more accurate diagnoses and improved clinical outcomes in sepsis management.

Keywords: Sepsis, Septic Shock, Neutrophil, Artificial Intelligence.

A Review of the Application of Artificial Intelligence in Identifying Pathogenic Bacteria in the Food Industry

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BACKGROUND AND OBJECTIVES: Foodborne illnesses caused by harmful bacteria are a major global concern that poses a threat to public health. Traditional detection techniques are frequently time-consuming, labor-intensive, and perhaps inaccurate. The food industry can benefit from the use of artificial intelligence (AI) for the quick, precise, and automated detection of these microorganisms.

MATERIALS AND METHODS: Machine learning (ML) approaches, such as Support Vector Machines, Random Forests, and k-Nearest Neighbors, are included in AI techniques, as are deep learning (DL) models, such as Convolutional Neural Networks. These models analyze data from microscopy, Raman/hyperspectral imaging, and genomic sequences. Data gathering, preprocessing, feature extraction, model training, validation, and deployment are all part of the AI workflow.

RESULTS AND DISCUSSION: AI models are capable of identifying pathogens like Salmonella, Listeria, and E. coli with accuracy rates of over 90%. AI facilitates automation and non-destructive testing, which minimizes human labor and errors. Integrating AI with sensor networks makes it possible to monitor food production in real time. The difficulties include securing high-quality datasets, enhancing model transparency, establishing uniform procedures, and securing regulatory approval. Ongoing research aims to solve these problems by developing better data sharing, explainable AI, and standards.

Keywords: Artificial intelligence, pathogenic bacteria, food safety, machine learning, deep learning,

A study on gut microbiota in patients with inflammatory bowel disease from northwest Iran

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BACKGROUND AND OBJECTIVES: A disturbance in the composition of intestinal microbiota has been linked to the onset of various gastrointestinal diseases, such as inflammatory bowel disease (IBD).IBD is a recurring infammatory disease that afects diferent parts of the human digestive system.This disease is a global public health challenge and millions of people in the world are sufering from this disease.The present study aimed to evaluate four main phyla(Bacteroidetes, Firmicutes, Proteobacteria, and Actinobacteria)of gut microbiota in IBD patients in comparison to the control group.

MATERIALS AND METHODS: In this study, 40 stool samples from patients with IBD (20 patients with Crohn's disease (CD) and 20 patients with ulcerative colitis (UC)) and 20 stool samples from healthy controls were included. The predominant bacterial phylum of gut microbiota were evaluated using Quantitative PCR .

RESULTS AND DISCUSSION: In the analysis of SCFAs, a significant decrease was observed in the amount of butyric acid in both UC and CD compared to control, while significant reductions were noted in the amount of acetic acid and propionic acid only in UC patients compared to control subjects. Our research revealed the some changes in bacterial metabolites within the intestines of patients with IBD compared to the healthy people. Considering the protective effect of intestinal microbiota and their metabolites, restoring these factors may be beneficial in the management of patients with IBD.

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

A study on microbial short-chain fatty acids in patients with inflammatory bowel disease from northwest Iran.

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BACKGROUND AND OBJECTIVES: Gut microbiota is essential for the synthesis of short-chain fatty acids (SCFAs). The amount of SCFA in fecal samples seems to be associated with certain illnesses, including inflammatory bowel disease (IBD). Nevertheless, further investigations are needed to substantiate this relationship. The present study aimed to evaluate main SCFAs in IBD patients in comparison to the control group.

MATERIALS AND METHODS: In this study, 40 stool samples from patients with IBD (20 patients with Crohn's disease (CD) and 20 patients with ulcerative colitis (UC)) and 20 stool samples from healthy controls were included. The concentration of the main SCFAs (butyric acid, propionic acid, and acetic acid) were evaluated using High-performance liquid chromatography system.

RESULTS AND DISCUSSION: In the analysis of SCFAs, a significant decrease was observed in the amount of butyric acid in both UC and CD compared to control, while significant reductions were noted in the amount of acetic acid and propionic acid only in UC patients compared to control subjects.Our research revealed the some changes in bacterial metabolites within the intestines of patients with IBD compared to the healthy people. Considering the protective effect of intestinal microbiota and their metabolites, restoring these factors may be beneficial in the management of patients with IBD.

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

A Study on the Prevalent Nosocomial Infection Agent and Its Antibiotic Resistance Pattern in ICU Patients at Iran Hospital, Iranshahr (2024)

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BACKGROUND AND OBJECTIVES: Hospital-acquired infections (HAIs), particularly in intensive care units (ICUs), remain a significant challenge for healthcare systems. The emergence and spread of antibiotic resistance among common pathogens complicate treatment processes, increase mortality rates, and impose a heavy economic burden. This study aimed to identify the most prevalent causative agent of hospital-acquired infections and assess its antibiotic resistance pattern among ICU patients at Iran Hospital in Iranshahr during the year 2024 (1403 in the Iranian calendar).

MATERIALS AND METHODS: In this cross-sectional study, 30 ICU patients who developed hospital-acquired infections over a four-month period (from Khordad to shahrivar 1403) were evaluated. Urine samples were collected and cultured from all patients. Isolates were cultured on EMB and blood agar media. Preliminary identification was based on colony morphology and Gram staining. Antimicrobial susceptibility testing was performed using the disk diffusion method, according to CLSI guidelines.

RESULTS AND DISCUSSION: Among 30 samples, 16 isolates were identified as Klebsiella pneumoniae. Colonies appeared as mucoid pink on EMB and white with gamma-hemolysis on blood agar. Gram staining confirmed Gram-negative bacilli. Imipenem showed the highest sensitivity (87.5%), while cefepime had the lowest (75%). Klebsiella pneumoniae was the most prevalent pathogen responsible for HAIs in ICU patients. The observed resistance pattern highlights the need for stricter infection control policies, rational antibiotic use, and preventive strategies such as minimizing prolonged catheterization. Additionally, incorporating antimicrobial surfaces—particularly copper, which has proven effectiveness against K. pneumoniae—may help reduce the spread of nosocomial infections in critical care settings.

Keywords: Nosocomial Infection- Intensive Care Unit (ICU)- Klebsiella pneumoniae- Antibiotic Resistance-

A Surveillance Study on Synergism of Fosfomycin and Imipenem to Combat Drug-resistant Enterobacteriaceae Clinical Isolates

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BACKGROUND AND OBJECTIVES: Combining different antibiotics to enhance antimicrobial effectiveness is a promising approach to combat multidrug resistance in Enterobacteriaceae. This study aimed to investigate the effect of fosfomycin in combination with imipenem on eliminating multidrug-resistant Enterobacteriaceae.

MATERIALS AND METHODS: This study involved the collection of 376 clinical specimens from hospitalized patients between 2022 and 2025. Antibiotic resistance patterns were assessed using the Kirby-Bauer method by the CLSI-2021 guidelines. The minimum inhibitory concentration (MIC) of fosfomycin was determined both individually and in combination with imipenem using the broth microdilution method.

RESULTS AND DISCUSSION: The distribution of isolates was as follows: Escherichia coli (129 isolates, 62%), Klebsiella pneumoniae (34 isolates, 16.5%), Proteus mirabilis (29 isolates, 14%), and Enterobacter cloacae (16 isolates, 7.5%). Out of the resistant isolates, 153 (73.56%) were classified as multidrug-resistant (MDR), 85 (40.86%) as extensively drug-resistant (XDR), and 23 (11.06%) as pandrug-resistant (PDR). The MIC90 of the combination of fosfomycin and imipenem was found to be 256 µg/ml, which was 4 to 8 times lower than the MIC90 for fosfomycin alone (MIC90 ≥ 1024 µg/ml). The combined effect of fosfomycin and imipenem was 2.5 times more effective against multidrug-resistant E. coli isolates and 1.4 times more effective against multidrug-resistant K. pneumoniae (P0.05).The emergence of MDR, XDR, and PDR uropathogenic E. coli isolates poses a significant health threat to society. Given the favorable in vitro antimicrobial efficacy of fosfomycin in combination with imipenem, particularly against uropathogenic isolates, this combination warrants further investigation.

Keywords: Enterobacteriaceae, Fosfomycin, Drug Resistance, Imipenem, Synergy

A Systematic Review of Antibiotic Resistance Patterns in Methicillin-Resistant Staphylococcus aureus (MRSA) Isolates in Iran (2015–2025)

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BACKGROUND AND OBJECTIVES: Methicillin-resistant Staphylococcus aureus (MRSA) has become one of the most important nosocomial and community-acquired pathogens in Iran, leading to high morbidity and mortality rates and treatment failure. This systematic review aims to evaluate the prevalence and antibiotic resistance profiles of MRSA isolates in Iran over the past decade.

MATERIALS AND METHODS: A comprehensive literature search was conducted in PubMed, Scopus, SID, and Google Scholar for studies published between January 2015 and May 2025, using the following keywords: "MRSA", "antibiotic resistance", "Iran", and "Staphylococcus aureus". The inclusion criteria were original studies that reported MRSA prevalence and antimicrobial susceptibility testing from clinical samples. Data were extracted on sample size, geographic location, detection methods, and resistance rates to key antibiotics. Meta-analysis was not performed; descriptive analysis was used.

RESULTS AND DISCUSSION: Result From 286 screened studies, 32 were eligible to be included that covered 18 provinces around the country. The overall prevalence of MRSA within S. aureus isolates was 43.7%. Highest resistances were reported against erythromycin (82.5%), clindamycin (68.4%), and ciprofloxacin (61.2%). In contrast, linezolid and vancomycin showed good susceptibility (resistance 5% and 2%, respectively). The variability among regions was observed, mainly for ICU and dairy-related isolates. Conclusion: MRSA remains highly prevalent in Iran and demonstrates considerable multidrug resistance. Nevertheless, vancomycin and linezolid remain reliable therapeutic options. These findings underscore the importance of region-specific antibiotic stewardship, regular resistance monitoring, and updated treatment guidelines across healthcare facilities.

Keywords: MRSA, Iran, Antibiotic Resistance, Vancomycin, Linezolid

Advancements in Bacterial and Viral Vaccines: Efficacy and Future Prospects

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BACKGROUND AND OBJECTIVES: Vaccines are pivotal in controlling infectious diseases caused by bacteria and viruses, with ongoing advancements addressing emerging challenges such as antimicrobial resistance and vaccine hesitancy. This comprehensive review aims to evaluate the current landscape of bacterial and viral vaccines, highlight recent technological innovations, and explore prospects to enhance vaccine efficacy, safety, and accessibility.

MATERIALS AND METHODS: A systematic literature review was conducted, analyzing peer-reviewed studies, clinical trial data, and recent advancements in vaccine technology. The review covers historical developments, classification of existing vaccines, novel platforms such as mRNA and viral vector vaccines, and emerging strategies like reverse vaccinology and nanoparticle-based delivery systems. Challenges and limitations in current vaccine programs are also discussed to identify research gaps and future directions.

RESULTS AND DISCUSSION: The review illustrates the evolution from early attenuated and inactivated vaccines to sophisticated platforms like mRNA and recombinant vaccines, which offer improved safety profiles and immunogenicity. Conjugate vaccines and adjuvant innovations have significantly enhanced bacterial vaccine responses, exemplified by the Hib and pneumococcal vaccines. Emerging technologies, including nanoparticle vaccines and reverse vaccinology, promise to accelerate vaccine development against difficult pathogens. Despite these advances, challenges such as vaccine hesitancy, production costs, cold chain requirements, and pathogen variability remain. The integration of novel adjuvants, delivery systems, and genomic approaches holds potential to overcome these hurdles, guiding future research towards more effective, broad-spectrum, and globally accessible vaccines.

Keywords: Vaccine, Nano-particles, Adjutant, Bacteria, Virus

AI-Driven Design of Novel Abaucin Derivatives Targeting Multidrug-Resistant Acinetobacter baumannii

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BACKGROUND AND OBJECTIVES: acinetobacter baumannii is a Gram-negative nosocomial pathogen that exhibits high-level resistance to a wide range of antibiotics, earning a place on the World Health Organization's (WHO) list of critical-priority pathogens. It is a leading cause of hospital-acquired infections, with mortality rates reported up to 42.6%. Since the 1970s, resistance in A. baumannii has progressively increased, and the bacterium now demonstrates multidrug resistance to most conventional antibiotics. This organism harbors a small core genome and a large accessory genome, enabling exceptional adaptability to environmental changes. Clinical isolates are dominated by international clones ICL1 and ICL2.

MATERIALS AND METHODS: Recent progress in machine learning has facilitated the discovery of novel antibiotics. Abaucin, an experimental compound, served as the basis for the virtual design of thousands of derivatives. These molecules were computationally optimized to selectively bind outer membrane proteins of A. baumannii. We utilized AlphaFold for protein structure prediction, DataWarrior for molecular design, and AutoDock Vina for docking simulations.

RESULTS AND DISCUSSION: Promising derivatives were selected based on their high binding affinity to A. baumannii targets and low predicted affinity toward commensals like Escherichia coli, suggesting narrow-spectrum activity. Our results demonstrate the effectiveness of AI-driven drug design in producing selective, next-generation antibacterial agents such as Abaucin. These candidates show potential to combat all resistant strains of A. baumannii while preserving the host microbiota.

Keywords: Acinetobacter baumannii,Drug Resistance,Anti-Bacterial Agents ,Artificial Intelligence,Narrow-Spectrum Antibiotics

Alpha antigen of Clostridium perfringens biotype A

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BACKGROUND AND OBJECTIVES: Clostridium perfringens(C. perfringens) is one of the most pathogenic species in the Clostridium genus that produces many toxins. This bacterium is divided into different types (A to G) based on the main toxins secreted. C. perfringens type A, due to its ability to secrete alpha toxin, causes cell membrane destruction and damage, followed by vascular, muscular, and hemolytic damage.

MATERIALS AND METHODS: At first, different strains of C. perfringens biotype A isolates were cultured in nutrient media. To reconfirm using molecular methods and performing Multiplex PCR using specific primers. After genotyping and sequencing, it was used in tests of minimum lethal dose(MLD), sterility, residual toxicity, safety, and histopathology. The number of three The strain was used for passage and preparation of suspension. To measure C. perfringens alpha toxin, the Inviro ELISA method was used, and the minimum lethality(MLD) test was performed as an Invivo method for each of the strains using an activated suspension and injection into a laboratory animal. In the following, several steps of precipitation were performed using different concentrations of aluminum sulfate. In the next step, protein measurement was performed using SDS-PAGE, and the presence of alpha toxin was confirmed. A non-toxicity and harmlessness controls were performed.

RESULTS AND DISCUSSION: Based on the obtained results, it was determined that the selected strains can be used as candidates for the vaccine strain, so it is suggested that these selected strains be evaluated in the form of a field trial study.

Keywords: Vaccine, Clostridium perfringens, Toxin

Amino acid alterations in the β-lactam binding residues of penicillin-binding proteins and Helicobacter pylori amoxicillin resistance phenotype

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BACKGROUND AND OBJECTIVES: Helicobacter pylori infection is a leading cause of gastrointestinal disorders and a recognized precursor to gastric cancer, posing a major public health concern. The increasing resistance to amoxicillin threatens the effectiveness of standard eradication therapies. This study aimed to evaluate the pattern of amoxicillin resistance and identify key mutations in the pbp1A and pbp2 genes among H. pylori clinical isolates collected from patients at Firoozgar Hospital in Tehran, Iran.

MATERIALS AND METHODS: A total of 164 H. pylori isolates from adult patients with gastritis were tested for amoxicillin susceptibility using the E-test method to determine minimum inhibitory concentrations (MICs). PCR amplification, sequencing, and bioinformatics analysis were conducted to detect amino acid mutations in penicillin-binding proteins PBP1A and PBP2, particularly in regions involved in β-lactam antibiotic binding. Statistical analyses were performed using SPSS version 26 and GraphPad Prism version 8.4.3 with chi-square and Fisher's exact tests.

RESULTS AND DISCUSSION: Amoxicillin resistance was observed in 32.1% of the isolates. In the pbp1A gene, mutations D535N, S543R, S417T, and E406A were prevalent, while T573P, A592R, and D561N were specific to resistant strains. In the pbp2 gene, I508V and H344R appeared in all isolates, whereas L400Y and E403Q were found only in resistant strains. The co-occurrence of D535N (PBP1A) and I508V (PBP2) was detected in 100% of the isolates. These findings highlight the growing resistance of H. pylori to amoxicillin and the emergence of specific mutations, emphasizing the need for ongoing resistance monitoring and updated treatment strategies to improve patient outcomes.

Keywords: Helicobacter pylori, Amoxicillin resistance, E-test, pbp1A, pbp2, Mutation

An Overview of Bartonellosis from a One Health Perspective: Humans, Animals, and Vectors in the World Health Organization Eastern Mediterranean Region

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BACKGROUND AND OBJECTIVES: Bartonellosis is an emerging infectious disease caused by Bartonella spp. It can infect a wide range of domestic and wild animals. This study aimed to investigate the prevalence of Bartonella and the distribution of Bartonella species in the WHO Eastern Mediterranean Region (WHO-EMR).

MATERIALS AND METHODS: The databases such as PubMed, Google Scholar, Web of Science, and Scopus were searched. Inclusion and exclusion criteria were considered for screening studies.

RESULTS AND DISCUSSION: A total of 45 papers out of 240 were included in the analysis. The results showed that the prevalence of Bartonella infection among endocarditis patients was 3.8% and the seroprevalence of Bartonella among other people was 27.5%. The overall prevalence of Bartonella spp. among animals, as determined by molecular, serological, and culture methods, was 11.9%, 38.9%, and 1.7%, respectively. Furthermore, the prevalence of Bartonella spp. in ectoparasites was 3.9%, with fleas (6.2%) showing a higher prevalence compared to lice (4.9%) and ticks (1.0%). Eighteen different species of Bartonella were reported in WHO-EMRO countries. Also, only human cases of B. henselae and B. quintana infections were reported from WHO-EMRO. Bartonellosis is an emerging infectious disease. Besides no studies were found from 10 countries, also few studies used One Health approach. Countries and international agencies should invest more in research and surveillance on Bartonella spp.

Keywords: Bartonellosis, EMRO, One Health

An overview of the latest status of Q fever in Iran

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BACKGROUND AND OBJECTIVES: Q fever is a zoonotic disease caused by the gram-negative, obligate intracellular bacterium Coxiella burnetii. Q fever infections in humans are asymptomatic in more than 60 % of cases, and the clinical manifestations of Q fever in humans include acute Q fever, chronic Q fever, and fatigue syndrome. Acute Q fever is known as a self-limiting febrile illness and may lead to pneumonia or hepatitis. Endocarditis occurs in 75 % of cases of chronic Q fever, with a reported mortality rate of around 25 %.

MATERIALS AND METHODS: In this review, we reviewed the status of Q fever in Iran.

RESULTS AND DISCUSSION: A very high rate of seroprevalence of Coxiella burnetii has been reported among domestic animals from all over Iran in recent years. Coxiella burnetii has been reported to have a significant prevalence in milk and dairy products, cases of animal abortion, and other environmental samples in Iran. Also, Q fever has high seroprevalence among the human population, especially in high-risk groups. On the other hand, a very significant and concerning prevalence of Q fever has been reported in cases of blood culture-negative endocarditis as well as in patients with fever of unknown origin in Iran. Based on available information, Q fever is an important and endemic disease in Iran but has been ignored by the health system and clinical experts. Unfortunately, despite very strong evidence about the importance of Q fever in Iran, there is still no human or animal health surveillance system for this disease

Keywords: Q Fever, Coxiella burnetti, Iran.

Antagonistic Effects of Lactobacillus Isolates from Traditional Cheese of Ardabil Province Against Selected Intestinal Pathogens

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BACKGROUND AND OBJECTIVES: Introduction: Cheese is a natural probiotic product with potential health benefits. Traditional cheeses, in particular, have been shown to improve bodily functions and modulate physiological activities. These products can enhance the survival and gastrointestinal delivery of probiotic microorganisms, thereby promoting a beneficial balance of gut microflora. This balance can inhibit harmful bacteria through the production of antimicrobial compounds such as bacteriocins. In the face of rising antibiotic resistance, the development of novel antimicrobial agents is crucial. Certain strains of lactic acid bacteria (LAB) with probiotic potential may contribute to the prevention and treatment of gastrointestinal infections. In this study, the antagonistic activity of Lactobacillus strains isolated from traditional cheeses of Ardabil province was evaluated against selected intestinal pathogens.

MATERIALS AND METHODS: Method: Cheese samples were enriched in MRS broth and cultured on MRS agar. Isolates were identified based on colony morphology, catalase test, Gram staining, carbohydrate fermentation patterns, growth at 10°C and 45°C, and tolerance to 6.5% NaCl. The antimicrobial activity of the cell-free supernatants was assessed using the agar well diffusion method against Escherichia coli, Staphylococcus aureus, Pseudomonas aeruginosa, and Klebsiella pneumoniae.

RESULTS AND DISCUSSION: From eight cheese samples, 26 Lactobacillus isolates were identified. Lactobacillus agilitis showed the highest prevalence (31%) and the most potent inhibitory effect, especially against S. aureus (inhibition zone diameter: 39 mm), while E. coli exhibited the greatest resistance. Given their notable antagonistic activity, Lactobacillus strains from traditional Ardabil cheese show promise as natural probiotics and may serve as functional food ingredients for gastrointestinal health.

Keywords: antagonistic effect, probiotic, pathogenic bacteria, Lactobacillus

Anti-bacterial and anti-inflammatory efficiency of chitosan nanoparticles carrying mesenchymal stem cells secretome in a cholera mouse model

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BACKGROUND AND OBJECTIVES: Reports of increasing antibiotic resistance in Vibrio (V). cholerae are considered a major health challenge. We aimed to evaluate the anti-bacterial and anti-inflammatory activity of chitosan nanoparticles (CSNPs) incorporated with mouse mesenchymal stem cell secretome (MSC/sec-CSNPs) in a cholera mouse model.

MATERIALS AND METHODS: MSC/sec-CSNPs were synthesized by the ionic gelation method. To characterize nanoparticle dynamic light scattering, scanning electron microscopy, and zeta potential analyses were performed. Encapsulation efficiency (EE) and protein release were also investigated under the pH conditions of 7 and 2 for 72 hours. C57BL/6 mice were infected with V. cholerae, and after 24 hours, treatment with the prepared nanostructure was administered orally for 7 days. Clearance of the bacteria from the small intestine, pro-inflammatory, and anti-inflammatory responses were measured.

RESULTS AND DISCUSSION: Characterization of nanostructures showed that they were correctly synthesized. The prepared MSC/sec-CSNPs exhibited 87% EE and 88% protein release. Compared to controls, the infection was cleared from all mice treated with the new compound (p0.05). The percentage of clearance was as follows: MSC/sec-CSNPs (ns): 97%, CSNPs: 73%, MSC/sec: 55%, and erythromycin: 100% (p0.05). Moreover, inflammatory cytokines in the serum of mice treated decreased, and anti-inflammatory cytokines increased (p0.05). MSC/sec-CSNPs exhibited favorable antibacterial and immunomodulatory properties, which could be exploited as a novel and effective alternative therapeutic strategy for cholera.

Keywords: Anti-bacterial, Anti-inflammatory, Chitosan nanoparticle, Mesenchymal stem cell secretome, Vibrio cholerae

Antibacterial Activity of Milk-Isolated Lactobacillus casei Against Multidrug-Resistant Human Pathogens

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BACKGROUND AND OBJECTIVES: The global rise of antibiotic-resistant infections has intensified the search for alternative antimicrobial strategies. Probiotics, particularly lactic acid bacteria like Lactobacillus casei, are promising candidates due to their ability to inhibit pathogens via competitive exclusion, acid production, and bacteriocin synthesis. This study aimed to evaluate the antibacterial activity of L. casei strains isolated from human and cow milk against multidrug-resistant clinical pathogens, namely Staphylococcus aureus and Pseudomonas aeruginosa.

MATERIALS AND METHODS: Milk samples were collected under sterile conditions from Karaj and Tehran and cultured in MRS Broth and Agar. Suspected probiotic colonies were identified as Lactobacillus using Gram staining, catalase, TSI, SIM, and sugar fermentation tests. Antimicrobial activity was assessed through spot agar and well diffusion assays, and inhibition zones were measured. pH changes and antibiotic susceptibility (ciprofloxacin, imipenem) were also evaluated.

RESULTS AND DISCUSSION: The study confirmed successful isolation of Lactobacillus casei from human and cow milk samples. These isolates exhibited antibacterial effects against Staphylococcus aureus and Pseudomonas aeruginosa, with inhibition zones measuring 18–19 mm in spot tests and 12 mm in well diffusion assays. The pH of the culture medium dropped from 6.8 to 4.6, indicating lactic acid production as the main antimicrobial factor. Causality tests showed minimal roles for other compounds such as hydrogen peroxide. While the pathogens were sensitive to ciprofloxacin and imipenem, L. casei was resistant to both, highlighting its probiotic strength and therapeutic potential. In conclusion, milk-derived Lactobacillus casei strains exhibit significant antibacterial activity against multidrug-resistant pathogens.

Keywords: Probiotics, Lactobacillus casei, Antibacterial Activity, Pseudomonas aeruginosa, Staphylococcus aureus.

Antibacterial Activity of Satureja khuzistanica Extract against MRSA and S. aureus via Disk and Well Diffusion Methods

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BACKGROUND AND OBJECTIVES: Antibiotic resistance, particularly against Methicillin-resistant Staphylococcus aureus (MRSA), poses a significant global health threat. With the diminishing efficacy of antibiotics like vancomycin, novel therapeutic strategies are urgently needed. This study investigates the antibacterial efficacy of the ethanolic extract of Satureja khuzistanica, a native Iranian plant with antimicrobial activity, against MRSA and Staphylococcus aureus (S. aureus).

MATERIALS AND METHODS: Satureja khuzistanica aerial parts were dried, powdered, Soxhlet-extracted with 96% ethanol, and rotary-evaporated at 40°C. Antibacterial activity was evaluated by disk diffusion and well diffusion assays on Mueller-Hinton agar. The extract, vancomycin (positive control), absolute ethanol (negative solvent control), and blank were applied to disks or wells. After 24 hours of incubation at 37°C, inhibition zone diameters were measured.

RESULTS AND DISCUSSION: The extract demonstrated significant antibacterial activity against both MRSA and S. aureus, with stronger inhibition observed against MRSA (disk: 29.66 ± 0.58 mm (n=3) vs. 26.00 ± 1.00 mm (n=3) for S. aureus; well: 32.33 ± 3.21 mm (n=3) vs. 29.66 ± 3.78 mm (n=3) for S. aureus). Vancomycin was ineffective against MRSA and showed limited activity against S. aureus. Although absolute ethanol exhibited minor inhibitory effects, the extract's antibacterial activity was significantly greater, indicating a specific effect. The well diffusion method produced larger inhibition zones than the disk method, suggesting better diffusion and suitability for evaluating the extract's antibacterial potential. Therefore, Satureja khuzistanica extract possesses notable antibacterial effects against drug-resistant bacteria, particularly MRSA, and presents a promising natural alternative for combating these infections.

Keywords: Methicillin-Resistant Staphylococcus aureus, Satureja, Anti-Bacterial Agents, Plant Extracts.

Antibacterial Activity of UV-Treated and CFS Postbiotics from Lactococcus lactis Against Salmonella enterica

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BACKGROUND AND OBJECTIVES: Salmonella enterica is a major foodborne pathogen, with some multidrug-resistant serovars posing treatment challenges. Postbiotics have recently emerged as promising non-antibiotic agents. This study aimed to compare the antibacterial effects of two types of Lactococcus lactis derived postbiotics one obtained via UV inactivation and the other as a cell-free supernatant (CFS) against S. enterica.

MATERIALS AND METHODS: For the UV-inactivated postbiotic, a bacterial suspension (0.5 McFarland) was exposed to UV-C light (254 nm, 39 W) at 70 cm for 0, 15, and 20 minutes. Complete inactivation was confirmed by MRS agar plating. For CFS preparation, the culture was centrifuged (8000 rpm, 5 min) and filter-sterilized (0.22 µm). Sterility of CFS was confirmed by MRS agar plating. Antibacterial activity was assessed using agar well diffusion on Mueller-Hinton agar seeded with S. enterica. Three wells were created using a sterile sampler: well 1 with MRS broth (blank), well 2 with CFS, and well 3 with UV-inactivated postbiotic suspension. After filling wells with respective samples, plates were incubated at 37°C for 24 hours.

RESULTS AND DISCUSSION: No bacterial growth was observed after 15 minutes of UV exposure. MRS plating of CFS also showed no viable cells. The UV-inactivated postbiotic produced a clear inhibition zone (22.0 ± 2.3 mm, n=4), while the CFS sample showed no inhibition. Therefore UV-inactivated postbiotics demonstrated strong antibacterial activity against S. enterica, whereas sterile CFS showed none, suggesting superior efficacy of UV-inactivated formulations as biotherapeutic agents.

Keywords: Agar diffusion method, cell-free supernatant, Lactococcus lactis, postbiotics, Salmonella enterica

Antibacterial and Antibiofilm Potential of Common Antidepressants Against Clinical Staphylococcus aureus Isolates

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BACKGROUND AND OBJECTIVES: Antibiotic resistance in Staphylococcus aureus poses a significant clinical challenge, particularly due to its ability to form biofilms that reduce treatment efficacy. Notably, some antidepressants have shown promising antibacterial activity in preliminary research. This study evaluated the antimicrobial and antibiofilm efficacy of four commonly used antidepressants — sertraline, fluoxetine, amitriptyline, and citalopram — in vitro on clinical isolates of S. aureus and standard bacterial strains

MATERIALS AND METHODS: Five clinical isolates of S. aureus and standard strains, including S. aureus ATCC 25923, Escherichia coli ATCC 25922, and Staphylococcus epidermidis RP62A, were evaluated using broth microdilution to determine minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC). Biofilm inhibition was assessed by safranin staining to determine the minimum biofilm inhibitory concentration (MBIC). To ensure repeatability, measurements were performed in triplicate.

RESULTS AND DISCUSSION: Sertraline demonstrated the most potent antibacterial activity (MIC: 64 µg/mL; MBC: 256 µg/mL). In contrast, amitriptyline showed the weakest effects (MIC: 1024 µg/mL; MBC: 2048 µg/mL). Fluoxetine and citalopram showed moderate activity. Sertraline exhibited the most potent antibiofilm effect (MBIC: 16–32 µg/mL), whereas citalopram showed the weakest performance (MBIC: 64–256 µg/mL). Conclusion: Our findings demonstrate the significant antibacterial and, notably, antibiofilm potential of sertraline against clinical S. aureus isolates. Antidepressants, particularly sertraline, may be potential candidates for use in controlling chronic biofilm-associated infections, although their definitive efficacy requires further study

Keywords: Staphylococcus aureus, Biofilms, Drug Resistance, Antidepressants, Sertraline

Antibacterial and Antioxidant Activites of Nanoemulsion Prepared using Ethanolic of Euonymus japonicus Extract

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BACKGROUND AND OBJECTIVES: Recently, bacterial infection has become a serious threat to human health because it can develop into a severe infectious disease if not prevented, controlled and treated in time. The use of antibiotics is one of the most common methods for treating various infectious diseases. Therefore, Considering the progress of science in the field of nanotechnology, therefore, the aim of this project is to synthesize nanoemulsions (NEs) using ethanolic extract of Euonymus japonicus leaves and investigate its antibacterial and antioxidant properties.

MATERIALS AND METHODS: In this project, (NEs) of Euonymus japonicus leaves ethanolic extract (EJ-NEs) were formulated and characterized. The NEs were formulated using an ultrasonic device using 15% ethanolic extract (w/w), 80% water (w/w) and 5% surfactant (w/w). The EJ-NEs was characterized using transmission electron microscopy (TEM), zeta potential and dynamic light scattering (DLS). Also, their antibacterial activity against Gram-positive (Staphylococcus aureus) and Gram-negative (Escherichia coli) bacteria was investigated using minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) methods and their antioxidant effect was investigated using DPPH0 assay.

RESULTS AND DISCUSSION: The results showed that the zeta potential value was -22.4. mV and size of the EJ-NEs was between 50 and 300 nm, EJ-NEs was effective on both Gram-positive and Gram-negative bacteria and also showed a free radical inhibition percentage of 86.35 and an value of 2.97 µg/mL. Therefore, EJ-NEs can be good candidates for food, cosmetic, therapeutic and biomedical applications.

Keywords: Euonymus japonicus, Nanoemulsions (NEs), TEM, MIC, DPPH0, Biomedical applications.

Antibacterial effects of Cuminum cyminum L. essential oil nanoemulsion on gram-positive and gram-negative bacteria

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BACKGROUND AND OBJECTIVES: The purpose of this study was to investigate the antibacterial effect and antibiofilm of cumin essential oil nanoemulsion on S.aureus, P.aeruginosa, K. pneumoniae and E. coli bacteria by microbroth dilution (MIC)(MBC) and Microtiter Plate method.

MATERIALS AND METHODS: For each bacterial strain, one standard sample (ATCC) and one clinical sample, with essential oil and nanoemulsion (L. Cuminum cyminum) and antibiotics, gentamicin (K. pneumoniae and E. coli), colistin and tetracycline (P.aeruginosa), vancomycin and Tetracycline (Staphylococcus aureus), MIC and MBC) was study Broth Microdilution method. The synergistic effect of nanoemulsion with the corresponding antibiotic was determined for each bacterium. From the concentrations lower than the Sub-MIC, the antibiofilm test was done by the Microtiter Plate method. The type and amount of cumin essential oil compounds were obtained by Gas Chromatography-Mass Spectrometry technique.

RESULTS AND DISCUSSION: The MIC and MBC of cumin essential oil nanoemulsion for gram-negative bacteria with a concentration of 62.5 mg/ml were the same, but for S.aureus it was slightly different with MIC-15.6 and MBC-5.62. The MIC level for nanoemulsion was much higher than essential oil, but it had no bactericidal effect for Escherichia coli and Pseudomonas, and it was 2.5 mg/ml for Klebsiella. This value for Staphylococcus aureus was 312 µg/ml. Conclusion: Cumin essential oil nanoemulsin had a moderate antibacterial effect for the studied bacteria, which was more effective for S. bacteria. These effects were the same for standard and clinical strains. Nanoemulsion increases the antibacterial effect of essential oil compounds. Also, nanoemulsion prevented the production of strong biofilm in bacteria.

Keywords: Nanoemulsion ،Cuminum cyminum ،Antibacterial

Antibacterial Effects of Eucalyptus Leaf Essential Oil on Multi-Drug-Resistant Clinical Isolates

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BACKGROUND AND OBJECTIVES: The increasing prevalence of bacterial resistance to antibiotics is one of the most significant global public health challenges of the 21st century.The ineffectiveness of conventional antibiotics has prompted a growing interest in safe, natural alternatives with potent antimicrobial properties. Plant-derived essential oils have emerged as promising sources of antibacterial agents. This study aims to investigate the antibacterial activity of eucalyptus leaf essential oil (EL-EO) against clinical isolates resistant to levofloxacin, to determine its potential as a natural alternative or supplement to conventional antibiotic therapy.

MATERIALS AND METHODS: Eucalyptus leaves were collected from the central region of Tehran, Iran, and underwent hydrodistillation for essential oil extraction. Gas chromatography-mass spectrometry analysis was conducted to identify its chemical composition. The antibacterial activity of EL-EO was evaluated using the broth microdilution method, with concentrations ranging from 100% to 0.2% (v/v). Additionally, the minimum bactericidal concentration and hemolytic activity of EL-EO were evaluated.

RESULTS AND DISCUSSION: EL-EO was found to be rich in eucalyptol and α-pinene, exhibiting significant antibacterial activity against levofloxacin-resistant isolates of S. aureus and P. aeruginosa. Complete inhibition was observed at a concentration of 12.5% (v/v). The MIC and MBC values of EL-EO were notably lower than conventional antibiotics in the test. Hemolysis assays indicated non-hemolytic activity (5%) at concentrations 15%. Eucalyptus leaf essential oil exhibited promising potential as a natural antimicrobial agent effective against multidrug-resistant isolates of S. aureus and P. aeruginosa. Its potent antibacterial activities and favorable safety profile suggest potential applications as a complement or alternative to conventional antibiotics.

Keywords: Essential Oil,Eucalyptus,Anti-Bacterial Agents,Drug Resistance

Antibacterial Efficacy of Biosynthesized Silver Nanoparticles Against Staphylococcus aureus Biofilms

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BACKGROUND AND OBJECTIVES: Biofilm formation by Staphylococcus aureus contributes significantly to antibiotic resistance, complicating hospital-acquired infection treatment. This study investigates the efficacy of silver nanoparticles (AgNPs) biosynthesized by Bacillus subtilis in inhibiting S. aureus biofilms, offering a biotechnological alternative to conventional antibiotics. AgNPs were synthesized extracellularly, characterized using UV-Vis spectroscopy (peak at 420 nm), and TEM (average size: 20 nm). Antibiofilm activity was assessed via crystal violet assay on clinical S. aureus isolates (n=50). Results showed a dose-dependent inhibition, with 50 µg/mL AgNPs reducing biofilm biomass by 85% (p0.01) compared to controls. Minimum inhibitory concentration (MIC) ranged from 10–25 µg/mL, significantly lower than standard antibiotics like vancomycin (MIC: 50 µg/mL). SEM analysis revealed disrupted biofilm architecture post-treatment. The nanoparticles exhibited low cytotoxicity on human fibroblast cells (IC50: 100 µg/mL), suggesting biocompatibility. Mechanistically, AgNPs likely penetrate biofilms, releasing Ag+ ions that disrupt bacterial cell membranes and inhibit quorum sensing. These findings highlight the potential

MATERIALS AND METHODS: AgNPs were biosynthesized using Bacillus subtilis supernatant, characterized by UV-Vis and TEM. Antibiofilm activity was tested on 50 S. aureus isolates via crystal violet assay. MIC, SEM, and cytotoxicity on fibroblasts were assessed.

RESULTS AND DISCUSSION: AgNPs (50 µg/mL) reduced biofilm biomass by 85% (p0.01). MIC ranged from 10–25 µg/mL, outperforming vancomycin. SEM showed disrupted biofilms, with low cytotoxicity (IC50: 100 µg/mL).

Keywords: , Silver Nanoparticles, Biofilms, Staphylococcus aureus, Drug Resistance

Antibiotic Resistance

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BACKGROUND AND OBJECTIVES: Antimicrobial resistance (AMR) threatens global health, particularly in low- and middle-income countries (LMICs) where healthcare resources are limited. This systematic review aims to evaluate the prevalence of AMR, identify contributing factors, and assess strategies to mitigate resistance in these settings.

MATERIALS AND METHODS: Data from 30 peer-reviewed articles covering 220 hospitals across India, Nigeria, Bangladesh, Egypt, and Pakistan were systematically reviewed. Resistance patterns in pathogens such as Escherichia coli and Staphylococcus aureus were analyzed to assess antibiotic resistance levels and factors influencing AMR spread.

RESULTS AND DISCUSSION: High resistance rates were identified, including 42% penicillin resistance in E. coli and 37% in Klebsiella pneumoniae. Fluoroquinolone resistance reached 50%, and 37% of S. aureus isolates were resistant to erythromycin. These rates were significantly higher than in developed countries, where resistance generally remains below 20%. Contributing factors included antibiotic overuse in agriculture, self-medication, lack of professional training, poor regulatory oversight, and insufficient surveillance programs. The absence of standardized stewardship initiatives was notable and likely exacerbates the issue. These findings emphasize the urgent need for improved antibiotic management and policy reforms in LMICs. These findings highlight the urgent need for comprehensive antimicrobial stewardship policies and capacity-building in LMICs to mitigate AMR.

Keywords: Keywords: Antimicrobial Resistance (AMR), LMICs, Escherichia coli, Staphylococcus aureus, Stewardship,

Antibiotic resistance pattern and frequency of spiA, bcsA and csgA genes involved in the biofilm of Salmonella enteritidis isolates from chicken meat

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BACKGROUND AND OBJECTIVES: Salmonella is one of the most common pathogens associated with foodborne illnesses caused by the consumption of contaminated food. The emergence of antibiotic resistance in zoonotic bacteria such as Salmonella enteritidis is a significant concern in both human and veterinary medicine.The presence of virulence genes in multidrug-resistant strains of Salmonella is linked to severe infections and poses a major public health threat.Consequently, identifying and screening these genes is essential to prevent the emergence of multidrug-resistant strains.The aim of this study was to determine the antibiotic resistance patterns and the prevalence of the spiA, bcsA, and csgA genes involved in biofilm formation in Salmonella enteritidis isolates from chicken meat.

MATERIALS AND METHODS: A total of 50 chicken meat samples were collected from various sources.The presence of Salmonella species was identified using biochemical tests.Antibiotic susceptibility of the isolates was assessed using the disk diffusion method against 14 antibiotics.The prevalence of the spiA, bcsA, and csgA genes in biofilm-producing Salmonella enteritidis was determined using polymerase chain reaction.

RESULTS AND DISCUSSION: The highest resistance rates were observed for nalidixic acid(92%),cotrimoxazole(92%),The highest sensitivity rates were seen for amikacin(100%), ceftriaxone(80%). The prevalence of the spiA, bcsA, and csgA genes in biofilm-producing isolates was 100%, 62%, and 42%,respectively.This study highlights the high prevalence of multidrug resistance in Salmonella enteritidis isolates from chicken meat, which can be transmitted to humans.The findings indicate that while the virulence genes spiA, csgA, and bcsA are associated with antibiotic resistance,not all resistance-related genes are expressed in the isolates.

Keywords: salmonella enteritidis, antibiotic resistance, spiA, bcsA, csgA, chicken

Antibiotic Resistance Patterns of Bacteria Isolated from ICU Computer Keyboards

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BACKGROUND AND OBJECTIVES: Environmental surfaces in Intensive Care Units (ICUs), particularly computer keyboards, are frequently touched and may act as unnoticed reservoirs for multidrug-resistant (MDR) bacteria, potentially contributing to the transmission of hospital-acquired infections (HAIs). This study aimed to investigate the extent of bacterial contamination and the antibiotic resistance profiles of isolates obtained from ICU computer keyboards.

MATERIALS AND METHODS: Samples were collected from computer keyboards within the ICU of a referral hospital. Bacterial isolation was performed using selective media including Mannitol Salt Agar, MacConkey Agar, and Blood Agar. Identification was achieved through standard biochemical tests (catalase, coagulase, and oxidase), and antibiotic susceptibility was determined by the Kirby-Bauer disk diffusion method in accordance with CLSI guidelines.

RESULTS AND DISCUSSION: Staphylococcus spp. and Klebsiella spp. were the predominant organisms isolated, both of which are well-documented agents of nosocomial infections. Several isolates exhibited resistance to commonly used antibiotics in ICU settings, notably beta-lactams and aminoglycosides. A subset of isolates showed resistance to multiple antibiotic classes, confirming their MDR status. These findings indicate that ICU computer keyboards may act as silent reservoirs for MDR pathogens and contribute to cross-transmission between healthcare workers and patients. The study highlights the necessity for enhanced disinfection protocols and targeted hygiene practices to mitigate contamination risks in critical care environments.

Keywords: ICU, antibiotic resistance, multidrug resistance, hospital-acquired infections, contamination, infection control

Antibiotic Resistance Profiles of Abortion-Associated Bacterial Isolates from Vaginal Secretions

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BACKGROUND AND OBJECTIVES: Vaginal infections during pregnancy can lead to serious complications, including spontaneous abortion and preterm delivery. Antibiotic therapy plays a critical role in managing infectious miscarriages. This study examines the antibiotic susceptibility patterns of bacteria isolated from vaginal secretions of women who experienced abortion.

MATERIALS AND METHODS: In this descriptive-analytical study, 220 vaginal discharge samples were collected from women with abortion and control subjects. Bacterial isolates were identified through biochemical testing, and their antibiotic resistance profiles were determined using the disk diffusion method by Clinical and Laboratory Standards Institute (CLSI) guidelines.

RESULTS AND DISCUSSION: Among the isolates, Streptococcus agalactiae (9.1%, 20/220) was the most prevalent, followed by Listeria monocytogenes (1.4%, 3/220) and Brucella abortus (0.5%, 1/220). S. agalactiae exhibited the highest sensitivity to ceftriaxone and vancomycin but showed significant resistance to clindamycin and tetracycline. Among L. monocytogenes isolates, one demonstrated resistance to tetracycline, ampicillin, and gentamicin, while all three remained sensitive to clindamycin, erythromycin, and vancomycin. The single B. abortus isolate was susceptible to all tested antibiotics, including rifampin, tetracycline, doxycycline, norfloxacin, and streptomycin.Given the high prevalence of S. agalactiae in vaginal samples, prompt treatment is essential to mitigate adverse pregnancy outcomes. Based on the findings, ceftriaxone and vancomycin may serve as effective therapeutic options for beta-lactam-resistant S. agalactiae infections. These results underscore the need for targeted antibiotic stewardship to prevent resistance and improve clinical outcomes in high-risk pregnancies.

Keywords: Abortion, Antibiotic Resistance, Streptococcus agalactiae, Listeria monocytogenes, Brucella abortus

Antibiotic Susceptibility Patterns of Vibrio cholerae Isolates to Using Disk Diffusion Method

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BACKGROUND AND OBJECTIVES: Vibrio cholerae is a waterborne pathogen responsible for cholera outbreaks, especially in regions with poor sanitation. Although oral rehydration therapy is the primary treatment, antimicrobial agents are essential in severe cases to reduce disease duration, prevent complications, and limit transmission. However, growing concerns about antimicrobial resistance in V. cholerae highlight the need for ongoing surveillance. This study aimed to evaluate the susceptibility patterns of V. cholerae isolates to cefepime, amikacin, and meropenem three broad-spectrum antibiotics commonly used against Gram-negative bacteria—using the disk diffusion method.

MATERIALS AND METHODS: A total of 40 V. cholerae isolates were tested using the Kirby-Bauer disk diffusion method according to CLSI M45 guidelines. Disks of cefepime (30 µg), amikacin (30 µg), and meropenem (10 µg) were applied to Mueller-Hinton agar plates. The plates were incubated aerobically at 35±2°C for 18–24 hours. After incubation, inhibition zones were measured in millimeters, and susceptibility was interpreted according to CLSI M45 breakpoints.

RESULTS AND DISCUSSION: Among the 40 isolates, 20 (50%) showed intermediate susceptibility to cefepime, while the remaining 20 were sensitive. All isolates (100%) were sensitive to amikacin. For meropenem, 3 isolates (7.5%) showed intermediate susceptibility, while 37 (92.5%) were sensitive. The complete sensitivity to amikacin suggests it may be a promising option for treatment. The intermediate responses observed with cefepime and meropenem highlight the importance of continuous surveillance to detect emerging resistance.

Keywords: Vibrio cholerae, antibiotic susceptibility, disk diffusion

Anticancer activity of hydatid cyst fluid antigens on tumors induced by MCF7 breast cancer cells

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BACKGROUND AND OBJECTIVES: Studies on the experimental model of breast cancer have shown that hydatid cyst fluid (HCF) has antitumor activity. We aimed to investigate the effect of HCF and antigen B on MCF7 breast tumor cells in BALB/c mice.

MATERIALS AND METHODS: Mouse breast adenocarcinoma cell line (MCF7) was cultured in an rpm medium and fetal bovine serum was added to it along with L-glutamine. These mice were divided into 5 groups, the first PBS group and the second, third, fourth, and fifth groups intraperitoneally with concentrations of 100, 200, 300, and 500 µg/ml HCF and AgB in 100 µl PBS. It was injected with naltrexone and naloxone. Help to determine the preventive effect of HCF and AgB antigens on the growth of MCF7 mammary tumor in BALB/c mice, 10 days after the inoculation of cancer cells, animals in each group in terms of tumor and tumor growth, blood was taken from one side of the mice.

RESULTS AND DISCUSSION: The results showed that in the mice that received the combination of HCF and AgB along with the adjuvant naltrexone and naloxone, the size of the tumor was significantly smaller in them and it was quite clear compared to the control group. And the higher the doses of our antigen combination, the smaller the tumor size.

Keywords: Anticancer activity, hydatid cyst, MCF7, breast cancer

Antimicrobial effects of Pseudomonas aeruginosa toxins on azole antifungal resistance in Candida albicans species

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BACKGROUND AND OBJECTIVES: The azole antifungals are the most frequent class used to treat Candida infections. Therefore, in the present study, the antagonistic effect of Pseudomonas aeruginosa toxins on azole antifungal resistance in C. albicans species was investigated.

MATERIALS AND METHODS: In this study, 28 C. albicans species with azole antifungal resistance were obtained from patients at Shohadaye Tajrish Hospital. The effect of toxins, such as phenazine, pyocyanin, pyoverdine, and fluorescein, was examined on C. albicans species. The antifungal activity of these toxins against C. albicans spp. was determined using methods such as minimal inhibitory concentration (MIC90), radial diffusion assay (RDA), and detection of reactive oxygen species (ROS).

RESULTS AND DISCUSSION: The prevalence of C. albicans strains in urinary catheters, surgical wounds, respiratory tracts, blood, and standard strains was 46.3%, 21.4%, 25%, 7.14%, and 3.57%, respectively. The MIC values were reported as 32 µg/ml for phenazine, and 128 µg/ml for pyoverdine, pyocyanin, and fluorescein. The results showed that phenazine exhibited higher inhibitory effects against C. albicans isolated from clinical samples compared to the other toxins. After exposure to phenazines (20 µg/ml), 65-70% of yeast cells of C. albicans spp. showed rhodamine 123 fluorescence, indicating high intracellular reactive oxygen species (ROS) production.The antifungal effect of different toxins in C. albicans spp. may be due to ROS-mediated apoptotic death. The results suggest that phenazine has high potential in controlling C. albicans. This natural compounds are a potential alternative for eliminating this yeast.

Keywords: Antagonistic effect Toxins of Pseudomonas aeruginosa Candida albicans

Antimicrobial Activity of Chemically Synthesized ZnO Nanoparticles Against Staphylococcus epidermidis

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BACKGROUND AND OBJECTIVES: Metal oxide nanoparticles, particularly zinc oxide (ZnO), show great potential in addressing infectious diseases and antibiotic resistance. Staphylococcus epidermidis, a major cause of device-related hospital infections, poses a serious therapeutic challenge due to its multidrug resistance and biofilm formation. This study aimed to evaluate the antimicrobial, antibiofilm, and antioxidant potential of ZnO nanoparticles against resistant strains of S.epidermidis.

MATERIALS AND METHODS: ZnO nanoparticles were synthesized via a microwave-assisted chemical precipitation method using zinc nitrate and NaOH. After microwave irradiation, the product was washed, dried, and incubated. Characterization was conducted using FESEM and XRD. Antibacterial and antibiofilm activities were evaluated using disk diffusion, MIC, MBC, and biofilm inhibition assays. Antioxidant activity was assessed using DPPH radical scavenging and total antioxidant capacity (TAC) methods

RESULTS AND DISCUSSION: FESEM confirmed uniform surface morphology with an average size of 79.35 nm. XRD revealed sharp peaks at 2θ angles of 31.8°, 34.4°, 36.2°, 47.5°, and 56.6°, corresponding to standard ZnO patterns. The inhibition zone against S. epidermidis was 5 mm, equal to erythromycin. MIC and MBC values were 3.125 and 6.25 mg/mL, and biofilm inhibition reached 75.49%. Antioxidant activity increased by approximately 25% and 30% at 500 and 1000 mg/mL, respectively. Significant absorption at 0.2 µg/mL confirmed the bioactivity of the nanoparticles. According to the U.S. FDA, ZnO is classified as GRAS (generally recognized as safe), supporting its biomedical application. These findings suggest that ZnO nanoparticles are promising candidates for combating resistant and biofilm-forming S.epidermidis strains.

Keywords: Antimicrobial, Synthesis, ZnO, nanoparticles

Antimicrobial Activity of Fresh Pistachio Peel Extract: A Natural Alternative to Conventional Antimicrobials agents.

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BACKGROUND AND OBJECTIVES: Introduction: The increasing prevalence of antibiotic-resistant bacteria has prompted the search for effective natural antimicrobial agents. In this context, plant-derived byproducts are gaining attention as sustainable and bioactive resources. This study investigates the antibacterial potential of fresh pistachio peel extract against a range of Gram-positive and Gram-negative bacteria. The peel, commonly discarded as agricultural waste, is rich in polyphenolic compounds known for their antimicrobial properties. Our results demonstrate significant inhibitory effects, particularly against Bacillus cereus and Escherichia coli, suggesting a broad-spectrum antibacterial activity.

MATERIALS AND METHODS: Extract of fresh pistachio peel was extracted using 96% ethanol. Serial dilution was prepared (100- 6.2 mg/ml). Antimicrobial effects were evaluated by well diffusion. Method on 6 bacterial strains (E. coli, P. aeruginosa, K. pneumonia, M. luteus, S. aureus and B. cereus), and Candida albicans as a fungal agent.

RESULTS AND DISCUSSION: Anti-bacterial activity of extract of fresh pistachio peel was observed in all of bacterial strains by using all concentrations of extract. The largest inhibition zone was observed 20 mm using 100 mg/ml of extract in E. coli, M. luteus and B. cereus. In C. albicans just wasn't observed at 6.2 mg/ml of extract and the largest inhibition zone was observed at 100 mg/ml by 23 mm. These findings indicate that fresh pistachio peel extract could serve as a natural and eco-friendly antimicrobial agent with potential applications in food preservation, pharmaceuticals, and alternative medicine. Further studies are needed to isolate active constituents and determine their mechanisms of action.

Keywords: Pistachio peel, Antibacterial activity, Natural antimicrobial compounds , Antibiotic resistance.

Antimicrobial activity of thymol as the main monoterpene phenol against bacterial food-borne pathogens

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BACKGROUND AND OBJECTIVES: Thymol is the main monoterpene phenol occurring in essential oils isolated from plants belonging to the Lamiaceae family (Thymus, Ocimum, Origanum, and Monarda genera), and other plants such as those belonging to the Verbenaceae, Scrophulariaceae, Ranunculaceae, and Apiaceae families.

MATERIALS AND METHODS: The antimicrobial property of L. verbena extract was evaluated against bacterial food-borne pathogens, including Staphylococcus aureus, Listeria monocytogenes, Salmonella typhimurium, and Escherichia coli, using minimum inhibitory/bactericidal concentration (MIC/MBC) assay.

RESULTS AND DISCUSSION: The MICs of thymol against S. aureus, L. monocytogenes, S. typhimurium, and E. coli were 20, 20, 30, and 40 µg/ml, respectively. The MBCs of thymol against corresponding bacteria were 40 µg/ml. Thymol cause damage to the bacterial cell membrane and reduce in ATP, ATPase (Na+K+-ATPase and Ca2+-ATPase) activity and respiratory chain complex activity. Thymol presents appropriate antimicrobial activity against common food-borne pathogenic bacteria. It has been indicated that Thymus, Ocimum, Origanum, and Monarda genera (with 67% thymol) had high antimicrobial activity against E. coli, Streptococcus pneumoniae, Bacillus cereus, Clostridium perfringens, Candida albicans, Candida krusei, Acinetobacter lwoffii, and Klebsiella pneumoniae.

Keywords: antibacterial activity, medicinal plants, thymol

Antimicrobial and Anti-Adhesive Properties of Intestinal Lactobacillus rhamnosus Against Clinical Escherichia coli Isolates Linked to Gastrointestinal Infections

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BACKGROUND AND OBJECTIVES: Diarrhea remains a leading cause of childhood mortality in low-income countries. The rise of antibiotic-resistant microbes highlights the need for alternative treatments, such as probiotics. This study aimed to evaluate the antimicrobial and anti-adhesive properties of standardized Lactobacillus rhamnosus against clinical Escherichia coli isolates.

MATERIALS AND METHODS: A total of 160 clinical samples were collected and analyzed for E. coli using standard biochemical and microbiological methods. Antibiotic resistance was assessed via disk diffusion. Probiotic L. rhamnosus was cultured, and its cell-free supernatant was prepared. Antimicrobial effects were tested with agar well diffusion, and adhesion to HT-29 epithelial cells was evaluated.

RESULTS AND DISCUSSION: The L. rhamnosus supernatant significantly inhibited E. coli growth at 400 and 800 µg/ml concentrations and reduced intestinal cell adhesion, particularly for Enterotoxigenic E. coli. L. rhamnosus demonstrates strong probiotic activity against resistant E. coli, suggesting its therapeutic potential for diarrhea prevention in children. These findings reinforce the promising role of L. rhamnosus in enhancing gut mucosal defenses and preventing pathogen colonization, supporting its use in probiotic therapies for gastrointestinal infections.

Keywords: Diarrhea, Escherichia coli, Lactobacillus rhamnosus, Probiotics, Anti-adhesive properties

Antimicrobial and antibiofilm activity of a novel endolysin (LysSW21) against Methicillin-resistant Staphylococcus aureus

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BACKGROUND AND OBJECTIVES: The increasing prevalence of Methicillin-resistant Staphylococcus aureus (MRSA) underscores the urgent need for new antimicrobial agents. Endolysins present a viable solution through their targeted cell wall degradation. This study focuses on expressing, purifying, and analyzing phage-derived LysSW21's anti-MRSA and anti-biofilm activity, while evaluating its stability across diverse conditions to assess therapeutic viability.

MATERIALS AND METHODS: The LysSW21 gene was PCR-amplified from the genomic content of Staphylococcus bacteriophage vB_SauR_SW21 (GenBank: OR683639), digested with NcoI/XhoI, and cloned into pET28a (+) for expression in E. coli BL21(DE3). Recombinant LysSW21 was purified via Ni-NTA chromatography under denaturing conditions. Two reference strains (ATCC43300, ATCC33591) and one clinical MRSA isolate were used to evaluate the antimicrobial and antibiofilm properties of the recombinant LysSW21 using MIC/MBC, crystal violet staining for biofilm disruption, and time-kill kinetics. Thermal (4–70°C) and pH (4.5–10.5) stability were evaluated. Structural damage was analyzed using FE-SEM. Statistical significance (p 0.05) was determined via one-way ANOVA (SPSS), with triplicate experiments and controls.

RESULTS AND DISCUSSION: The study demonstrates that LysSW21, a phage-derived endolysin, exhibits potent antibacterial and anti-biofilm activity against MRSA. Its amidase domain enables peptidoglycan cleavage, resulting in rapid bactericidal effects (5-log CFU reduction) and significant biofilm disruption. SEM confirmed extensive cell wall damage, validating its lytic mechanism. LysSW21's stability across a broad temperature (4–70°C) and pH (4.5–10.5) ranges enhances its therapeutic potential. LysSW21's targeted action and low resistance risk position it as a viable alternative to conventional antibiotics in combating MRSA.

Keywords: Methicillin-resistant Staphylococcus aureus; Biofilm; Bacteriophage; endolysin

Antimicrobial and antibiofilm properties of green synthesized copper oxide-zinc oxide coated nanoparticles against bacteria isolated from urinary tract

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BACKGROUND AND OBJECTIVES: Antibiotic resistance is a global challenge that forces researchers to replace common antibiotics with natural substances. The present study addresses the issue of urinary tract infections, which are commonly caused by uropathogenic Escherichia coli, and its antibiotic resistance. The aim of this study was to present a new therapeutic approach by synthesizing zinc-doped copper oxide-coated nanoparticles using a green method with Artemisia Turcomanica extract and evaluating their antibacterial and antibiofilm activity against UPEC strains as well as their cytotoxic effects on colon cancer cells.

MATERIALS AND METHODS: The antibacterial activity of nanoparticles against E. coli from UTI patients was evaluated using disk diffusion and broth microdilution methods to determine MIC and MBC, and the anti-biofilm properties were analyzed using microtiter plate method and expression of related genes by real-time PCR. Cytotoxicity was tested using MTT assay and confirmed using SEM and TEM electron microscopy.

RESULTS AND DISCUSSION: The results of the study showed that the synthesized nanoparticles had a size range of 31.01-58.08 nm. Their MIC and MBC values were significantly lower than those of A. turcomanica extract, indicating superior antibacterial activity. The significant reduction in the expression of fimA, fimB, and fimH genes confirmed the anti-biofilm effect and also showed significant cytotoxicity against HT-29 colon cancer cells with an IC50 value of 25.46 µg/mL. In conclusion, this study highlights the properties of nanoparticles as an effective antibacterial, anti-biofilm, and anti-cancer agent. This study paves the way for the development of therapeutic strategies to combat resistant bacterial infections and cancer.

Keywords: Nanoparticles, Antibacterial, Anti-biofilm, Urinary tract infections

Antimicrobial compounds Activity of Isolated Probiotic Strains Against Pathogens

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BACKGROUND AND OBJECTIVES: The emergence of antibiotic resistance has led to the use of antimicrobial compounds from probiotics as alternative therapeutic strategies.

MATERIALS AND METHODS: Nineteen molecularly confirmed probiotic strains (Bonda faravar) were evaluated using the well-agar diffusion method. Fifty microliters of active crude supernatant (ACS) from each strain were added to wells in MRS agar plates. The wells were sealed with a soft agar layer, followed by an overlay of soft BHI agar containing 1% of each pathogen standardized to 0.5 McFarland (10^6 CFU/mL). The tested pathogens included P. aeruginosa (ATCC9027), S. aureus (ATCC33591), S.sonnei (ATCC9290), C.albicans (ATCC11006), K. pneumoniae (ATCC13883), and E. coli (ATCC10536). Zones of inhibition were recorded, and minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) values were subsequently determined.

RESULTS AND DISCUSSION: Among 19 tested probiotic strains, E. faecium demonstrated broad-spectrum antimicrobial activity by inhibiting all six pathogenic microorganisms. Five strains (B. longum, B. lactis, L. plantarum, L. paracasei, and L. helveticus) showed strong inhibitory effects against five of six pathogens. Additionally, four strains (B. bifidum, L. brevis, L. salivarius, and S. salivarius) exhibited moderate antimicrobial activity against four pathogens. Notably, Gram-negative bacteria (P. aeruginosa and K. pneumoniae) were more susceptible to probiotic inhibition than C. albicans, which showed the lowest susceptibility. E. faecium showed MICs of 125-250 µg/mL (Gram-negatives) and 62.5-125 µg/mL (Gram-positives), with MBCs of 250-500 µg/mL and 125-250 µg/mL, respectively.The increasing prevalence of XDR and PDR pathogens underscores the urgent need for novel interventions. Probiotic-derived antimicrobial metabolites offer a potential solution to address this critical challenge.

Keywords: Antimicrobial compounds, Probiotics

Antimicrobial Effects of Ethanolic and Acetonic Extracts Rind of Citrus Limon on Burn Wounds from Escherichia coli in Mice

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BACKGROUND AND OBJECTIVES: Escherichia coli remains one of the most common causes of bacterial infections in humans and animals. The increasing prevalence of multidrug-resistant E.coli strains has raised global concern. Due to the growing antibiotic resistance, natural compounds with antimicrobial properties have gained significant attention. This study aimed to evaluate the antimicrobial effects of acetonic and ethanolic extracts of lemon rind on E.coli.

MATERIALS AND METHODS: After collecting and grinding Citrus Limon rinds, the soaking method was used for extraction. A microbial suspension with a concentration of 0.5mg/mL (0.5McFarland standard) was prepared. Using a 24-well plate, antimicrobial activity was assessed. Agar and broth culture media were employed to determine the Minimum Inhibitory Concentration (MIC) and Minimum Bactericidal Concentration (MBC) through macro dilution and serial dilution methods.

RESULTS AND DISCUSSION: Both ethanolic and acetonic extracts showed inhibitory effects against E.coli. Based on serial dilution tests, MIC values ranged from 7.8µl/ml (ethanolic) to 3.2µl/ml (acetonic). MBC values were between 15.6µl/ml (ethanolic) to 7.8µl/ml (acetonic), indicating stronger bactericidal activity in the acetonic extract. In animal models (mice), the acetonic extract showed greater antimicrobial efficacy, particularly at burn sites. It led to reduced bleeding and faster wound healing. In contrast, the ethanolic extract was less effective and associated with slower recovery. These findings suggest that acetonic Citrus Limon rind extract has promising potential as a natural antimicrobial agent against resistant E.coli strains.

Keywords: Antibacterial activity, serial dilution, bactericidal, microbial resistance

Antimicrobial Effects of Ethanolic and Acetonic Extracts Rind of Cydonia Oblonga on Burn Infections Caused by Pseudomonas aeruginosa in Mice

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BACKGROUND AND OBJECTIVES: Due to the growing problem of drug resistance in pathogenic bacteria, the identification of natural compounds with antimicrobial properties has become increasingly important. This study aimed to evaluate the antibacterial effects of ethanolic and acetonic extracts rind of Cydonia oblonga on clinical isolates of Pseudomonas aeruginosa.

MATERIALS AND METHODS: After collecting and identifying rind of Cydonia Oblonga , extracts were prepared using ethanol and acetone solvents. The minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) were determined by serial dilution in nutrient broth using microtiter plates. A pseudomonas aeruginosa suspension with a concentration of 5×10^5 CFU/mL was used for inoculation. The prepared extracts at MBC concentrations were then applied to treat burn wounds in mice.

RESULTS AND DISCUSSION: Both extracts showed antimicrobial activity against P. aeruginosa. The MIC values for the ethanolic and acetonic extracts were 15.6 µg/mL and 31.2 µg/mL, respectively, while the MBC values were 31.2 µg/mL and 62.5 µg/mL. In vivo experiments demonstrated that the ethanolic extract had stronger antimicrobial effects, leading to reduced bleeding and faster wound healing. In contrast, the acetonic extract showed weaker efficacy and slower recovery. The ethanolic extract rind of Cydonia Oblonga demonstrated greater antimicrobial activity compared to the acetonic extract and may be considered a natural therapeutic option for burn infections caused by Pseudomonas aeruginosa.

Keywords: Drug resistance, serial dilution, nutrient broth, natural extract, Pseudomonas aeruginosa

Antimicrobial effects of rhizospheric Bacillus strains of native Allium hirtifolium against drug-resistant clinical isolates

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BACKGROUND AND OBJECTIVES: The emergence of drug resistance is the main factor in the increased prevalence of difficult-to-treat microbial infections and serious challenges in the global health system. Studies show that the drug-resistant pathogens, especially Gram-negative bacteria and Candida species, are major contributors to mortality among hospitalized patients. The issue has led to increased interest in bioactive metabolites of important rhizospheric microorganisms. Therefore, this study aimed to evaluate the antimicrobial activity of Bacillus species isolated from the rhizosphere of Persian shallot (Allium hirtifolium) on drug-resistant pathogens.

MATERIALS AND METHODS: The Persian shallot rhizospheres were collected from the agricultural areas of Lorestan, Isfahan, and Chaharmahal and Bakhtiari provinces in the spring of 2024. After an appropriate period of thermal treatment (30 min at 70 °C) and cultivation on TSA, spore-forming bacteria were identified using phenotypic and genotypic methods. The antimicrobial potential of the isolates was screened using the spread patch method on two Candida species and two Gram-negative bacteria. The drug-resistant pathogens were isolated from pulmonary infections of hospitalized patients.

RESULTS AND DISCUSSION: Among 30 Bacillus isolates, strain L2B showed an inhibition zone of 23mm only on C. glabrata. Strain E10B also had inhibition zones of 18 and 22mm on C. albicans and C. glabrata, respectively (without effect on bacteria). Strain CB16Rh showed significant inhibition against Enterobacter hormaechei (20mm)and Klebsiella pneumoniae (25mm), but it did not inhibit the Candida species.These results highlight the potential of Bacillus strains isolated from the Persian shallot rhizosphere as natural sources with significant antimicrobial effects.

Keywords: Antimicrobial activity, Clinical isolates, Drug-resistant, Iranian Allium hirtifolium, Rhizospheric Bacillus

Antimicrobial Peptides as a Next Step in the Post-Antibiotic Era

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BACKGROUND AND OBJECTIVES: The alarming rise in multidrug-resistant (MDR) pathogens has created an urgent global need for novel antimicrobial strategies. Traditional antibiotics are increasingly ineffective, and antimicrobial peptides (AMPs)—natural components of the innate immune system—have emerged as promising alternatives due to their broad-spectrum activity and rapid bactericidal effects.

MATERIALS AND METHODS: This abstract synthesizes key findings from recent studies over the past ten years, focusing on AMP mechanisms, clinical applications, and optimization approaches. Emphasis was placed on their synergistic potential with bacteriophages and the use of chemical modifications to overcome development barriers.

RESULTS AND DISCUSSION: AMPs primarily act by disrupting microbial membranes or targeting intracellular pathways, offering an advantage over traditional antibiotics. Their effectiveness against MDR pathogens is enhanced when used in combination with antibiotics or phages. Major development challenges include enzymatic degradation, short half-life, toxicity, and high production costs. Strategies such as amino acid substitution, cyclization, and nanoparticle-based delivery have improved peptide stability and therapeutic potential. Several AMP candidates are now progressing through early clinical evaluation. Conclusion: AMPs are a powerful tool for addressing antibiotic resistance. With advancements in peptide design and delivery systems, they hold significant promise for future antimicrobial therapies, particularly in combination strategies.

Keywords: antimicrobial peptides; multidrug resistance; peptide engineering; phage synergy; antibiotic

Antimicrobial property of Lemon verbena extract against bacterial food-borne pathogens

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BACKGROUND AND OBJECTIVES: Lemon verbena as a tropical perennial shrub belongs to the Verbenaceae family. This plant is rich in phenolic constituents, particularly flavonoids and anthocyanins, which contribute to its broad-spectrum antioxidant and antimicrobial activities.

MATERIALS AND METHODS: The antimicrobial property of L. verbena extract was evaluated against bacterial food-borne pathogens, including Staphylococcus aureus, Listeria monocytogenes, Salmonella typhimurium, and Escherichia coli, using minimum inhibitory/bactericidal concentration (MIC/MBC) assay.

RESULTS AND DISCUSSION: The MIC and MBC of the L. verbena extract did not differ between gram negative and positive bacteria. S. aureus, L. monocytogenes, S. typhimurium, and E. coli had similar sensitivity to the extract (MIC and MBC = 40 µg/ml). The antimicrobial mechanism of plant extract is probably associated with the destabilization of the phospholipid bilayer structure, disruption of the cellular membrane, and interaction with membrane enzymes and proteins. The present study showed that L. verbena extract had appropriate antimicrobial activity against common food-borne pathogenic bacteria. Further research is necessary to examine the antimicrobial activity of L. verbena against S. aureus, L. monocytogenes, S. typhimurium, and E. coli in food products during refrigerated storage conditions.

Keywords: Antimicrobial property, Lemon verbena, bacterial pathogens

Antimicrobial Resistance in Gram-negative Bacilli: MALDI-TOF MS and WHONET Surveillance in Tehran

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BACKGROUND AND OBJECTIVES: Multidrug-resistant (MDR) Gram-negative bacilli are increasingly implicated in hospital-acquired infections. This study investigates the distribution and resistance profiles of isolates across Tehran hospitals, employing MALDI-TOF MS for rapid identification and WHONET software for integrated antimicrobial resistance surveillance.

MATERIALS AND METHODS: Between November 2023 and April 2025, different clinical specimens were collected from different hospitals in Tehran, totaling 260,772 samples, and analyzed. Bacterial identification was performed using MALDI-TOF MS with 98% accuracy, confirmed by conventional biochemical methods. Antimicrobial susceptibility testing followed CLSI 2025 guidelines via disk diffusion; MDR isolates underwent MIC determination using the VITEK 2 system. WHONET software enabled standardized data entry and resistance trend analysis across institutions.

RESULTS AND DISCUSSION: Among collected isolates (n=51,142), 28,276 (55.3%) were Gram-negative bacilli and 22,866 (44.7%) were Gram-positive cocci. The most frequent MDR Gram-negative organisms included Klebsiella pneumoniae (14,007; 49.5%), Acinetobacter baumannii (6,385; 22.6%), Pseudomonas aeruginosa (5,031; 17.8%), and Providencia stuartii (227; 0.8%). Resistance in P. aeruginosa exceeded 70% to amikacin and ciprofloxacin. K. pneumoniae showed 57.7% resistance to amikacin and over 73% to carbapenems. A. baumannii demonstrated over 90% resistance to multiple antibiotic classes.This study underscores the use of MALDI-TOF MS with WHONET-based surveillance for monitoring of antimicrobial resistance in Tehran hospitals. The high prevalence of MDR isolates, highlights the need to revise empirical therapy protocols. Implementing advanced diagnostics within a centralized monitoring framework enables antimicrobial stewardship and contributes to more effective infection control strategies, offering a scalable model for resource-limited healthcare settings.

Keywords: MDR bacteria, Gram-negative bacilli, Antimicrobial resistance, MALDI-TOF MS.

Antimicrobial resistance of pathogenic protozoa in Iran

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BACKGROUND AND OBJECTIVES: Antimicrobial resistance in pathogenic microbial infections has been one of the major public health challenges in Iran over the past decade. With the increase in inappropriate drug use and lack of strict control, various species of microbes including parasites have shown resistance to antimicrobial drugs, making the treatment of infectious diseases difficult. The aim of this study was to determine the antimicrobial resistance of pathogenic protozoa in Iran.

MATERIALS AND METHODS: This study was conducted as a systematic review of published articles and reports of the Iranian Ministry of Health from 2015 to 2025. Data were extracted from PubMed, Scopus, SID, and Magiran databases and categorized based on the type of parasite, drug used, and level of resistance.

RESULTS AND DISCUSSION: The most common antimicrobial-resistant parasites in Iran were: Giardia lamblia, Leishmania spp., Entamoeba histolytica, Plasmodium spp., and Toxoplasma gondii. Giardia lamblia has shown significant resistance to metronidazole (30-40% of cases). Leishmania spp. has been reported to have a 20-25% resistance to pentavalent antimony (Pentostam), and Miltefosine in the southern and western regions of Iran. Entamoeba histolytica has also been recorded to have resistance to Metronidazole at a rate of about 15%. Plasmodium falciparum has shown low rates of resistance to Chloroquine and Artemisinin (less than 10%). Toxoplasma gondii has been reported to be rarely resistant to Sulfadiazine and Pyrimethamine. It is concluded that antimicrobial resistance in pathogenic parasites is increasing in Iran, and closer surveillance and updated treatment strategies are critical to control the problem.

Keywords: Antimicrobe, Resistance, Parasitic Infections, Pathogenic Protozoa, Iran

Application of F57, IS1311, hspx, Map02, ISmav2 and L 255 for detection of Mycobacterium avium subsp. paratuberculosis

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BACKGROUND AND OBJECTIVES: Mycobacterium avium subsp. paratuberculosis (Map) causes Johne's disease (paratuberculosis) in ruminants. Map represents the slowest growth rate of the cultivable mycobacteria as culture of Map-suspected specimens can take 16 weeks or even more before its colonies are visible. Currently, the IS900 is the most frequently-used genetic marker in PCR-based diagnostic protocols of Map. Specificity of this however, has come into question as IS900-like elements have been reported in genome of other mycobacteria. Aims Here application of IS900 along with six further genetic loci specific to Map including F57, IS1311, HspX, Map02, ISMav2 and Locus 255 has been described.

MATERIALS AND METHODS: PCRs, conducted in singleplex format were of conventional type. Optimization measures on thermal and MgCl2-concentration were employed in a way that a single optimized thermal protocol was applicable for all the markers. This strategy was applied on 30 Iranian bovine (N=24), caprine (N=2) and ovine (N=4) Map isolates representing Alborz, Fars, Isfahan, Zanjan, Qazvin and Tehran provinces.

RESULTS AND DISCUSSION: Amplification in all PCR reactions on the whole panels of 30 isolates along with Map laboratory strain of 316f was successful as the expected PCR products of 560, 704, 608, 211, 278, 507, and 404 bp related to the IS900, F57, IS1311, HspX, Map02, ISMav2 and Locus 255 markers respectively, were produced. We assume in Iranian environment where IS900 remains the backbone in molecular diagnosis of Map, pairing any of the six extra markers described here with IS900 element, will improve the capability of the laboratory setting in accurate diagnosis of Map.

Keywords: Map, PCR, amplification

Applications of Microbial Laccase enzyme in Biomedicine, Biomaterial synthesis, and advanced drug delivery systems

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BACKGROUND AND OBJECTIVES: Laccase enzyme (EC 1.10.3.2) is one of the important oxidases in biological processes, due to its ability to oxidize phenolic and non-phenolic compounds, and has attracted attention in recent years in the fields of medicine, pharmaceuticals, cosmetics, and biotechnology. This study aims to investigate the various applications of laccase in the development of innovative therapies, targeted drug delivery systems, safe cosmetic products, and valuable biological compounds.

MATERIALS AND METHODS: In medicine, laccase plays a significant role in the synthesis and activation of various drugs, including Remdesivir, anti-inflammatory compounds, and antibiotics. Research has demonstrated the antiproliferative activity of laccase derived from the fungus Trametes versicolor in the field of cancer treatment. Additionally, the use of nanocarriers such as halloysite nanotubes, silver nanoparticles, functional twin liposomes, and laccase@zeolitic imidazolate framework-8 not only enhances enzyme stability and treatment effectiveness but also facilitates the activation of antitumor compounds like quercetin in the acidic environment of cancer cells. In the cosmetic industry, laccase serves as a safe alternative to hydrogen peroxide for skin and hair lightening agents. Moreover, in the field of biomaterials, laccase has been employed in the production of biocompatible hydrogels used in tissue engineering and wound dressings. These hydrogels exhibit high cross-linking efficiency and reduced toxicity, thereby creating a more suitable environment for reactions.

RESULTS AND DISCUSSION: In conclusion, laccase, by utilizing modern technologies, plays a key role in the development of treatment, health, and the production of valuable compounds.

Keywords: Laccase, Targeted drug delivery, Anticancer, Hydrogels, Biocatalysts, Nanotechnology

Artificial Intelligence–Driven Discovery of Plant-Based Antimicrobials: A Novel Strategy Against Drug-Resistant

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BACKGROUND AND OBJECTIVES: The increasing emergence of antimicrobial resistance presents a significant global health challenge. Bioactive phytocompounds, derived from medicinal plants, have demonstrated potent antimicrobial properties with lower toxicity. However, the identification and development of effective phytocompound-based drugs require advanced tools to manage the complexity and volume of data involved.

MATERIALS AND METHODS: This review examines recent advances in the use of artificial intelligence (AI) and machine learning (ML) in the discovery and development of phytochemical-based antimicrobial agents. Relevant literature was selected from peer-reviewed databases, focusing on AI models applied in compound screening, structure optimization, and antimicrobial activity prediction.

RESULTS AND DISCUSSION: AI technologies, particularly ML algorithms, have proven effective in rapidly analyzing large datasets, identifying promising phytochemicals, predicting their antimicrobial potential, and optimizing their bioactivity. These tools significantly reduce time, cost, and trial redundancy compared to traditional drug discovery methods. Additionally, AI can model microbial resistance trends, aiding in the development of more robust therapies. The integration of AI into phytochemical research introduces a transformative approach to antimicrobial drug discovery. By accelerating the identification of potent plant-based agents and enhancing their design, AI offers a timely solution to combat multidrug-resistant pathogens. Future research should focus on expanding curated phytochemical databases and refining predictive models for better translational outcomes.

Keywords: Anti-Bacterial Agents, Artificial Intelligence, Drug Discovery, Plant Extracts, Drug Resistance,

Assay of the antimicrobial and synergistic effects of nisin and colistin resistance pmr gene in clinical isolates of Klebsiella pneumoniae isolated from patients

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BACKGROUND AND OBJECTIVES: Klebsiella pneumoniae is a Gram-negative bacterium and a significant cause of nosocomial infections. This study aimed to evaluate the biochemical characteristics, antibiotic resistance patterns, and the effects of antimicrobial agents such as nisin and colistin on K. pneumoniae isolates.

MATERIALS AND METHODS: The study was conducted on 16 K. pneumoniae isolates. Bacteria were identified using Gram staining and biochemical tests, including TSI, Methyl Red (MR), Voges-Proskauer (VP), citrate, indole, and oxidase. Antibiotic resistance was assessed through antibiograms and well-diffusion tests for nisin and colistin. The presence of the pmr gene was analyzed using PCR.

RESULTS AND DISCUSSION: In biochemical tests, the MR reaction was positive and the VP test was negative. In the antibiogram test, colistin showed greater efficacy with an average inhibition zone diameter of 21.69 mm, compared to nisin with 21.31 mm. The minimum inhibitory concentrations (MICs) were determined to be 31.25 µg/mL for nisin and 15.625 µg/mL for colistin. PCR assays did not detect the pmr gene, indicating its absence in the isolates. Furthermore, the combination of nisin and colistin demonstrated a synergistic effect, with the well diffusion assay showing inhibition zones up to 23 mm. MIC tests also confirmed this synergism, as complete inhibition of K. pneumoniae growth was observed at very low concentrations, with most isolates inhibited at 0.005 µg/mL. Klebsiella pneumoniae demonstrates considerable resistance to some antibiotics; however, colistin and nisin exhibit significant inhibitory effects. These findings could guide the development of improved treatment strategies for drug-resistant infections.

Keywords: Klebsiella pneumoniae, Antibiotic resistance, Nisin, Colistin, pmr gene

Assay of the antimicrobial effect of nisin and the presence of the colistin resistance pmr gene in clinical isolates of Klebsiella pneumoniae isolated from patients in Bonab city in 1403

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BACKGROUND AND OBJECTIVES: Klebsiella pneumoniae is a Gram-negative bacterium and a significant cause of nosocomial infections. This study aimed to evaluate the biochemical characteristics, antibiotic resistance patterns, and the effects of antimicrobial agents such as nisin and colistin on K. pneumoniae isolates.

MATERIALS AND METHODS: The study was conducted on 16 K. pneumoniae isolates. Bacteria were identified using Gram staining and biochemical tests, including TSI, Methyl Red (MR), Voges-Proskauer (VP), citrate, indole, and oxidase. Antibiotic resistance was assessed through antibiograms and well-diffusion tests for nisin and colistin. The presence of the pmr gene was analyzed using PCR.

RESULTS AND DISCUSSION: In biochemical tests, the MR reaction was positive and the VP test was negative. In the antibiogram test, colistin showed greater efficacy with an average inhibition zone diameter of 21.69 mm, compared to nisin with 21.31 mm. The minimum inhibitory concentrations (MICs) were determined to be 31.25 µg/mL for nisin and 15.625 µg/mL for colistin. PCR assays did not detect the pmr gene, indicating its absence in the isolates. Furthermore, the combination of nisin and colistin demonstrated a synergistic effect, with the well diffusion assay showing inhibition zones up to 23 mm. MIC tests also confirmed this synergism, as complete inhibition of K. pneumoniae growth was observed at very low concentrations, with most isolates inhibited at 0.005 µg/mL. Klebsiella pneumoniae demonstrates considerable resistance to some antibiotics; however, colistin and nisin exhibit significant inhibitory effects. These findings could guide the development of improved treatment strategies for drug-resistant infections.

Keywords: Klebsiella pneumoniae, Antibiotic resistance, Nisin, Colistin, pmr gene,

Assessing the Burden of Antibiotic Resistance in Pseudomonas aeruginosa Associated with Pediatric Respiratory Tract Infections

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BACKGROUND AND OBJECTIVES: This study aimed to investigate the prevalence of beta-lactamase encoding genes in Pseudomonas aeruginosa isolates associated with respiratory tract infections (RTIs). P. aeruginosa is a significant pathogen in RTIs, particularly among pediatric patients and those with compromised immune systems. Understanding the resistance mechanisms of such pathogens is crucial for effective treatment strategies.

MATERIALS AND METHODS: The analysis involved 315 bronchoalveolar lavage (BAL) and tracheal tube samples collected from patients in surgery and ICU, which were analyzed by conventional microbiological tests, while the Kirby–Bauer disc diffusion method was utilized to evaluate antibiotic resistance. Additionally, PCR was performed to amplify resistance genes from isolated strains.

RESULTS AND DISCUSSION: Out of the samples examined, P. aeruginosa was identified in 30 cultures (9.52%), from 20 (66.7%) males and 10 (33.3%) females, aged between 0.049 and 14 years, with a mean age of 5.82 years. Resistance rates were highest for aztreonam (70%), imipenem (60%) and piperacillin-tazobactam (53.3%), with 63.3% of the isolates exhibiting carbapenem resistance. Multidrug resistance was present in 16 isolates (53.3%), half of which were resistant to all tested antibiotics. Furthermore, beta-lactamase genes were detected in 83.3% of the isolates, with blaVIM being the most common with 46.7%. These findings underscore the emerging threat of antibiotic resistance in P. aeruginosa associated with RTIs, highlighting the importance of ongoing surveillance and the need for effective strategies to combat resistant strains. Such strategies are essential to preserve the efficacy of existing antibiotics and ultimately improve patient outcomes.

Keywords: P. aeruginosa, Antibiotic Resistance, Respiratory Tract Infection

Assessing the transmissibility and persistence of tet(X4)-tetA-floR-bearing IncX1-type plasmid harbored by pan-tetracycline resistant Escherichia coli

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BACKGROUND AND OBJECTIVES: Tet(X), is a FAD-dependent monooxygenase that hydroxylates and inactivates all tetracyclines, including tigecycline as well as other newer FDA-approved derivatives such as eravacycline, and omadacycline. In this study we investigated the transferability and stability of tet(X4)-bearing plasmid identified in two tigecycline resistant E. coli isolates

MATERIALS AND METHODS: The transferability of tet(X4)-carrying elements was assessed by conjugation assay. A 1:5 ratios of donor (tet(X4)-harboring E. coli strains) to recipient cell (two different mcr-negative colistin resistant- E. coli strains) were mixed in LB broth and incubated overnight at 37°C. Transconjugants were selected on Mueller Hinton agar supplemented with 16 mg/L tigecycline and 4 mg/L colistin. Conjugation frequency was determined as the number of transconjugants divided by the number of recipients. Plasmid stability testing was performed by continuously subculturing the tet(X4)-positive donors and transconjugants in daily refreshed antibiotic-free LB broth for 10 consecutive days.

RESULTS AND DISCUSSION: The tet(X4)-bearing element in each donor isolate could be successfully transferred to recipient strains, with conjugation frequencies of approximately 1.0 ×10−9 and 5.6 ×10-10. All the tet(X4)-carrying transconjugants exhibited increased MICs of tigecycline and tested positive for the presence of tet(X4) by PCR. All tet(X4) donor isolates and their transconjugants retained the tet(X4)-bearing elements at rates 70% to 96% after 10 consecutive passages in antibiotic-free media. The successful transmissibility of tet(X4)-harboring elements and their high stability in the absence of tigecycline selective pressure pose a serious threat for the therapeutic utility of third-generation tetracyclines against emerging MDR bacterial pathogens.

Keywords: Tigecycline resistance, tet(X4), Conjugation, Escherichia coli, IncX1 Plasmid

Assessment of Antibiotic Resistance in Bacterial species Isolated from Patients with Prostate Adenocarcinoma and Urinary Tract Infections Using the Kirby-Bauer Disk Diffusion Method.

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BACKGROUND AND OBJECTIVES: In prostate cancer patients, microbial contamination of tumor biopsies is common, and immunosuppressive therapy further increases susceptibility to infections, including UTIs. this study aims to evaluate the prevalence of bacterial isolates in patients with prostate adenocarcinoma and UTIs, as well as assess their antibiotic resistance patterns.

MATERIALS AND METHODS: 72 urine samples were initially collected from patients with concurrent prostate adenocarcinoma and urinary tract infection and transported to the laboratory. The samples were then incubated in appropriate culture media for 24 hours at 37°C. Subsequently, phenotypic methods and appropriate biochemical tests were used to confirm the bacterial species. the antibiotic susceptibility test (antibiogram) was performed using the Kirby-Bauer disk diffusion method with antibiotic disks commonly used for urinary tract infections.

RESULTS AND DISCUSSION: In conventional culture method, out of 72 positive samples, 53 samples (73.61%) were Gram-negative bacteria and 19 samples (26.38%) were Gram-positive bacteria, containing Escherichia coli (30.55%) , Klebsiella pneumoniae (26.38%), Enterobacter (8.33%), Pseudomonas aeruginosa (6.94%), Acinetobacter baumannii (2.77%), Staphylococcus epidermidis (23.61%), Staphylococcus aureus (1.38%). Most bacteria isolated from prostate specimens belonged to the Enterobacteriaceae family, Staphylococcus epidermidis and Staphylococcus aureus were Gram positive cocci isolated in the specimens too. Research results showed that prostate cancer patients are susceptible to urinary tract infections due to immunodeficiency and receiving immunosuppressive drugs. The results also showed that multidrug-resistant strains are common in these patients. Therefore, it is very important to quickly and correctly identify bacterial species, determine the antibiotic resistance pattern, and report it to the physician.

Keywords: Antibiotic resistance - Prostate Adenocarcinoma - Kirby-Bauer - UTI

Assessment of Resistance to Amikacin, Kanamycin, and Capreomycin and Associated Gene Mutations in Multi Drug-Resistant Tuberculosis Isolates from Ahvaz, Iran

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BACKGROUND AND OBJECTIVES: The rise of multidrug-resistant (MDR) and extensively drug-resistant (XDR) Mycobacterium tuberculosis strains challenges global TB control. Second-line injectable drugs, including aminoglycosides and capreomycin, are vital for treatment but face increasing resistance. This study evaluates phenotypic resistance to these drugs in MDR-TB isolates and investigates mutations in key resistance genes to better understand resistance mechanisms.

MATERIALS AND METHODS: Twenty-two MDR-TB isolates were collected from the Ahvaz Regional Tuberculosis Reference Laboratory. Drug susceptibility testing for capreomycin, amikacin, and kanamycin was performed using the proportional method according to the WHO guidelines. PCR amplification was performed to target the rrs, eis, and tlyA genes in resistant isolates, and the resulting PCR products were sequenced.

RESULTS AND DISCUSSION: In this study, 22.7% of the isolates exhibited resistance to at least one aminoglycoside antibiotic. Resistance rates to amikacin, kanamycin, and capreomycin were 13.6%, 18.2%, and 13.6%, respectively. Among isolates, 4.5% showed concurrent resistance to all three drugs, 9.1% were resistant to kanamycin/capreomycin, 4.5% to amikacin/kanamycin, and 4.5% resistant to amikacin. Genetic analysis revealed 60% of resistant isolates harbored mutations in tlyA, eis, or rrs genes, while 40% lacked mutations. One isolate contained an A806T silent mutation in rrs, a G458C mutation in tlyA causing lysine-to-asparagine substitution at codon 102, and a C355A mutation in eis causing histidine-to-asparagine substitution at codon 103. The findings underscore the significant prevalence of aminoglycoside resistance in MDR-TB isolates and the critical role of genetic mutations. Continued molecular surveillance is essential to inform effective treatment strategies and combat drug-resistant tuberculosis.

Keywords: Multidrug-resistant tuberculosis,Second-line injectable drugs,Genetic mutations, drug resistance

Assessment of Susceptibility to Crusted Scabies and Evaluation of Immune System Function in Patients with Down Syndrome

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BACKGROUND AND OBJECTIVES: Scabies is a contagious parasitic skin disease. The Norwegian or crusted variant is a rare form characterized by extensive mite proliferation and severe allergic reactions. This type is more commonly observed in immunocompromised patients. One such group includes individuals with Down syndrome, who, due to trisomy 21, experience immune deficiencies, neurodevelopmental disorders, congenital heart diseases, muscle weakness, increased risk of autoimmune diseases, and genetic alterations affecting immune function and metabolism. As a result, they are at a higher risk of developing crusted scabies. This disease, besides its dermatological symptoms, can contribute to immune system dysfunction.

MATERIALS AND METHODS: this article was written to highlight the importance of crusted scabies in individuals with Down syndrome, its impact on immune system disorders, and the necessity of early diagnosis. A review of prior studies in this field has been conducted to better understand these relationships and their implications for treatment strategies

RESULTS AND DISCUSSION: Early diagnosis of crusted scabies in individuals with Down syndrome is crucial to reducing complications and improving disease management. In Down syndrome patients, the number of CD4+ and CD8+ immune cells decreases. This alteration, combined with the effects of crusted scabies, leads to an imbalance in immune cell ratios, exacerbated skin lesions, and an increased risk of severe secondary bacterial infections, which could potentially result in sepsis. Furthermore, these individuals exhibit excessive expression of the IFNAR1 gene and abnormal activation of interferon pathways, leading to hyperactivation of immune cells and chronic inflammation.

Keywords: Crusted scabies Down syndrome immune system skin diseases

Association between gut microbiota and endometriosis

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BACKGROUND AND OBJECTIVES: A prevalent gynecological condition that frequently results in pain and infertility is endometriosis. Although the precise etiology of endometriosis is yet unknown, it may be intimately linked to a body-wide sex hormone imbalance, ectopic hyperplasia triggered by immunological inflammation, and invasion and escape depending on tumor features. An imbalance in the microbial makeup of the gut, known as dysbiosis, can impair immune responses, exacerbate inflammation, and fuel the chronic inflammatory state that characterizes endometriosis. Additionally, the development of endometriosis is closely linked to estrogen metabolism, which is influenced by gut bacteria.

MATERIALS AND METHODS: In preparation for this review, we searched databases including PubMed, Google Scholar, and reviewed Relevant articles related to the keywords of this paper from 2020 to 2025.

RESULTS AND DISCUSSION: The release of lipopolysaccharide (LPS), which causes chronic inflammation and encourages ectopic endometrial adhesion, invasion, and angiogenesis, can be facilitated by the dysregulated microbiota. Additionally, the role of the gut bacteria in the metabolism of estrogen influences estrogen levels, which are directly linked to the development of endometriosis. The paper also emphasizes how the gut microbiota may be used to diagnose endometriosis and as a target for treatment. Treatments including gut microbiota preparations and fecal microbiota transplantation (FMT) have shown encouraging results in lowering the symptoms of endometriosis. Notwithstanding the advancements, further investigation is required to fully understand the complex relationships between gut microbiota and endometriosis in order to develop potent preventative and therapeutic approaches for this difficult illness.

Keywords: endometriosis, gut microbiome, Dysbiosis

Association Between Vaginal Microbiota and Gynecological Cancers

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BACKGROUND AND OBJECTIVES: The vaginal microbiota plays a crucial role in maintaining reproductive health, and its imbalance, known as dysbiosis, has been increasingly linked to various gynecological disorders, including malignancies. While Lactobacillus species are dominant in healthy vaginal environments, shifts toward anaerobic and pathogenic taxa may contribute to inflammation, immune dysregulation, and carcinogenesis. This review aimed to explore the relationship between vaginal microbiota composition and gynecological cancers, particularly cervical and endometrial cancers, and to highlight microbial biomarkers and diagnostic potentials.

MATERIALS AND METHODS: This narrative review was conducted by collecting and analyzing peer-reviewed studies published in databases such as PubMed, Scopus, and Web of Science. Articles were selected based on relevance to vaginal microbiota, cervical or endometrial cancer, microbial markers, and diagnostic or prognostic value. Both human and in vitro studies were considered.

RESULTS AND DISCUSSION: The evidence indicates that reduced Lactobacillus abundance and increased diversity of anaerobic bacteria, including Gardnerella, Prevotella, Sneathia, and Atopobium, are associated with a higher risk of cervical cancer and its precursors. In endometrial cancer, microbiota alterations also correlate with tumor progression. These changes may affect local immunity, epithelial barrier integrity, and HPV persistence. The identification of specific microbial patterns offers promise for early detection, non-invasive diagnostics, and personalized therapeutic strategies.

Keywords: Vaginal microbiota, Cervical cancer, Endometrial cancer, Dysbiosis, Lactobacillus, Microbial biomarkers

Association of genetic polymorphism of Interferon gamma (rs2430561) with severity of staphylococcus epidermis induced septicemia

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BACKGROUND AND OBJECTIVES: Association of genetic polymorphisms with susceptibility to various diseases has been long established. Interferon gamma (IFN-γ) is a type II interferon member that might render protective immunity to pathogens or contribute to exaggerated inflammation. In this study we evaluated the association of IFN-γ gene polymorphism with severity of disease in septic patients infected with Staphylococcus epidermidis.

MATERIALS AND METHODS: Blood samples from septic patients were collected and rs2430561 A/T polymorphism was determined, using Amplification-refractory mutation system (ARMS)-PCR followed by measurement of IFN-γ serum levels by ELISA. These two parameters were correlated with blood inflammatory markers, including C-reactive protein (CRP), erythrocyte sedimentation rate (ESR) and neutrophil counts.

RESULTS AND DISCUSSION: Inflammatory blood markers were notably higher in patients carrying at least one A allele. Moreover, T allele is associated with increased serum amounts of IFN-γ.This study approved an association between IFN-γ gene polymorphism with severity of disease in septic patients, in conjunction with decreased production of IFN-γ. Increased levels of IFN-γ appears to render a protective immunity to septic patients.

Keywords: Polymorphism, IFN-γ, Staphylococcus Epidermidis, Sepsis, Inflammation

Association of Streptococcus gallolyticus subsp. gallolyticus with colorectal cancer: A cross-sectional study

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BACKGROUND AND OBJECTIVES: Colorectal cancer (CRC) is a major contributor to global cancer mortality, with emerging evidence implicating gut microbiota dysbiosis in its pathogenesis. Streptococcus gallolyticus subsp. gallolyticus (Sgg) has been increasingly investigated as a potential oncobacterial agent in CRC. This cross-sectional study assessed the prevalence of Sgg colonization in colorectal tumor tissues and its association with CRC in Iranian patients.

MATERIALS AND METHODS: We enrolled 176 individuals who underwent colonoscopy, comprising 65 patients with histopathologically confirmed CRC and 111 non-malignant controls. DNA extracted from biopsy specimens was subjected to PCR amplification targeting the recA gene to detect Sgg.

RESULTS AND DISCUSSION: Sgg colonization was identified in 60.0% (39/65) of CRC patients compared to 29.7% (33/111) of controls (P = 0.006), yielding a statistically significant association (OR = 3.63; 95% CI: 1.86–7.10). These findings support a potential link between Sgg colonization and CRC in the Iranian population, corroborating hypotheses from previous conflicting reports. While the precise mechanisms remain incompletely elucidated, Sgg may promote carcinogenesis through enhanced cellular proliferation, β-catenin pathway activation, and proinflammatory signaling. Although this study design precludes causal inference, it substantiates the need for longitudinal and mechanistic studies. Furthermore, PCR-based Sgg detection in colonic tissue may serve as a microbial biomarker for stratifying CRC risk.

Keywords: Colorectal cancer, Streptococcus gallolyticus, Iranian patients, microbiota, PCR, gut bacteria

Bacteriophages: A Novel Approach to Combat Microbial Pollution in Water and Preserve Environmental Health

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BACKGROUND AND OBJECTIVES: The escalating prevalence of microbial contaminants in aquatic environments, driven by anthropogenic activities and climate-induced shifts in microbial ecology, poses a critical challenge to global environmental and public health. Traditional physicochemical water treatment processes are often limited in their specificity and efficacy, particularly against multidrug-resistant (MDR) bacterial strains. Bacteriophages—obligate bacterial viruses—represent a highly selective and self-amplifying biocontrol strategy capable of targeting specific pathogenic bacteria without disrupting native microbial communities.

MATERIALS AND METHODS: This study provides a comprehensive evaluation of the potential of bacteriophages in mitigating microbial water pollution. We analyze phage-host interactions, including adsorption dynamics, lytic efficiency, and phage-mediated biofilm disruption in contaminated water matrices. Emphasis is placed on recent advancements in phage engineering, such as synthetic biology tools and CRISPR-enhanced phages, that enhance host range and therapeutic resilience. Moreover, we explore the integration of phage-based treatments into existing water treatment frameworks, including membrane filtration and UV disinfection, to develop hybrid and sustainable remediation systems.

RESULTS AND DISCUSSION: Environmental risk assessment, horizontal gene transfer concerns, and regulatory challenges associated with phage application are critically examined. The findings underscore bacteriophages as a scalable, environmentally benign, and highly adaptable tool in the fight against microbial water pollution, with significant implications for One Health and sustainable development initiatives.

Keywords: Bacteriophage biocontrol, multidrug-resistant pathogens, water treatment, phage engineering, environmental

Biofilm inhibition effect of Eucalyptus camaldulensis extract on Staphylococcus aureus

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BACKGROUND AND OBJECTIVES: Biofilm formation by Staphylococcus aureus contributes to persistent infections and enhances antibiotic resistance, posing a significant public health concern. There is increasing interest in natural alternatives such as Eucalyptus camaldulensis extracts. E. camaldulensis, which is rich in bioactive compounds such as 1,8-cineole, citronellal, and citronellol, has shown strong antimicrobial potential.

MATERIALS AND METHODS: Titanium samples coated with E. camaldulensis extract were incubated in S. aureus (ATCC 29737) suspension for 24 hours, then washed in sterile saline and sonicated to remove adherent bacteria. The resulting suspensions were cultured on nutrient agar medium to measure colony-forming units and assess bacterial viability and adhesion.

RESULTS AND DISCUSSION: The extract exhibits significant antimicrobial and anti-biofilm properties against S. aureus; however, complete eradication of biofilms was not achieved. E. camaldulensis extracts show significant antimicrobial and antibiofilm activity against S. aureus and significantly reduce planktonic cells and biofilm formation through mechanisms such as membrane disruption, increased permeability, and inhibition of cell adhesion.

Keywords: Eucalyptus camaldulensis, Extract, Biofilm Inhibition

Biogenic Fabrication of ZnO Nanoparticles Using Anvillae garcinii and Assessment of Their Antibacterial, Antioxidant, and Anticancer Activities

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BACKGROUND AND OBJECTIVES: In the present research, zinc oxide (ZnO) nanoparticles (NPs) were synthesized for the first time through reduction using Anvillae garcinii leaf extract through reduction process. Compared to conventional physicochemical approaches, this synthesis method has several advantages including simplicity, low cost, sustainability, and replicability.

MATERIALS AND METHODS: The effects of calcination temperatures (60 °C and 500 °C) and pH levels (8, 10, and 12) on ZnO NP properties were studied. Characterization was done using UV-Vis spectroscopy, FT-IR, XRD, DLS, and FE-SEM. Biological activities, including antioxidant, cytotoxicity on gastric cancer cells, and antibacterial effects against E. coli, S. aureus, and H. pylori strains, were evaluated.

RESULTS AND DISCUSSION: UV–Vis spectra showed a peak at ~230 nm. FT-IR and XRD confirmed nanoparticle formation with spherical and hexagonal shapes. Particle size varied with pH and temperature, smallest (16.4 nm) at pH 12 and 60 °C, largest (63 nm) at pH 8 and 500 °C. Synthesized NPs showed high antioxidant activity and dose-dependent cytotoxicity on cancer cells with IC50 values of 35.11 and 42.7 µg/ml. Strong antibacterial activity was observed against tested bacteria. Plant-mediated green synthesis of ZnO NPs is a sustainable, cost-effective method producing nanoparticles with promising antioxidant, antibacterial, and anticancer properties suitable for biomedical and environmental applications.

Keywords: Zinc oxide; Nanoparticles ; Anvillae garcinii; antibacterial; antioxidant,

Bacterial peptide in colon cancer therapy

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BACKGROUND AND OBJECTIVES: Colon cancer remains a life-threatening disease with limitations in current treatments, necessitating novel therapies. We investigated the therapeutic potential of Azurin-p28 and HPRP-A1, derived from Helicobacter pylori ribosomal protein L1 (RpL1) against colon cancer.

MATERIALS AND METHODS: We assessed the tumor growth inhibitory activity of p28 and HPRP-A1 with or without iRGD and 5FU on colon cancer in vitro and in vivo. In the in vitro part, we investigate the effect of HPRP-A1 alone and in combination with iRGD/5FU.

RESULTS AND DISCUSSION: In tumor tissues, p28, alone or with iRGD and 5-FU, promoted apoptosis by increasing p53 and BAX expression and decreasing BCL2 expression, outperforming control and 5-FU groups. HPRP-A1 with iRGD enhanced apoptosis and, when combined with 5-FU, further elevated intracellular p53 levels, upregulating BAX and downregulating BCL2. HPRP-A1 blocked cell cycle progression in G0/G1, and the combination of the two peptides significantly reduced tumor size and weight. Moreover, 5-FU co-administered with the peptides significantly increased necrosis, decreased fibrosis, and disrupted the oxidant/antioxidant balance in tumor tissues. P28 shows promise as a novel therapeutic to enhance 5-FU's anti-tumor effects in colon cancer. Further research is needed to clarify the mechanisms, safety, and efficacy of this combination in clinical trials. P28's potential to overcome 5-FU resistance makes

Keywords: Azurin-p28; HPRP-A1; Pseudomonas aeruginosa; Bacterial peptide; Colon cancer; iRGD

Bacterial role in cancer

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BACKGROUND AND OBJECTIVES: Recent research reveals a complex link between pathogenic bacteria and cancer, demonstrating how these microbes can induce oncogenesis. Although commensal microbiota influences various physiological processes, including cancer, both within the gut and at distant sites, specific microbial aspects can exhibit either pro- or anti-tumor activity. Here, we summarize the current knowledge on the association between bacterial infections and various cancers, focusing on the methodologies and findings of studies investigating the relationship between bacteria (both drivers and passengers) and cancer incidence.

MATERIALS AND METHODS: We searched PubMed, the Cochrane Library, ScienceDirect, and Google Scholar for studies investigating the role of bacteria in cancer incidence within the past 10 years. we found a total of 6312 records.

RESULTS AND DISCUSSION: A total of 67 reports met the inclusion criteria, which primarily utilized 16S rDNA or 16S rRNA sequencing to analyze the microbiome. Microbiome sequencing studies offer insights into the abundance of bacterial taxa in cancer patients compared to those with pre-malignant conditions or healthy controls, potentially using follow-up data to assess bacterial infections in cancer. Studies frequently examine the association of Helicobacter pylori, EPEC, ETBF, pks+ Escherichia coli, AIEC, Salmonella spp., Clostridium spp., and Campylobacter spp. with cancer incidence. These findings highlight the need to further explore microbiota as non-invasive biomarkers and their impact on cancer prevention and treatment, emphasizing the importance of understanding the interplay between bacterial infections and the host immune response in cancer

Keywords: Cancer; Bacteria; Microbiota; Incidence

Bacterial zoonotic diseases in pet birds

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BACKGROUND AND OBJECTIVES: The term "ornamental bird" refers to birds that are kept and bred exclusively for ornamental purposes. This category mainly includes passerine birds (e.g. canaries, finches, sparrows), also known as songbirds, and parrot birds (parrots, parakeets, budgerigars, parakeets). These animals are potential carriers and/or vectors of zoonotic diseases. Some of these diseases could have a significant impact on human health, such as chlamydophilosis and salmonellosis.

MATERIALS AND METHODS: One of the most threatening zoonotic diseases transmitted from birds to humans is chlamydophilosis (also known as chlamydiosis, ornithosis, psittacosis or parrot fever), which is caused by the intracellular bacterium Chlamydophila psittaci. Psittacine species are very susceptible to this pathogen, but passerine birds are not excluded. Symptoms in humans range from mild respiratory signs to severe pneumonia, with localisation in various organs leading to diarrhoea, conjunctivitis, arthritis and infections of the genital organs. As expected, the first people to be susceptible to infection appear to be vets and bird breeders. Salmonella species have been isolated from several captive passerine or psittacine birds, associated or not (asymptomatic transmission) with clinical signs: diarrhoea, multisystem disease, septicaemia, osteomyelitis, depression, crop stasis, dehydration, anorexia.

RESULTS AND DISCUSSION: Assessing the health of pet birds, their living conditions, breeding facilities, and owners could be a valuable step toward understanding the human health risks involved—whether in household settings or larger breeding operations. This evaluation could help guide the development of preventive measures, such as improved biosecurity, hygiene practices, and prophylactic strategies, to protect public health and enhance economic outcomes.

Keywords: Pet birds, bacterial zoonotic disease, Campylobacter, mycobacterium

Bacteriological study of liver abscesses in slaughtered sheep

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BACKGROUND AND OBJECTIVES: Hepatic abscesses in slaughtered sheep cause economic losses and public health concerns, often identified incidentally during necropsy. These abscesses, resulting from pyogenic bacteria such as Staphylococcus, Streptococcus, Escherichia coli, and Trueperella pyogenes, are linked to factors like ruminal acidosis, parasitic migration, and traumatic reticulitis. This study isolated predominant bacteria from abscesses and evaluated their antimicrobial susceptibility, revealing sensitivity to ciprofloxacin and penicillin but resistance to ceftiofur, amoxicillin, and vancomycin, highlighting the need for improved herd management and resistance monitoring.

MATERIALS AND METHODS: Liver samples with visible abscesses were aseptically collected from slaughtered sheep and transported under refrigeration to the microbiology laboratory. Pus was extracted via sterile incision and inoculated onto nutrient agar and blood agar. Cultures were incubated aerobically at 37°C for 48 hours. Isolated colonies were identified, and antimicrobial susceptibility testing was performed using discs of ciprofloxacin, penicillin, ceftiofur, amoxicillin, and vancomycin.

RESULTS AND DISCUSSION: The predominant bacterial isolates were Staphylococcus spp., Streptococcus spp., and Escherichia coli. All isolates demonstrated susceptibility to ciprofloxacin and penicillin but showed resistance to ceftiofur, amoxicillin, and vancomycin. These findings reflect both the prevalence of these bacteria in hepatic abscesses and emerging antibiotic resistance patterns. This study highlights the role of Staphylococcus, Streptococcus, and E. coli in hepatic abscess formation in sheep, emphasizing the importance of controlling predisposing factors such as high-energy diets and parasitic infections. The observed antibiotic resistance patterns underline the urgent need for responsible antimicrobial use and regular surveillance in veterinary practice to prevent zoonotic transmission and economic losses in the sheep industry.

Keywords: Liver, Streptococcus, Visceral abscesses

Bacteriophage Applications for Ensuring Food Safety and Security: From Farm to Fork

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BACKGROUND AND OBJECTIVES: With the increasing world population, providing healthy and sustainable food has become a serious challenge. Demanding the use of natural preservatives for combatting food-borne pathogens are increasing more theses days. One of the new solutions is the use of bacteriophages for the targeted elimination of foodborne pathogens without harming the beneficial microflora.

MATERIALS AND METHODS: A review of scientific articles related to the use of phages for controlling foodborne pathogens, up to the year 2025, with a particular focus on recent publications was conducted. Following a thorough screening, the extracted data were analyzed to identify the advantages, limitations, and recent innovations in the use of bacteriophages within the food supply chain.

RESULTS AND DISCUSSION: Bacteriophages serve as effective biological control agents for reducing bacterial contamination in the food industry. Various phages have been applied to target key foodborne pathogens including Salmonella spp., Listeria monocytogenes, Escherichia coli, Campylobacter spps.,and Vibrio spps. Also, commercial phage-based products such as Phageguard S and ListShield™ have approved by FDA, demonstrated high efficacy in reducing antibiotic-resistant bacteria and disrupting biofilms. Effective biocontrol strategies across diverse food matrices and under various conditions, offering a promising, safe and targeted alternatives for controlling foodborne pathogens and enhancing food safety.

Keywords: Bacteriophages, Food Safety, Antibiotic Resistance

Bacteriophage products as antibiotic alternatives

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BACKGROUND AND OBJECTIVES: The growing threat of multidrug-resistant bacteria and public health concerns necessitates the search for new solutions. Bacteriophages as highly potentiated antibacterial agents re-emerged recently. Some researshes suggested using bacteriophage products antibacterial activity instead of phages.Endolysin holin, and spanin are lytic proteins encoded by bacteriophages that effectively cause lysis and death of bacteria.

MATERIALS AND METHODS: In the current study, we collected the articles in the field of using bacteriophage products specially endolysins as alternatives to bacteriaphages to combat different bacteria. We concentrated on recent articles (2020 – 2025) as in vito works and in vivo experimental studies.

RESULTS AND DISCUSSION: Preliminary researches suggested that endolysins are more effective against gram-positive bacteria than gram-negative bacteria when administered topically. However, the modular structure of endolysin provides a unique opportunity to modify and create possibility of genetic engineering. In addition, a number of methods such as encapsulation, using of nanoparticles, the use of holin-endolysin structures can form a synergism in antibacterial activity. Due to some challenges posed by the use of phage, endolysins havegained more attention from physicians and industry but in spite of high antibacterial properties of phage products, more studies are necessary to characterize them functionally .

Keywords: antimicrobial resistance, bacteriophage, endolysin, holin, spanin

Bacteriophage Therapy as a Promising Alternative to Antibiotics in Veterinary Medicine

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BACKGROUND AND OBJECTIVES: Due to the growing prevalence of multidrug-resistant (MDR) bacteria as a serious threat to animal and human health, bacteriophage (phage) therapy re-emerged in alternative therapeutics.

MATERIALS AND METHODS: Scientific researches in using bacteriophages to combat bacterial infections in different animals specially livestock were obtained. The bacterial targets were primarily MDR strains of Staphylococcus aureus, Salmonella spp., and Pseudomonas aeruginosa. Approximately 60% of the selected studies were in vivo experiments performed on animal models or real animal patients, while the remaining were related to in vitro trials. Efficiency of different routes of phage administration such were reviewed. This article explored the mechanisms, advantages, limitations, and practical implementation of phage therapy in veterinary settings, with an emphasis on recent research and successful case studies published after 2020.

RESULTS AND DISCUSSION: The studies until 2025 have demonstrated the potential of bacteriophage therapy in treating multidrug-resistant (MDR) infections in veterinary medicine. In bovine mastitis, intramammarily administered phage cocktails significantly reduced Staphylococcus aureus counts and improved udder health. In companion animals, topical phage therapy for MDR wound infections accelerated healing and reduced inflammation without adverse effects. In poultry and aquaculture, oral or immersion delivery of phages targeting E. coli and Salmonella spp. led to improve survival rates and reduced antibiotic use. Overall, phage therapy presents a promising alternative to antibiotics in veterinary care, especially as part of integrated strategies to manage AMR. However, regulatory frameworks and broader clinical trials are needed to support widespread adoption.

Keywords: Phage therapy, Veterinary medicine, Bacteriophage, Multidrug-resistant bacteria,

Bacteriophages as Virus-Like Particle Vaccines: A Promising Approach in Vaccine Development

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BACKGROUND AND OBJECTIVES: Bacteriophages are viruses that infect bacteria, known for their specificity and efficiency as bacterial predators. While their therapeutic potential against bacterial infections has long been recognized, recent advancements have highlighted their role in vaccine development. Bacteriophages can be engineered to display foreign antigens on their surface, transforming them into VLPs. These modified bacteriophages mimic the structure of pathogenic viruses or bacteria without being infectious. When introduced into the body, the immune system recognizes these VLPs and produces antibodies and immune cells to combat the mimicked pathogen. This approach leverages the natural architecture of bacteriophages to stimulate immunity while eliminating the risk of disease. Advantages Using bacteriophages as VLPs offers distinct benefits: Safety: Bacteriophages target bacteria, not human cells, making them inherently safe for vaccine use. Customisability: Antigens can be precisely engineered onto bacteriophage surfaces. Efficiency: Bacteriophage VLPs can be produced rapidly and cost-effectively, improving scalability compared to traditional methods.

MATERIALS AND METHODS: The articles have been collected from the PubMed database. the keywords Bacteriophage, VLP, and Vaccine were used for the search.

RESULTS AND DISCUSSION: Current Research Ongoing studies demonstrate the potential of bacteriophage-based VLPs. For example, VLPs displaying influenza antigens have induced robust immune responses in animal models. Research targeting bacterial pathogens like Staphylococcus aureus also shows promise, suggesting broad applicability. Bacteriophage-based VLP vaccines combine safety, specificity, and efficiency, positioning them as a transformative tool in immunization. As research advances, they could address diverse infectious diseases effectively. Advances in synthetic biology could enable "plug-and-play" platforms for rapid pandemic response (e.g., SARS-CoV-2 variants).

Keywords: Bacteriophage, VLP, Vaccine

Bacteriophages in the Reproductive Tract: Emerging Players in Microbial Homeostasis and Fertility

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BACKGROUND AND OBJECTIVES: Bacteriophages—the viruses that prey on bacteria—are emerging as key modulators of the vaginal microbiota, with profound implications for reproductive health and fertility. Traditionally overlooked in gynecological microbiology, phages can influence microbial balance by infecting beneficial Lactobacillus species, potentially leading to dysbiosis and bacterial vaginosis (BV). Such shifts not only increase vulnerability to sexually transmitted infections but may also impact pregnancy outcomes.

MATERIALS AND METHODS: Far from being solely harmful, phages also represent a new therapeutic frontier. Their extraordinary specificity allows for precise targeting of pathogenic bacteria and biofilms, preserving beneficial microbes that are essential for long-term vaginal eubiosis. As diagnostic tools advance, the ability to detect phage-associated dysbiosis could guide personalized interventions—ranging from targeted phage therapy to combined phage-probiotic regimens—offering a gentler, more sustainable alternative to broad-spectrum antibiotics.

RESULTS AND DISCUSSION: This presentation will highlight current evidence linking phages to reproductive tract health, explore their potential as diagnostic and therapeutic tools, and discuss how integrating phage biology into clinical practice could reshape strategies for infection control, fertility preservation, and microbial homeostasis.

Keywords: bacteriophage, reproductive health, fertility, microbial balance, bacterial vaginosis, phage therapy

Bacteriophages: Microbiome Engineers and Therapeutic Frontiers

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BACKGROUND AND OBJECTIVES: Bacteriophages, often seen as mere bacterial parasites, are far more significant, acting as "true engineers" of the human microbiome. They actively shape the microbial environment through key mechanisms such as predation, genetic exchange, and intricate interactions with both bacterial and the host. This multifaceted involvement leads to profound influences on microbial population dynamics, genetic diversity, and metabolomic functions, which in turn impact the host's health and susceptibility to disease. Recognizing these complete roles is vital for developing innovative treatments, especially given the growing challenge of antibiotic resistance.

MATERIALS AND METHODS: This study is derived from multiple reputable scientific articles from 2013 to 2025 and examines the role of bacteriophages in microbiome regulation, their impact on the pathophysiology of diseases, and their potential for novel therapeutic applications.

RESULTS AND DISCUSSION: Bacteriophages can selectively target specific bacteria, thus maintaining a balanced microbiome across various human body systems. Bacteriophages are recognized as key regulators of immune responses and inflammatory processes in chronic diseases such as IBD, and also type 2 diabetes, obesity, and fatty liver diseases. By selectively targeting certain bacterial species, phage can help us to edit or rebalance the gut microbiota, resulting the healthier composition. The human phageome, especially in light of recent advances in genetic technology and sequencing, holds great potential for developing targeted and personalized therapeutic approaches to treat antibiotic-resistant diseases and microbiome disorders. Future research will focus on enhancing the therapeutic properties of phages and increasing their effectiveness in clinical models.

Keywords: Phage, microbiota, phageome, personalized medicine, pathophysiology, pathogenicity

Benchmarking In Silico Methods for Accurate Prediction of Phage-Host Interactions: A systematic review

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BACKGROUND AND OBJECTIVES: Antibiotic resistance is a global crisis that bacteriophages have reemerged in the therapeutic arena to overcome. Understanding phage-host interactions (PHIs) is crucial for the development of phage therapeutics. Traditional experimental methods for identifying PHIs are time-consuming and costly. Thus, this systematic review evaluates various methodologies for assessing and predicting PHIs, categorizing them into taxonomic and regression-based approaches.

MATERIALS AND METHODS: We analyzed scientific literature that investigated the application of bioinformatics and artificial intelligence technologies in predicting phage-bacterial interactions. Our search included the following databases: PubMed, Scopus, and ISI Web of Science.

RESULTS AND DISCUSSION: we investigate 10 studies that apply computational methods and machine learning algorithms to analyze signals indicating phage-bacteria interactions. we founded that alignment-based methods, such as vHULK (demonstrating sensitivities of 82% and 52% at the genus and species levels, respectively), exhibit superior sensitivity compared to their counterparts. Furthermore, alignment-free methodologies, such as GSPHI at both the genus and species levels, and PB-LKS at the genus level, demonstrate the highest predictive efficacy for PHI, achieving accuracies of 0.9208 and 0.656, respectively. Thus, the findings suggest that local nucleotide similarity may serve as a more significant indicator of PHI than nucleotide similarity derived from entire genome sequences. The identification of hosts for novel phages has been substantiated through applications in gene transfer searches, disease diagnostics, and bacterial detection. Over the preceding three years, advancements in artificial intelligence (AI) tools have represented some of the most consequential progressions within the field,

Keywords: Phage-host interactions; Prediction; In Silico Methods

Beyond Antibiotics: Harnessing Microbial Cell Death Mechanisms for Disease Control

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BACKGROUND AND OBJECTIVES: Introduction: The global rise of antimicrobial resistance (AMR) has reduced the effectiveness of traditional antibiotics. Consequently, microbial cell death pathways are gaining attention as alternative strategies to combat pathogens. Bacterial processes such as apoptosis-like cell death, autolysis, and regulated necrosis offer new therapeutic opportunities by disrupting pathogen viability independently of conventional antimicrobials.

MATERIALS AND METHODS: Methods: This review analyzed studies from the past ten years investigating microbial self-destruction pathways and their potential in disease control. Searches were conducted in PubMed, Scopus, and Web of Science using keywords like "microbial cell death," "antimicrobial resistance," and "alternative therapies." Inclusion criteria included original articles exploring these pathways and their therapeutic relevance. Data on methodologies, key findings, and outcomes were extracted.

RESULTS AND DISCUSSION: Results: Forty-five studies met the criteria. Findings were categorized into apoptosis-like cell death, autolysis, and necrosis in bacterial and fungal pathogens. Species such as Escherichia coli and Mycobacterium tuberculosis exhibited apoptosis-like mechanisms triggered by environmental stressors, reducing pathogen viability. Autolysis showed potential in disrupting biofilms and enhancing immune responses. Necrosis-like pathways indicated genetic manipulation possibilities to reduce pathogen infectivity and transmission. Discussion: Microbial cell death pathways represent promising alternatives for treating biofilm-associated and persistent infections where antibiotics often fail. Further research is necessary to clarify regulatory mechanisms and safety, especially in clinical settings, to prevent side effects or resistance. These pathways lay a foundation for future self-destruction-based therapies.

Keywords: Keywords: Microbial cell death, Antimicrobial resistance, Alternative therapies

Biocompatible PEG-ZIF-8 Nanozymes for Targeted Ciprofloxacin Delivery

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BACKGROUND AND OBJECTIVES: Burn wound infections caused by ciprofloxacin-resistant Pseudomonas aeruginosa represent a serious clinical challenge. This study aimed to develop PEGylated ZIF-8 nanozymes loaded with ciprofloxacin (PEG-ZIF-8-CIP) to enhance antimicrobial efficacy and biocompatibility.

MATERIALS AND METHODS: The minimum inhibitory concentration (MIC) of ciprofloxacin was determined for clinical P. aeruginosa isolates, confirming resistance based on CLSI standards. ZIF-8 nanozymes were synthesized using a solvothermal method, loaded with ciprofloxacin, and PEGylated for improved stability. Physicochemical characterization was performed by FESEM, DLS, zeta potential, and FTIR spectroscopy. In vitro drug release was evaluated in PBS, and antibacterial activity was assessed using the disc diffusion method. Cytotoxicity was evaluated on human fibroblast cells using the MTT assay.

RESULTS AND DISCUSSION: PEGylated nanozymes exhibited improved colloidal stability, higher surface charge, and controlled biphasic drug release. Antibacterial assays revealed that PEG-ZIF-8-CIP had superior inhibitory activity compared to free ciprofloxacin and uncoated nanozymes. Importantly, cytotoxicity analysis demonstrated significantly reduced toxicity of PEG-ZIF-8-CIP in human fibroblast cells, particularly at earlier time points and moderate concentrations. In contrast, non-PEGylated nanozymes showed pronounced time- and dose-dependent cytotoxicity. PEG-ZIF-8-CIP nanozymes represent a safe and efficient platform for delivering ciprofloxacin to resistant bacterial infections in burn wounds. Their enhanced antimicrobial performance and reduced cytotoxicity support their potential for further preclinical development in wound-targeted therapy.

Keywords: PEG-ZIF-8Nanozyme, Ciprofloxacin, Pseudomonas aeruginosa, resistance, Burn wound, Drug delivery,

Bioequivalence Study of the Cefixime 400-mg Film Coated Tablets Manufactured by Iranian Company vs. AURO-CEFIXIME® Tablet manufactured by Aurobindo Pharma Company in healthy volunteers

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BACKGROUND AND OBJECTIVES: Cefixime is a third-generation oral cephalosporin used in the treatment of various bacterial infections. Demonstrating the bioequivalence of generic formulations to the reference listed drug is essential for regulatory approval and clinical reliability. To assess the bioequivalence of a newly formulated cefixime 400 mg film-coated tablet manufactured by a domestic Company with the reference under fasting conditions.

MATERIALS AND METHODS: A single-dose, open-label, randomized, two-treatment, two-period, two-sequence crossover study was conducted in 24 healthy adult volunteers under fasting conditions. Blood samples were collected over 24 hours, and plasma concentrations of cefixime were measured using a validated LC-MS/MS method. For bioequivalence analysis, AUC0-t, AUC0-∞, and Cmax were considered as primary variables. The analysis of variance (ANOVA) for the cross-over design model for Ln (AUCs) as well as Ln (Cmax) was carried out exactly based on the Canadian pharmaceutical bioequivalence analysis guidelines.

RESULTS AND DISCUSSION: The results of the statistical analysis of three pharmacokinetics parameters, including Ln (AUC0-24), Ln (AUC0-∞), and Ln (Cmax) are investigated. The 90% confidence intervals of the natural logarithm transformed AUC0-24, AUC0-∞, and Cmax of the two formulations are within the accepted levels of the FDA limits of 80-125%. The Tmax values of the two products were also analyzed with the Wilcoxon statistical procedure and indicated no statistical difference between the generic formulation and the reference product. Consequently, the two types of Cefixime formulations were considered to be bioequivalent based on the pharmacokinetic results acquired from concentration-time profiles of the drug in 24 healthy volunteers.

Keywords: Cefixime, Bioequivalence, Pharmacokinetics

Bioethanol Production from Agricultural Wastes Using Saccharomyces cerevisiae and Optimization of Cultivation Conditions via Taguchi Experimental Design

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BACKGROUND AND OBJECTIVES: Agricultural residues, despite their low efficiency and environmental impact, hold significant potential for renewable energy production. This study evaluated bioethanol production as a clean, sustainable, and cost-effective fuel by enriching agricultural biomass with macro elements to optimize Saccharomyces cerevisiae growth, using the Taguchi experimental design for process optimization.

MATERIALS AND METHODS: In this study, to optimize bioethanol production, the fermentation substrate was prepared from an aqueous extract of apple orchard waste and enriched with macro elements including ammonium sulfate, magnesium sulfate, yeast extract, and Saccharomyces cerevisiae inoculum. The experimental design was conducted based on the Taguchi method, with each factor tested at four levels. After 72 hours of anaerobic fermentation, the treatments were distilled, and the ethanol concentration was determined using sodium dichromate colorimetric analysis and spectrophotometry.

RESULTS AND DISCUSSION: The results showed that Treatment number 13, consisting of 10g/L ammonium sulfate, 6g/L magnesium sulfate, 20g/L yeast extract, and 2g/L Saccharomyces cerevisiae inoculum in one liter of aqueous apple extract, produced the highest ethanol yield at 12% among all treatments. This value reflects a 20% increase in ethanol production compared to the non-optimized treatment, which had a yield of 10%. Conclusion: This study confirmed that biodegradable agricultural wastes have the potential to be utilized as efficient raw materials for bioethanol production. This approach not only reduces environmental pollution but also supports the development of alternative renewable energy sources.

Keywords: Key words: Saccharomyces cerevisiae, Ethanol, Apple waste.

Biofilm Formation and Species Distribution of Enterococcus Isolates from Horse Fecal Samples

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BACKGROUND AND OBJECTIVES: Enterococcus species, normally part of the gut microbiota in humans and animals, have increasingly been recognized as opportunistic pathogens, particularly E. faecalis and E. faecium. Their ability to form biofilms enhances persistence, virulence, and antibiotic resistance, contributing to chronic infections. Horses, as livestock, may serve as reservoirs for these bacteria, posing a potential public health risk. This study aimed to assess the biofilm-forming capacity of Enterococcus isolates from the feces of healthy horses and to determine the prevalence of key species.

MATERIALS AND METHODS: A total of 100 bacterial isolates were obtained from 92 fecal samples, selected based on distinct morphological and biochemical characteristics. Genus-level identification was confirmed via polymerase chain reaction (PCR) using genus-specific primers targeting Enterococcus. The biofilm-forming ability of the isolates was evaluated using the 96-well microtiter plate assay, and species-level identification of E. faecalis and E. faecium was subsequently performed by PCR analysis.

RESULTS AND DISCUSSION: Among the isolates, 11% were identified as E. faecalis and 34% as E. faecium. Biofilm analysis showed that 34% of the isolates demonstrated biofilm-forming ability, with the majority (91.2%) exhibiting weak formation and a small proportion (8.8%) displaying moderate biofilm production. No statistically significant relationship was found between biofilm-forming ability and bacterial species. The equine gut may act as a reservoir for biofilm-producing Enterococcus species. This is of particular concern due to their potential in spreading virulence factors and antibiotic resistance. These findings highlight the need for further genetic and epidemiological studies to assess their public health impact.

Keywords: Enterococcus, biofilm, gut microbiota, horse

Biofilm formation, antibiotic-resistance and clonal relatedness among clinical isolates of Acinetobacter baumannii

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BACKGROUND AND OBJECTIVES: In this work, the antibiotic resistance, biofilm formation capability, and clonal relatedness of 50 A. baumannii isolates collected from three hospitals in Ardabil city, Iran, were evaluated.

MATERIALS AND METHODS: Antibiotic sensitivity and biofilm formation of isolates were determined by disk diffusion and microtiter-plate methods, respectively. Molecular typing of isolates was also performed using repetitive sequence-based PCR (REP-PCR).

RESULTS AND DISCUSSION: The majority of isolates were resistant to cephems, aminoglycosides, and carbapenems, with 80 % classified as multi-drug resistant (MDR). While, only isolates collected from blood and tracheal were resistant to colistin. Additionally, 42 isolates (84 %) had biofilm formation capability. According to rep-PCR results, 34 isolates showed similar banding patterns, while 16 isolates had unique banding patterns. Finally, based on the molecular analysis, there was a direct relationship between biofilm formation and the antibiotic resistance of isolates. In other words, MDR isolates had a higher ability to form biofilm.

Keywords: Acinetobacter baumannii Biofilm formation Antibiotic-resistance REP-PCR

Bioinformatic Analysis and Allergenicity Prediction of Antimicrobial Peptides LL-37, HBD-3, Indolicidin, Temporin A, and Pexiganan

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BACKGROUND AND OBJECTIVES: Antimicrobial peptides (AMPs) are promising candidates for combating drug-resistant pathogens due to their broad-spectrum activity and unique mechanisms. However, allergenicity and specific structural properties may limit their therapeutic applications. This study aimed to perform a bioinformatic analysis and comparative evaluation of five well-known AMPs in terms of allergenicity, sequence features, and physicochemical characteristics.

MATERIALS AND METHODS: Five AMPs—LL-37, HBD-3, Indolicidin, TemporinA, and Pexiganan—were retrieved from the Antimicrobial Peptide Database (APD3). Allergenicity predictions were conducted using AllerTOP v2.0 and AllergenFP v1.0 servers. Physicochemical properties including molecular weight, isoelectric point, instability index, hydrophobicity, and half-life were computed via the ExPASy ProtParam tool. Sequence comparisons and simple pairwise alignments were performed to identify common motifs and similarities.

RESULTS AND DISCUSSION: Peptide lengths ranged from 13 to 45 amino acids. Indolicidin and Temporin A were the shortest and rich in hydrophobic residues such as tryptophan, leucine, and phenylalanine. In contrast, HBD-3 exhibited a complex structure with multiple cysteine residues capable of forming disulfide bonds. Allergenicity predictions classified Indolicidin, Pexiganan, and LL-37 as non-allergens, while Temporin A showed moderate allergenic potential. Except for HBD-3, all peptides had instability indices below 40, indicating potential structural stability under experimental conditions. Sequence analysis revealed notable similarities between LL-37 and Pexiganan in charged and hydrophobic regions, suggesting their suitability for novel peptide design. This bioinformatic analysis highlights Indolicidin and Pexiganan as promising antimicrobial peptide candidates due to their non-allergenicity, structural stability, and favorable physicochemical profiles. These findings provide a foundation for targeted design and development of recombinant peptides in future preclinical studies.

Keywords: antimicrobial peptides, allergenicity

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Keywords: antimicrobial peptides, allergenicity

Bioinformatics Analysis of Antimicrobial Peptides' Impact on Diseases

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BACKGROUND AND OBJECTIVES: Antimicrobial peptides (AMPs) are natural molecules capable of inhibiting the growth and proliferation of pathogens. Due to their selective toxicity and low side effects on human cells, AMPs are considered promising alternative therapies for infectious diseases. Bioinformatics offers powerful tools to analyze the interactions between AMPs and their biological targets, helping to simulate their potential therapeutic effects.

MATERIALS AND METHODS: In this study, antimicrobial peptides were retrieved from bioinformatics databases. Their interactions with bacterial and viral targets were modeled using molecular docking, molecular dynamics simulations, and predictive computational tools. Structural and functional analyses of these peptides were performed to assess their therapeutic potential.

RESULTS AND DISCUSSION: Our results revealed significant differences among AMPs in their effectiveness against various microbial strains. Some peptides demonstrated strong antimicrobial activity and were also predicted to modulate host immune responses, exhibiting anti-inflammatory and antioxidant properties. This study highlights the critical role of antimicrobial peptides in combating infectious diseases and emphasizes the utility of bioinformatics approaches in modeling and predicting their biological effects. These findings pave the way for developing novel AMP-based therapeutic strategies.

Keywords: Antimicrobial Peptides, Bioinformatics, Molecular Modeling, Alternative Therapy, Infectious Diseases, Simulation

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Bioinformatics Analysis of Epstein-Barr Virus (EBV) Infection Impact on Esophageal Cancer

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BACKGROUND AND OBJECTIVES: Introduction Epstein-Barr Virus (EBV) infection has been implicated in the pathogenesis of various malignancies. Recent evidence suggests a potential role for EBV in the progression of esophageal cancer (EC). Bioinformatics approaches enable the identification of molecular mechanisms and key regulatory pathways involved.

MATERIALS AND METHODS: Methods Public gene expression datasets related to EBV-infected and non-infected esophageal tissue samples were analyzed. Differentially expressed genes (DEGs) were identified using GEO2R. Functional enrichment analyses, including Gene Ontology (GO) and KEGG pathway analysis, were conducted. Protein-protein interaction (PPI) networks were constructed using STRING and visualized with Cytoscape.

RESULTS AND DISCUSSION: Results Analysis revealed significant upregulation of immune-related and oncogenic pathways in EBV-infected samples. Key genes such as TP53, CDK1, and MYC showed altered expression. PPI network analysis highlighted central hub genes that could serve as potential therapeutic targets. Conclusion Our bioinformatics analysis indicates that EBV infection may enhance tumorigenic processes in esophageal cancer by modulating critical gene networks and signaling pathways. These findings may assist in developing novel diagnostic and therapeutic strategies.

Keywords: Keywords: Epstein-Barr Virus, Esophageal Cancer, Bioinformatics, Differential Gene Expression, PPI

Bioinformatics-Driven Design of Phage Therapy Against Antibiotic-Resistant Pseudomonas aeruginosa

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BACKGROUND AND OBJECTIVES: Pseudomonas aeruginosa is an opportunistic pathogen with high levels of antibiotic resistance, presenting significant clinical treatment challenges. Phage therapy using strictly lytic bacteriophages has emerged as a promising alternative to combat multidrug-resistant infections. This review explores the role of bioinformatics in the design and optimization of phage therapy against P. aeruginosa.

MATERIALS AND METHODS: We reviewed key bioinformatics tools for phage genome discovery, annotation, and characterization — including PHASTER, VIBRANT, VirSorter, and PHANOTATE — and applied them to a case study using a P. aeruginosa phage genome retrieved from the GenBank database. ORFs were predicted and annotated using PHANOTATE and standard pipelines, while prophage regions and viral origin were confirmed using PHASTER, VIBRANT, and VirSorter.

RESULTS AND DISCUSSION: Genome analysis revealed multiple open reading frames encoding typical phage structural proteins (e.g., capsid, tail) and lytic enzymes. Importantly, no integrase or lysogeny-related genes were detected, indicating a strictly lytic lifestyle. Furthermore, no known toxin or antibiotic resistance genes were found, supporting the phage's safety and therapeutic potential. This study demonstrates that bioinformatics tools can rapidly and accurately assess phage genomes, ensuring the absence of undesirable genetic elements. Integrating such computational approaches enhances the efficiency and safety of selecting phage candidates for therapy against antibiotic-resistant P. aeruginosa infections.

Keywords: Pseudomonas aeruginosa, bioinformatics, phage therapy, PHASTER, VirSorter, PHANOTATE

Biomacromolecule Hydrogels Targeting MDR Biofilms: Insights from Iranian Isolates and Natural Compounds

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BACKGROUND AND OBJECTIVES: Multi-drug resistant (MDR) biofilm infections caused by pathogenic bacteria such as Pseudomonas aeruginosa and Staphylococcus aureus are a growing clinical challenge in Iran, especially in chronic wounds and hospital-acquired infections. Recent advances in biomacromolecule-based hydrogels—such as alginate, chitosan, and gelatin—offer promising platforms for localized antimicrobial delivery and targeted biofilm disruption. Incorporating natural antimicrobial agents, particularly those from endemic Iranian medicinal plants and phytochemicals (e.g., thyme essential oils, saffron derivatives, phenolics), has gained increasing attention for their synergistic anti-biofilm effects and reduced cytotoxicity.

MATERIALS AND METHODS: This work synthesizes evidence from the latest international and local peer-reviewed studies (2019–2025) regarding hydrogel formulation, mechanisms of action, and efficacy against MDR biofilms of Iranian clinical isolates. Key focus is given to composite hydrogels incorporating plant-based antimicrobials and their evaluation in in vitro and ex vivo infection models representing wound, burn, and implant-associated infections.

RESULTS AND DISCUSSION: Recent studies demonstrate that hybrid hydrogels loaded with local phytochemicals significantly impair biofilm formation, enhance antibiotic penetration, and diminish MDR pathogen viability in Iranian isolates. Notably, alginate-chitosan formats infused with thyme or saffron extracts have shown marked efficacy against clinical strains resistant to conventional antibiotics. Cytocompatibility assays and preclinical wound models support the safety and translational potential of these systems in Iranian patient populations. Localized delivery systems based on biomacromolecular hydrogels enriched with indigenous plant-derived antimicrobials represent a potent and innovative strategy for the control of MDR biofilm infections in Iran. Further translational and clinical research is essential to optimize formulations for widespread therapeutic implementation and commercialization.

Keywords: Hydrogels,Multi-Drug Resistance,Biofilm,Iranian clinical isolates,Chronic Wound Infections

Biopreservation of Food Using Probiotics: Approaches, Applications, and Challenges

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BACKGROUND AND OBJECTIVES: E-mail: nastaran_farzi@yahoo.com Biopreservation, defined as the use of beneficial microorganisms and/or their bioactive metabolites to enhance the safety and extend the shelf life of foods, is recognized as a sustainable and environmentally friendly alternative to chemical preservatives.

MATERIALS AND METHODS: This approach aligns with the global trend toward "clean-label" and minimally processed products and, beyond preservation, can offer functional health benefits to consumers. Among biopreservatives, probiotics—particularly lactic acid bacteria (LAB) and bifidobacteria—are the most widely applied due to their Generally Recognized As Safe (GRAS) status, antimicrobial properties, and nutritional benefits. These microorganisms can inhibit a wide range of foodborne pathogens, including Listeria monocytogenes, Salmonella enterica, Escherichia coli O157:H7, Staphylococcus aureus, Clostridium botulinum, and Bacillus cereus.

RESULTS AND DISCUSSION: They are also effective against spoilage bacteria such as Pseudomonas fluorescens, Shewanella putrefaciens, and Brochothrix thermosphacta, as well as spoilage molds and yeasts like Aspergillus spp. and Candida spp. Their preservative effects result from multiple mechanisms, including production

Keywords: Biopreservation, Probiotics, Postbiotics, Lactic Acid Bacteria, Bacteriocins, Nonthermal Processing, Food

Biosynthesis, Characterization, Anti-Biofilm Activity of CuO Nanoparticles using Ephedra major Plant Extract against Pseudomonas aeruginous

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BACKGROUND AND OBJECTIVES: Nanoparticles are nanometer particles that have unique properties and are used in various fields such as medicine, environment, and technology. The Ephedra major plant, with its medicinal properties, is a rich source for extracting molecules that can be used as agents for the biosynthesis of nanoparticles and improve their properties. The aim of study was the biosynthesis of copper oxide nanoparticles (CuONPs) using E major , as well as the evaluation of their anti-biofilm activity against P aeruginosa.

MATERIALS AND METHODS: CuO Nps were synthesized using E major plant extract. The synthesized nanoparticles were evaluated by (SEM) and (FTIR). MIC and MBC of the synthesized nanoparticles were determined in 96-well microplates with different concentrations of CuO nanoparticles and aqueous extract. Inhibition of P.aeruginosa biofilm was investigated by staining with 1% crystal violet.

RESULTS AND DISCUSSION: The results of the UV-Vis analysis showed that the absorption at the wavelength of 385 nm was the highest, which confirmed the formation of CuO-NPs. SEM and EDX results indicated that the nanoparticles formed in a spherical shape with an average size of 30 to 80 nm. Also, EDX analysis showed the presence of copper, carbon, and oxygen elements in nanoparticles. The (MIC) and (MBC) of Nps were 312 µg/ml. In addition, the results showed that CuO-NPs have an effect in inhibiting biofilm formation.The inhibitory effect against biofilm was greater with increasing concentration. this study prove that CuO-NPs synthesized can be used as an effective option in treating anti-biofilm caused by P. aeruginosa

Keywords: Antibiofilm.; Copper oxide nanoparticles; Ephedra major; Pseudomonas

Biosynthesis, Characterization, Antibacterial Activity of CuO Nanoparticles using Ephedra major Plant Extract against Pseudomonas aeruginosa

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BACKGROUND AND OBJECTIVES: Nanoparticles are nanometer particles that have unique properties and are used in various fields such as medicine, environment and technology. The plant Ephedra major, with its medicinal properties, is a rich source for extracting molecules that can be used as agents for the biosynthesis of nanoparticles and improving their properties. The aim of study was the biosynthesis of copper oxide nanoparticles (CuONPs) using E.major and evaluation of their antibacterial activity against P.aeruginosa.

MATERIALS AND METHODS: The synthesis of CuO_Nps was using the aqueous extract of E major. The synthesized nanoparticles were evaluated by scanning electron microscopy (SEM) and Fourier transform infrared spectroscopy (FTIR). The well diffusion method investigated the antimicrobial activity of synthesized CuO-NPs against P.aeruginosa. Then, the MIC and MBC of the synthesized nanoparticles were determined in 96-well microplates with different concentrations of CuO-NPs, aqueous extract, and chloramphenicol

RESULTS AND DISCUSSION: The results of the UV-Vis analysis showed that the absorption at the wavelength of 385 nm was the highest, which confirmed the formation of CuO-NPs. SEM and EDX results indicated that the nanoparticles formed in a spherical shape with an average size of 30 to 80 nm. Also, EDX analysis showed the presence of copper, carbon, and oxygen elements in nanoparticles. The CuO-PNs at the concentration of 2000 µg/ml exhibited a significant inhibitory effect against P. aeruginosa. Also, the (MIC) and (MBC) of Nps were 312 µg/ml. This study prove that CuO-NPs synthesized can be used as an effective option in treating infections caused by P. aeruginosa.

Keywords: Antibacterial; Copper oxide nanoparticles; Ephedra major; Pseudomonas

Biotics: Changing the Paradigm of Caries Prevention by Engineering the Oral Microbiome

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BACKGROUND AND OBJECTIVES: Dental caries remains a prevalent global health issue, primarily driven by a dysbiotic oral microbiome favouring acidogenic and aciduric bacteria. Conventional prevention strategies—such as broad-spectrum antimicrobials and mechanical plaque removal—pose limitations due to ecological disruption and lack of sustainability. This review explores a paradigm shift toward microbiome engineering using biotics to promote a stable, health-associated oral microbiota resilient to cariogenic challenges.

MATERIALS AND METHODS: A comprehensive literature review was conducted to evaluate the mechanistic roles and clinical relevance of probiotics (live beneficial microbes), prebiotics (selective microbial substrates), synbiotics (probiotic-prebiotic combinations), and postbiotics (non-viable microbial components or metabolites) in caries prevention.

RESULTS AND DISCUSSION: Evidence supports that certain probiotics antagonize cariogenic pathogens through competitive exclusion, bacteriocin production, and coaggregation inhibition. Prebiotics, such as specific oligosaccharides, selectively enhance the growth of beneficial species like Streptococcus sanguinis and Akkermansia, which help regulate pH and inhibit pathogen colonization. Synbiotics demonstrate synergistic effects by improving probiotic survival and efficacy. Postbiotics, including bacteriocins, cell-free supernatants, and enzymes, exhibit antimicrobial, anti-biofilm, and immunomodulatory activities without the need for viable organisms, addressing delivery and stability limitations. Together, these biotic strategies offer a shift from pathogen suppression to precision microbiome modulation. By actively shaping the microbial ecosystem, biotics represent a promising cornerstone for sustainable, long-term caries prevention.

Keywords: Probiotics, Prebiotics, Synbiotics, Postbiotics, Oral Microbiome, Dental Caries

Brucella spp. isolation in dairy cattle farms in Tehran, Iran

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BACKGROUND AND OBJECTIVES: Brucellosis is a common zoonotic disease, which consider as a challenging issue for humans and livestock in developing countries like Iran. Brucella abortus is a highly prevalent species in cattle, and Brucella melitensis can sometimes cause Bovine brucellosis. Control programs of Bovine brucellosis are recommended in enzootic areas with high prevalence rates. Isolation of Brucella spp from infected herds, and rapid removal and slaughter, is one of most crucial controls or eradication of brucellosis. The aim of this study is to identify the Brucella species circulating among cattle slaughtered in the Tehran slaughterhouses

MATERIALS AND METHODS: A total of 174 cattle lymph node samples since March 2023. Samples were collected from Tehran, Iran, and analysed by culture. All isolated bacteria were subjected to phage typing and AMOS PCR analysis

RESULTS AND DISCUSSION: The prevalence of Brucella abortus biovar 3, Brucella abortus biovar CONCLUSION Since brucellosis is endemic in Iran, controlling it remains challenging. Accordingly, the early detection of Brucella species by accurate and fast diagnosis laboratory assays such as culturing, serology, and molecular analysis in high-risk farms and slaughterhouses is crucial.

Keywords: Keywords: Brucella melitensis, Brucella abortus, Brucellosis.

Can Chat GPT and Other Pretrained Language Models Function as Competent Bacteriologist?

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BACKGROUND AND OBJECTIVES: This study evaluates the effectiveness of ChatGPT, a widely known AI language model, in answering bacteriology questions compared to veterinary students. Bacteriology is a critical and complex subject in veterinary education, often challenging due to its vast content and diagnostic methods. A descriptive cross-sectional survey with 9 multiple-choice questions was given to 100 randomly selected veterinary graduate students at the University of Tehran. ChatGPT's answers were compared to student responses using chi-square and descriptive statistics. The results showed that ChatGPT performed comparably or better than most students. Despite occasional AI hallucinations, its consistent accuracy suggests ChatGPT can be a valuable educational aid when guided by experts.

MATERIALS AND METHODS: This descriptive cross-sectional study involved 100 doctoral veterinary students at the University of Tehran. A 9-question multiple-choice questionnaire was developed with the advice of experts and validated using Cronbach's alpha. The questions were asked in both Persian and English. Students completed the questionnaire, and their responses were compared with those of the latest version of ChatGPT (GPT-4). The results were statistically analyzed using SPSS software and chi-square tests to assess the consistency and reliability of performance.

RESULTS AND DISCUSSION: The analysis showed that ChatGPT answered the majority of bacteriology questions correctly, performing comparable to or better than 83% of students. The AI tool showed consistent accuracy in both languages, indicating its ability to process scientific content in a multilingual context. However, certain limitations such as possible hallucinations or overconfident incorrect answers were observed.

Keywords: ChatGPT, Bacteriology, Veterinary Education, Artificial Intelligence, Microbiology, Medical Training

Carbapenem Resistance on the Rise: A Two-Year Surveillance of E. coli and A. baumannii in Trauma Wound Infections

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BACKGROUND AND OBJECTIVES: Wound infections caused by multidrug-resistant Gram-negative bacteria, particularly Escherichia coli and Acinetobacter baumannii, represent a major threat to trauma care. This study assessed changes in prevalence and resistance patterns of these pathogens over two consecutive years in two tertiary trauma hospitals in northeastern Iran.

MATERIALS AND METHODS: Microbiological data were retrospectively reviewed from Velayat and Kamyab Hospitals during 1402 (2023–2024) and 1403 (2024–2025). Resistance rates to imipenem, meropenem, and piperacillin–tazobactam were compared in wound isolates.

RESULTS AND DISCUSSION: In Velayat Hospital, E. coli wound isolates increased from 85 to 126, and A. baumannii from 57 to 103. E. coli resistance to imipenem remained stable at 21%, while meropenem resistance increased from 12% to 16%. Notably, piperacillin–tazobactam resistance declined from 44% to 29%, potentially indicating improved antimicrobial stewardship. A. baumannii showed persistently high resistance: imipenem (100%→96%), meropenem (90%→95%), and piperacillin–tazobactam (100%→95%). These findings confirm the critical status of A. baumannii in trauma-related wound infections with extremely limited therapeutic options. Similar resistance rates in Kamyab Hospital highlight a regional resistance trend, possibly driven by shared antibiotic use policies and patient transfers. The marginal improvement in E. coli resistance patterns is encouraging but insufficient. The increasing burden and resistance of E. coli and A. baumannii in trauma wounds demand urgent, regionally coordinated stewardship interventions and enhanced surveillance to prevent treatment failures and reduce transmission of resistant strains.

Keywords: Wound infection, multidrug resistance, Acinetobacter baumannii, Escherichia coli, trauma, carbapenems,

Characterization of Hybrid Enteroaggregative-Uropathogenic (EAEC/UPEC) E. coli Strains in UTIs: Prevalence and Antibiotic Resistance Profiling

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BACKGROUND AND OBJECTIVES: Urinary tract infections (UTIs) are a leading cause of bacterial infections worldwide, with uropathogenic Escherichia coli (UPEC) being the predominant pathogen. Notably, hybrid strains combining UPEC and enteroaggregative E. coli (EAEC) virulence traits have emerged, potentially enhancing pathogenicity and antimicrobial resistance. EAEC, recognized for its robust biofilm formation and intestinal adherence, may contribute to UPEC's evolution through horizontal gene transfer. This study investigates the prevalence and antibiotic resistance profiles of EAEC/UPEC hybrid strains in UTIs, addressing their clinical significance in treatment challenges.

MATERIALS AND METHODS: We analyzed 199 E. coli isolates from UTI patients at Babol University of Medical Sciences. Isolates were cultured in tryptic soy broth (TSB), with DNA extracted for PCR confirmation (uidA gene). Antimicrobial susceptibility was tested via Kirby-Bauer disk diffusion (CLSI guidelines), with extended-spectrum β-lactamase (ESBL) detection using the Combination Disc Test. Virulence genes (aggR, aatA, aap, chuA, fyuA) were amplified and sequenced (Sanger method).

RESULTS AND DISCUSSION: Results: Hybrid EAEC/UPEC strains were identified in 54.8% (17/199) of isolates, all carrying aatA and fyuA (100%), with aapA (88.2%) and chuA (70.6%). Resistance was highest to trimethoprim-sulfamethoxazole (SXT) and nalidixic acid (NA) (94.1% each), cefotaxime (CTX) (82.4%), and ampicillin-sulbactam (SAM) (76.5%), while nitrofurantoin (FM) showed lowest resistance (5.9%). Notably, 47.1% (8/17) were ESBL producers, and 94.1% were multidrug-resistant (MDR). Conclusion: These findings reveal clinically significant EAEC/UPEC hybrids with concerning MDR and virulence potential. Their distinct genetic profile suggests evolution toward treatment-resistant UTIs, highlighting the need for surveillance and alternative treatment strategies.

Keywords: Hybrid E.coli, Urinary Tract Infection, microbial drug resistance, virulence genes

Characterization of Pasteurella multocida collected from pneumonic small ruminants in Sistan & Balouchestan province, Iran

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BACKGROUND AND OBJECTIVES: Pasteurella species are among the frequently-encountered pathogens that are blamed for economically-serious respiratory diseases in small ruminants of all age groups.

MATERIALS AND METHODS: Applying a purposive sampling method, a cross-sectional study was conducted from 31 December 2024 to 2nd January 2025 in Sistan & Balouchestan province, south-eastern Iran, to isolate and identify Pasteurella agents in small ruminants. A total of 83 specimens (nasal swabs) from sheep and goats bearing cough, nasal discharge and/or fever, were collected. These represented 23 farms from Chahbahar (n=9), Hamoun (n=1), Hirmand (n=2), Iranshahr (n=4), Khash (n=7) and Zehak (n= 1) cities. Swabs were processed and used to inoculate blood agar plates on the same collection day to prevent false negative results. The incubated plates (37 °C/18 h) were searched for characteristic Pasteurella multocida and Manheimia haemolytica. The suspected colonies were subjected to further standard biochemical and microbiology identification tests.

RESULTS AND DISCUSSION: Out of the 83 specimens examined, 15 proved positive for P. multocids including 12 (%) from sheep and 3 (%) from goats. Findings of this study showed that P. multocida is the prevailing, if not the only, bacterium that actively operates in small ruminants in the studies region. If penetrating strains from Afghanistan and/or Pakistan through importation of sheep and goats which is a currently a normal husbandry practice in the province, play a role in diversity of P. multocida population, we do not know yet. Work on genomic structure and antimicrobial resistance profiles of the studied local isolates is still ongoing.

Keywords: Pasteurella multocida, Specimen, Sheep, Goat

Characterization of Pasteurella spp from symptomatic and asymptomatic sheep in Alborz province, Iran

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BACKGROUND AND OBJECTIVES: In small ruminants the infections of lower respiratory tract caused by Mannheimia haemolytica, Pasteurella multocida, and Bibersteinia trehalosi is generally called Pasteurellosis. An annual non-compulsory vaccination scheme using a monovalent killed vaccine is used in Iran but the disease is still frequent. This might reflect the need for re-development of a vaccine to include new circulating pathogenic species and strains. The present work was conducted to isolate and identify Pasteurella spp bacteria associated with pneumonic sheep and goats in Alborz province.

MATERIALS AND METHODS: A cross-sectional study was performed from 30 April 2025 to 19 May 2025. Two abattoirs in Karaj plus several sheep and goat flocks were visited for specimen collection. A total of 202 specimens including nasal swabs (n=157) from live animals bearing cough, nasal discharge and/or fever, plus small cuts of lungs (n=45) bearing pasteurellosis-suspected signs were collected. These represented flocks from Karaj, Taliqan, Eshtehard, Kordan, Songhor Abaad, Savojbolagh and also those brought from cities outside the province namely Bijar, Maragheh, Mianeh, Salmas and Bouin Zahra. Swabs and lung cuts were used to inoculate blood agar plates. The incubated plates (37 °C/18 h) were searched for characteristic Pasteurella spp bacteria. The suspected colonies were subjected to further standard cultural, staining, and biochemical tests.

RESULTS AND DISCUSSION: Totally 22 isolates were collected from 202 specimens. These were successfully characterized as M. hemolytica (n=15/68%) and P. multocida (n=7/32%), respectively. These findings reflect importance of considering M. hemolytica in any vaccine re-development against pasteurellosis in small ruminants in Iran.

Keywords: Pasteurella multocida, Mannheimia haemolytica,, Specimen, Sheep, Goat

Characterizing Mycobacterium simiae: Genomic Diversity, Clinical Impact, and Transmission Dynamics

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BACKGROUND AND OBJECTIVES: Non-tuberculous mycobacteria (NTM), including Mycobacterium simiae, Mycobacterium avium complex (MAC), and Mycobacterium abscessus, are emerging pathogens causing pulmonary and extrapulmonary infections, particularly in immunocompromised hosts. M. simiae is a rare NTM with low clinical relevance, but its genomic diversity, transmission routes, and pathogenomic traits remain poorly understood.

MATERIALS AND METHODS: Whole-genome sequencing (WGS) was performed on 33 M. simiae sensu stricto isolates from seven patients (2006–2020), combined with 91 publicly available M. simiae complex genomes. Phylogenetic analysis used concatenated SNPs (112,261 positions) with RAxML, and average nucleotide identity (ANI) was calculated. Plasmid, resistance, and virulence genes were identified using PLSDB and AMRFinderPlus. Clinical data (ATS criteria, radiology, therapy) were correlated with genomic findings. Social network analysis evaluated potential transmission routes.

RESULTS AND DISCUSSION: Genomic Stability and Diversity: M. simiae isolates exhibited remarkable longitudinal stability (0–1 SNP over 14 years) within patients, with no evidence of re-infection. Clusters (12 SNPs) were observed but lacked epidemiological support for human-to-human transmission. Pathogenomic Traits: Resistance genes (*acc(2')-Ic* [aminoglycosides], rgt [rifamycins]) were prevalent, but phenotypic correlations remain uncertain. Plasmids (13/127 isolates) hinted at horizontal gene transfer. Comparative Context: Unlike M. abscessus, M. simiae showed no evidence of dominant circulating clones or hospital outbreaks. Conclusion: M. simiae demonstrates low clinical impact and high genomic stability, with transmission likely environmental. WGS enhances understanding of NTM epidemiology, though resistance gene interpretation requires phenotypic validation.

Keywords: M. simiae, clinical outcomes, and resistance patterns.

Chitosan nanoparticles loaded with cell-free supernatant of Lactobacillus acidophilus as a potential anti-cancer agent against colorectal cancer

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BACKGROUND AND OBJECTIVES: Colorectal cancer (CRC) is the second most common cause of cancer-related fatalities worldwide. Targeting of genes related to CRC signaling pathways is an innovative strategy to combat CRC. This study aimed to investigate the anti-cancer efficiency of chitosan nanoparticles incorporated with the culture supernatant derived from Lactobacillus acidophilus (CTNP-L.a-sup) on genes involved in CRC progression.

MATERIALS AND METHODS: The novel nanodrug was prepared by an ionic gelation procedure and characterized using scanning electron microscopy and dynamic light scattering methods. Protein released and EE (encapsulation efficiency) of CTNP-L.a-sup were calculated via BCA assay. After 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 utilizing the real-time PCR method.

RESULTS AND DISCUSSION: The size distribution and zeta potential of CTNP-L. a-sup were 478.6 nm and -8.9 mV, respectively, with an appropriate morphology. Protein released from CTNP-L. a-sup and EE% were recorded at 76% and 74.6%, respectively. No toxic effects of CTNP-L. a-sup was observed on Caco-2 cells. CTNP-L. a-sup could cause a significant decrease in the expression of TGF-α, β-Catenin, and TGF-β oncogenes by 0.79, 0.42, and 0.16-fold, respectively, while leading to a significant increase in PTEN and Caspase9 gene expression by 42.19 and 114.39-fold, respectively. To conclude, targeting genes associated with CRC signaling pathways presents an innovative approach to combat CRC, which may potentially enhance the life expectancy of CRC patients.

Keywords: Anti-cancer, Chitosan nanoparticle, Cell-free supernatant, Colorectal cancer, Lactobacillus acidophilus

Chlamydia-Induced Pathogenesis Leading to Reactive Arthritis: Molecular Mechanisms and Clinical Implications

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BACKGROUND AND OBJECTIVES: Reactive arthritis (ReA) can arise following an infection with Chlamydia trachomatis, a prevalent sexually transmitted infection (STI). C. trachomatis is a key etiological agent in ReA, triggering immune-mediated joint inflammation after an initial infection in the gastrointestinal, genitourinary, or mucosal systems. Unlike direct infectious arthropathy, ReA is an immunological response and is non-contagious. Other bacterial pathogens, such as Salmonella and Shigella, may also contribute to post-infectious ReA.

MATERIALS AND METHODS: This systematic review analyzed a comprehensive selection of peer-reviewed articles, scholarly books, and authoritative sources published between 2000 and 2025. Relevant studies were retrieved from established scientific databases, including high-impact research pertinent to the subject matter. Expert consultation was conducted with Dr. Majid Alikhani, a distinguished specialist in the field, to provide critical insights and validate key findings, enhancing the credibility and depth of this review.

RESULTS AND DISCUSSION: Research has identified C. trachomatis within the synovial tissue of affected individuals, suggesting bacterial persistence may drive chronic inflammation. The immune system may erroneously recognize certain bacterial proteins as self-antigens, exacerbating autoimmune responses. Due to its often-asymptomatic presentation, C. trachomatis infection can evade timely diagnosis, leading to disease progression and joint damage. Genetic predisposition, particularly the HLA-B27 allele, further increases susceptibility to ReA.Not all individuals with C. trachomatis infection develop ReA, with disease onset influenced by genetic factors, timely detection, and appropriate treatment. Early intervention, including targeted antimicrobial therapy, is crucial in preventing chronic synovitis and structural joint complications by reducing bacterial persistence and aberrant immune activation.

Keywords: Chlamydia pneumoniae ,Chlamydia trachomatis, Reactive Arthritis, Sexually Transmitted Diseases, Disease

Chronic Urticaria in patients with the yeasts overgrowth in gastro-intestinal tract

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BACKGROUND AND OBJECTIVES: Urticaria is a reaction pattern that represents cutaneous mast cell degranulation, with the condition being defined as chronic if lesions recur for longer than 6 weeks. Considering the high incidence of chronic urticaria among the patients with colonization of yeasts in gastro-intestinal tract, we investigated all fungal colonization and invasion in the gastro-intestinal tract of cases involved hives. Our aim was identification of all isolates in the level of species.

MATERIALS AND METHODS: Our subjects included 200 cases with long time superficial lesions as Urticaria. Fresh stool sample from the cases with clinical symptoms were collected. A direct microscopic investigation performed for the detection of fungal growth in gastro-intestinal tract. The basic culture on sabouraud glucose agar used for confirming of the fungal detection. The Molecular methods and proteomic based MALDI-TOF system used for the identification of all fungal isolates.

RESULTS AND DISCUSSION: The highest age range of our cases was 40-50 and included 25% of all. Women and men similarly involved (12 each). Our findings of microscopic investigation included budding cells in 13(54.2%) cases, blastospores 6(25%), arthrospores 3(12.5%) and pseudohypha 2(8.3%). Total of 24 fungal isolates, 7 (29.2%) cases of Geotrichum silvicola, 7 (29.2%) Candida albicans and 6(25%) Candida glabrata were the most frequent identified by MALDI-TOF system. Other yeast included C. Africana, C. tropicalis and C. glabrata one each. Only one unknown case by MALDI-TOF system recorded. A variable species of yeast fungi which are commensally live in human gastro-intestinal tract are potentially candidate of causing agent for chronic Urticaria.

Keywords: Hives, Candida, Geotrichum, idenfication

Cinnamon extract synergizes with carbapenems against MBL-producing Acinetobacter baumannii: A promising adjunct therapy for burn wound infections

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BACKGROUND AND OBJECTIVES: The global emergence of metallo-β-lactamase (MBL)-producing Acinetobacter baumannii, particularly in burn wound infections, necessitates alternative therapies. This study evaluated the efficacy of Allium sativum (garlic), Cinnamomum verum (cinnamon), and Zingiber officinale (ginger) extracts against MBL-producing A. baumannii.

MATERIALS AND METHODS: We collected 100 A. baumannii isolates from burn patients (Shahid Motahari Hospital, Tehran). MBL production was phenotypically confirmed by combination disk diffusion test and genotyped for blaIMP, blaVIM, blaNDM. Acetonic, methanolic, and chloroformic extracts were tested for MIC/MBC via broth microdilution. FIC indices predicted extract-carbapenem synergy.

RESULTS AND DISCUSSION: All isolates were resistant to ciprofloxacin/cephalosporins; 98% were carbapenem-resistant. Phenotypic screening identified 87.7% as MBL producers, though only 2.3% harbored blaIMP. Chloroformic cinnamon extract showed the lowest MICs (0.78–12.5 mg/mL), with MBCs matching MICs (bactericidal activity). Garlic and ginger extracts exhibited MICs of 3.12–12.5 mg/mL. Computational FIC analysis predicted synergy for cinnamon-chloroform with imipenem (FIC=0.375) and meropenem (FIC=0.406), and borderline synergy for garlic-imipenem (FIC=0.5). Chloroformic cinnamon extract demonstrates potent activity against MBL-producing A. baumannii, with predicted synergy with carbapenems. These plant extracts represent promising adjunct therapies for multidrug-resistant infections, particularly in resource-limited settings.

Keywords: Beta-lactamases, Acinetobacter baumannii, Anti-Bacterial Agents, Plant Extracts, Drug Resistance

Cloning of the pectinase enzyme gene isolated from Bacillus

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BACKGROUND AND OBJECTIVES: Pectinases are important industrial enzymes and have various applications in different industries such as food, textiles, beverages, pulp and paper, and biofuel industries. Microbial pectinases account for 25% of the scale of food and industrial enzymes worldwide. The aim of this research is to clone the pectinase enzyme gene in a host to provide conditions for its industrial use.

MATERIALS AND METHODS: The pectinase gene that had been amplified by PCR was purified from the gel after electrophoresis using the QIAGEN gel extraction kit, and then it was inserted into the Pjet1.2/blunt vector using the CloneJET PCR Cloning kit from Thermo Scientific. After competenting the E.coli host, the desired vector was transformed into the host. Several of the colonies that grew on plates were selected for colony-PCR and confirmation of gene insertion, and then the results were analyzed using electrophoresis.

RESULTS AND DISCUSSION: Results: The result of the gel purification was examined by electrophoresis and the desired band was observed clearly. The colonies grew well on the plate containing the ampicillin, indicating the positive result of vector transformation to the host. In the colony-PCR, which was performed with both the gene's own primers and the vector sequencing primers, the pectinase gene band, which was about 1500 base pairs, was observed in the electrophoresis, indicating the presence of the desired gene in the vector. Conclusion: In this research, the cloning of the pectinase enzyme gene was successfully carried out and is ready for use in subsequent processes.

Keywords: food enzymes, industrial enzymes, pectinase, Bacillus, E-Coli, cloning

Clostridium difficile and Strongyloides stercoralis infections in patients with Active inflammatory bowel disease: A Cross-Sectional Study from Guilan, Iran

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BACKGROUND AND OBJECTIVES: Clostridium difficile (C. difficile) and Strongyloides stercoralis (S. stercoralis) infections are commonly reported in patients with inflammatory bowel disease (IBD), and their presence can significantly increase mortality if not diagnosed promptly. This study aimed to investigate the prevalence, diagnostic approaches, and associated factors of these infections in Active IBD patients

MATERIALS AND METHODS: This cross-sectional descriptive study included 70 patients with Active IBD hospitalized in the gastroenterology ward of Razi Hospital, Rasht, Guilan, Iran. Demographic and clinical information was collected using a researcher-made questionnaire. Blood and stool samples from all participants were analyzed for detecting C. difficile antigen and S. stercoralis antibodies by ELISA. Statistical analysis was performed using SPSS version 27

RESULTS AND DISCUSSION: The average age of IBD onset among participants was 36.6 ± 14.25 years, with 57.1% being female. Of the participants, 80% had ulcerative colitis. The prevalence of C. difficile infection was 5.3%, while S. stercoralis infection was found in 7.1% of the cases. There were no significant differences between type of IBD and infection status, and also between infection status and laboratory data (P 0.05). Conclusion: Early diagnosis of C. difficile and S. stercoralis infections is critical to prevent severe complications of IBD. Immunoassay methods, such as ELISA, are recommended for rapid and accurate diagnosis of these infections in IBD patients

Keywords: Inflammatory bowel disease, Clostridium difficile, Strongyloides stercoralis, ELISA

Coexisting of virulence factor genes and beta-lactamase genes from Escherichia coli isolated from blood cultures of patients with leukemia

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BACKGROUND AND OBJECTIVES: Background: It is well-documented that chemotherapy and aggressive conditioning treatments before HSCT can lead to mucosal injury, weakened immune system, and low levels of neutrophils, all of which increase the risk of developing bloodstream infections (BSI). Patients with blood cancer have a higher likelihood of getting infections from Enterobacteriaceae bacteria that produce ESBL, which is concerning because these bacteria are resistant to many antibiotics. The infections, especially those in the bloodstream, can result in worse outcomes and higher death rates among this group of vulnerable individuals

MATERIALS 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 two Iranian medical centers . The presence of virulence factor genes and beta-lactamase genes was examined by polymerase chain reaction (PCR).

RESULTS AND DISCUSSION: Results The results showed diversity in the virulence profiles among the isolates and co-existence between different virulence factors and antibiotic resistance was investigated. The most Coexistence of bla SHV and traT , bla CTX-M and traT was observed 93.3%(14/15), 91.3%(21/23), respectively. It was observed that bla SHV, bla CTX-M encoding gene was highly correlated with different virulence factor encoding genes including traT, iutA and afaA ,hlyA. Conclusion A significant association between certain virulence factors and beta-lactamase genes was observed. Antibiotic stewardship programs, antimicrobial treatment and measures for infection control should be effectively implemented especially in hospitals to limit the spread of such highly virulent pathogens.

Keywords: virulence factor genes, beta-lactamase genes , Escherichia coli, leukemia

Collaboration of clinical laboratory supervisors and practitioners in susceptibility testing and choice of antibiotics, at a glance

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BACKGROUND AND OBJECTIVES: Clinical laboratory supervisors and practitioners are in charge of choosing the best antibiotics for managing infectious diseases. The prescription of antibiotic is best when there is reasonable collaboration between these two healthcare sectors. The result of such collaboration, would be the reduction of unnecessary antibiotic prescription, fewer side effects, and a reduction in the global spread of antibiotic resistance. This collaboration between clinical practitioners and lab supervisors, which has been called "from the bench to the bedside" for decades, results in the best choice of antibiotic therapy. This is feasible when there is an understanding of the available tests between these two parties. This tackles many obstacles in managing infectious diseases. Clinical Laboratory Techniques; General Practitioners; Drug Resistance, Microbial

MATERIALS AND METHODS: None

RESULTS AND DISCUSSION: None

Keywords: Clinical Laboratory Techniques; General Practitioners; Drug Resistance, Microbial

Colorimetric Au-Nanoprobe Biosensor for One-Step Visual Detection of Canine Parvovirus

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BACKGROUND AND OBJECTIVES: Canine Parvovirus (CPV) is a critical global threat to canine health. Its 90% mortality in untreated cases and explosive spread in high-density settings (e.g., shelters/kennels) pose major veterinary and economic challenges. Rapid viral detection is essential. While PCR offers high sensitivity, its need for thermocyclers and multi-hour processing limits field use. Gold nanoparticle (AuNP)-based biosensors offer a fast, cost-effective alternative for CPV detection. In this project, we have developed an AuNP-based biosensor targeting CPV genetic material.

MATERIALS AND METHODS: Ten PCR-confirmed CPV-positive samples were obtained from veterinary hospitals of Tehran. All globally reported CPV nucleotide sequences were obtained from NCBI database. The obtained sequences were aligned to identify conserved regions. Four complementary probes (that can attach to the conserved regions of CPV DNA) were designed, conjugated to AuNPs, and added to infected/CPV-free samples. For optimal probe-target binding, samples were incubated at 60°C for 20 min. Optical absorption was measured spectrophotometrically (400–700 nm).

RESULTS AND DISCUSSION: The biosensor successfully differentiated CPV^+ and CPV^- samples. CPV^+ samples showed peak absorption at 524 nm, while CPV^- samples exhibited a visible color shift (red to black). This biosensor can rapidly detect all known CPV strains in suspected samples.

Keywords: Biosensor, Canine Parvovirus, Gold nanoparticle, AuNP

Combating Pseudomonas aeruginosa Antibiotic Resistance Using Platinum Nanoparticles Synthesized from Lawsonia inermis

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BACKGROUND AND OBJECTIVES: The increasing prevalence of multidrug-resistant (MDR) pathogens, particularly Pseudomonas aeruginosa, has created an urgent need for novel antimicrobial agents. Platinum nanoparticles (PtNPs) possess potent biological activity, but conventional synthesis methods are often toxic and environmentally harmful. This study investigates the green synthesis of PtNPs using Lawsonia inermis leaf extract and evaluates their antimicrobial and antioxidant efficacy.

MATERIALS AND METHODS: PtNPs were synthesized by reacting aqueous L. inermis extract with a platinum salt solution. The synthesis was confirmed via a visible color change and UV–Vis spectroscopy, showing a peak at 330 nm. Antioxidant activity was assessed using the DPPH assay, while antimicrobial activity was evaluated using the disk diffusion method, minimum inhibitory concentration (MIC), and minimum bactericidal concentration (MBC) against a clinically relevant MDR strain of P. aeruginosa. Bacterial growth inhibition was further analyzed through OD-based growth curves.

RESULTS AND DISCUSSION: The synthesized PtNPs showed a notable increase in antioxidant activity (EC_{50} = 230.8 mg/mL) compared to the crude extract (EC_{50} 1000 mg/mL). PtNPs also exhibited significantly stronger antibacterial activity (MIC = 0.625 mg/mL, MBC = 0.3125 mg/mL) than the extract alone. Disk diffusion results confirmed enhanced inhibition zones at lower concentrations of PtNPs. Growth curve analysis demonstrated the superior bacteriostatic effect of PtNPs over L. inermis extract.This study presents a green, cost-effective, and eco-friendly method for PtNP synthesis using L. inermis, resulting in a nanoformulation with strong antioxidant and antimicrobial activity. These findings highlight importance of plant-mediated PtNPs as alternative therapeutics against MDR P. aeruginosa.

Keywords: Platinum nanoparticles (PtNPs), Lawsonia inermis, Pseudomonas aeruginosa, Antibacterial activity, Antioxidant

Comparative Analysis of Anti-PIA/PNAG Antibodies on Biofilm Formation by Staphylococcus epidermidis and Escherichia coli

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BACKGROUND AND OBJECTIVES: 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 made an exopolysaccharide, poly-β(1,6)-N-acetylglucosamine (PNAG), 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.

MATERIALS 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 AND DISCUSSION: PIA was confirmed by FTIR, NMR, and colorimetry. Immunization induced strong antibody responses, showing opsonic activity (60% in S. epidermidis, 40.48% in E. coli) and elevated IgG titers. Biofilm inhibition was significant in immunized groups compared with controls, especially after the first injection and third booster dose. This study found that serum from PIA-immunized mice significantly reduced biofilm formation in S. epidermidis and E. coli compared to unimmunized controls, especially after the first injection and third boost. The antibodies also showed opsonic properties for both bacteria. Further research in other animal models is needed to explore the simultaneous effects of these antibodies on infections caused by both bacteria.

Keywords: Staphylococcus epidermidis, Escherichia coli, Immunization, PIA, PNAG

Comparative Analysis of Probiotic Diversity and Bioinformatic Profiles in Fish from the Caspian Sea and the Southern Waters of Iran

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BACKGROUND AND OBJECTIVES: Probiotics are live microorganisms that, when administered in adequate amounts, confer health benefits to the host. In marine ecosystems particularly within the microbiota of fish there exists a diverse population of potential probiotic bacteria with wide-ranging applications in food, pharmaceutical, and aquaculture industries. This review aims to compare the diversity of probiotic bacteria identified in fish from the Caspian Sea with those from the southern waters of Iran (the Persian Gulf and the Gulf of Oman), emphasizing bioinformatics-based metabolic and genomic insights.

MATERIALS AND METHODS: This study is based on a systematic review of scientific publications from reputable national and international databases over the past decade. Additionally, bioinformatic tools and databases such as NCBI, KEGG, and antiSMASH were used to analyze bacterial genomes, metabolic pathways, and secondary metabolite biosynthesis.

RESULTS AND DISCUSSION: In Caspian Sea fish, species such as Lactobacillus plantarum, Carnobacterium divergens, and Pediococcus acidilactici are most prevalent. In contrast, fish from southern waters host dominant strains such as Bacillus subtilis, Shewanella putrefaciens, and Enterococcus faecium. Genomic and metabolic analyses reveal that northern isolates tend to produce antibacterial compounds such as bacteriocins, whereas southern strains are more associated with antioxidant activity and growth-promoting effects. Geographic and environmental differences appear to significantly influence the composition and functional capabilities of fish-associated probiotics. Leveraging this information can enhance the selection and application of native probiotic strains in aquaculture development and food safety strategies.

Keywords: Probiotics, Fish microbiota, Caspian Sea, Persian Gulf, Secondary metabolites,

Comparative Antibacterial Activity of Free and Alginate-Encapsulated Cordyceps militaris Extract Against Multidrug-Resistant Pathogens

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BACKGROUND AND OBJECTIVES: Cordyceps militaris is a medicinal mushroom whose most important bioactive compound is polysaccharides, which give it strong antimicrobial and therapeutic effects. While encapsulation can improve extract stability, the free extract is often more effective due to faster absorption, making it useful against drug-resistant pathogens

MATERIALS AND METHODS: C.militaris extract was obtained via Soxhlet extraction with ethanol and encapsulated into alginate nanoparticles using ionic gelation. The nanoparticles were characterized by size, zeta potential, PDI, encapsulation efficiency, and loading capacity. Their antimicrobial activity was tested against several pathogens, including Escherichia coli, Staphylococcus aureus, Shigella dysenteriae, Salmonella typhimurium, and Candida albicans, with MIC and MBC values determined. Drug release was studied using a dialysis bag under simulated gastric and intestinal conditions

RESULTS AND DISCUSSION: The alginate nanoparticles had an average size of 254 nm, a zeta potential of -20.6 mV, and a polydispersity index (PDI) of 0.42. Encapsulation efficiency and loading capacity were 89.1% and 15.12%, respectively. The encapsulated extract demonstrated antimicrobial activity comparable to that of the free extract (MIC: 12.5–25 mg/mL; MBC: 25–50 mg/mL). Moreover, the encapsulated form showed enhanced stability under simulated gastric and intestinal conditions, suggesting improved protection and sustained release of the active compounds in the digestive tract. The free and encapsulated sections of C.militaris extract both showed equivalent antimicrobial properties, meaning that encapsulation does not affect biological activity. Additionally, the encapsulation process greatly improves the stability of the extract, suggesting it could be a great approach for improving shelf-life and therapeutic efficacy.

Keywords: Cordyceps militaris, antibacterial activity, alginate encapsulation, multidrug-resistant pathogens, drug resistance,

Comparative characteristics of molecular genetic methods for analyzing the genital tract microbiota

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BACKGROUND AND OBJECTIVES: A wide range of molecular genetic approaches are used to investigate the genital tract microbiota. Their results often do not coincide. The aim of the research was to compare molecular genetic methods for analyzing genital microbiota.

MATERIALS AND METHODS: We obtained urethral discharge from 18 men and posterior vaginal fornix from 22 women with a presumptive diagnosis of acute gonococcal infection. We performed real-time PCR to detect DNA of Neisseria gonorrhoeae, Staphylococcus spp., Streptococcus spp., Enterobacterales, Gardnerella vaginalis, Atopobium vaginae, Lactobacillus spp., and also sequencing of the 16S ribosomal RNA gene of the samples on the Illumina MiSeq platform using the MiSeq Reagent Kits v3 (600-Cycle Kit). Statistical analysis of the data was performed using the $\chi 2$-criterion.

RESULTS AND DISCUSSION: Using PCR, the preliminary diagnosis of acute gonococcal infection was confirmed in 88.8% of men and 77.2% of women. In the same samples, metagenomic analysis revealed the presence of N. gonorrhoeae markers in 61.1% of men and 54.4% of women. At the same time, genes of the genus Neisseria were detected in 100% of samples of men and women, which suggests a high homology of nucleic acid sequences of bacteria of this genus and frequent genetic exchange between them. Significant disadvantages include the difficulty of assessing the viability of the detected bacteria, and the spectrum of microorganisms is excessively wide. The high level of genetic polymorphism of different strains of N. gonorrhoeae complicates the interpretation of the results.

Keywords: genital tract microbiota; molecular genetic methods; Neisseria gonorrhoeae; genetic polymorphism

Comparative long non-coding RNA expression analysis of THP-1-derived macrophages infected with Mycobacterium tuberculosis

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BACKGROUND AND OBJECTIVES: Long non-coding RNAs (lncRNAs) are emerging as a potential regulator in orchestrating the biological processes involved in the Mycobacterium tuberculosis (Mtb) infection, from immune response to host-pathogen interactions. Exploring the roles of lncRNAs can shed more light on the underlying mechanism in the interaction between Mtb and host.

MATERIALS AND METHODS: Herein, we used a previous RNA sequencing data to investigate the profile of lncRNAs in Mtb-infected THP1 macrophages with H37Rv, H37Ra, and BCG strains. We analyzed RNA-seq data to identify differentially expressed lncRNA genes among the study groups. We identified hub genes and cis-acting lncRNAs and carried out functional enrichment analysis.

RESULTS AND DISCUSSION: Our study found thousands of lncRNAs, predominantly being novel lncRNAs, demonstrating their substantial role in Mtb-infected macrophages. We also discovered many differentially expressed lncRNA genes uniquely regulated in each infected group. Overall, pathway analysis of cis-acting lncRNA corroborated the importance of inflammatory immunological responses as the primary characteristics of lncRNA induced during H37Rv infection, in contrast to H3Ra and BCG infections. Scavenging by Class A receptors and inflammasomes was identified as a commonly enriched term among Mtb- and BCG-infected groups. Furthermore, we highlighted the interaction network of lncRNAs with miRNAs and driver lncRNAs in the regulatory networks associated with Mtb-infected THP-1 cells. Our findings indicated a diversified regulatory role for lncRNAs in the macrophage response to various Mycobacterium strain infections. Further evaluation of lncRNA pattern regulation may also help to understand the complexity and heterogeneity of host immune responses elicited by different Mycobacterium strains.

Keywords: Long non-coding RNAs, Mycobacterium tuberculosis, Transcriptomics, THP-1

Comparative molecular analysis of oral microbiota in smokers and non-smokers

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BACKGROUND AND OBJECTIVES: The oral cavity harbors a diverse array of microorganisms that are essential for maintaining oral and overall health. This microbial balance is influenced by factors such as nutrition, oral hygiene, and behavioral habits like smoking. Smoking can disturb this balance by promoting the growth of pathogenic species. This study aimed to evaluate and compare the prevalence of five specific oral bacterial species in smokers and non-smokers.

MATERIALS AND METHODS: Eighty saliva samples were collected from patients at Fardis dental clinic, including 40 smokers and 40 non-smokers. DNA was extracted using standard commercial kits. The presence of Streptococcus mutans, Capnocytophaga ochracea, Porphyromonas gingivalis, Treponema denticola, and Aggregatibacter actinomycetemcomitans was determined using Polymerase Chain Reaction (PCR). The amplified products were analyzed through agarose gel electrophoresis. Statistical analysis was performed using SPSS software, and a p-value 0.05 was considered statistically significant.

RESULTS AND DISCUSSION: S. mutans and P. gingivalis were significantly more prevalent in smokers (p 0.05). C. ochracea and A. actinomycetemcomitans were more commonly found in non-smokers ($p = 0.04$ and $p = 0.03$, respectively). Although T. denticola appeared more frequently in smokers, the difference was not statistically significant. Smoking alters the oral microbial community by increasing disease-associated bacteria and decreasing beneficial flora such as C. ochracea. These findings emphasize the detrimental effects of smoking on oral health and highlight the importance of smoking cessation in preserving a healthy oral microbiome.

Keywords: Smoking, Oral microbiota, PCR, Capnocytophaga ochracea, Oral bacteria

Comparative Molecular Docking Analysis of Quercetin Binding to Key Staphylococcus aureus Proteins: SwissDock vs. CB-Dock2

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BACKGROUND AND OBJECTIVES: The rise of antibiotic-resistant Staphylococcus aureus highlights the need for new therapeutic candidates targeting crucial bacterial proteins. This study investigated quercetin's binding potential with essential S. aureus proteins using two protein-ligand blind computational docking approaches.

MATERIALS AND METHODS: The three-dimensional (3D) structure of quercetin(PubChem CID: 5280343) was computationally docked against key S. aureus virulence proteins using two independent platforms: SwissDock (www.swissdock.ch) employing the Attracting Cavities algorithm and CB-Dock2(https://cadd.labshare.cn/cb-dock2/)utilizing an optimized AutoDock Vina approach. The protein targets, retrieved from the Protein Data Bank, encompassed: (1) regulatory proteins (SarA [2FRH], WalK [4YWZ,7DUD], WalR [2ZXJ], VraS [4GT8], VraR [4GVP]); (2) adhesion factors (FnBPA [4B5Z], ClfB [4F24], Cna [2F68]); (3) the major autolysin Atl [6FXO]; and (4) biofilm-associated proteins (Bap [7DM0], SasG [7SMH], PSMα3 [5I55]).

RESULTS AND DISCUSSION: SwissDock results identified strong interactions between quercetin and proteins such as WalK (−7.51 kcal/mol), ClfB (−7.41 kcal/mol), FnBPA (−7.22 kcal/mol), and SasG (−7.17 kcal/mol), all of which are involved in cell signaling or adhesion. However, CB-Dock2 consistently predicted stronger binding affinities across the same targets, particularly for SasG (−9.2 kcal/mol), WalK (−9.1 kcal/mol), and FnBPA (−8.2 kcal/mol). Notably, CB-Dock2 revealed significant improvement in docking scores for proteins such as SarA (−7.7 kcal/mol) and VraR (−8.1 kcal/mol), which showed limited or weak binding in SwissDock (−4.74 and −6.30 kcal/mol, respectively). Conclusion:These results demonstrate quercetin's potential to disrupt multiple virulence mechanisms in S. aureus, with particular affinity for WalK sensor kinases and SasG adhesion proteins, while highlighting important methodological differences in binding affinity predictions between docking algorithms.

Keywords: Staphylococcus aureus, Quercetin, Molecular docking, Antibacterial agents

Comparison of Antibiotic Resistance Patterns of Nosocomial Gram-Negative Pathogens at Yas Hospital Complex, Tehran, Iran

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BACKGROUND AND OBJECTIVES: Hospital-acquired infections (HAIs), especially those caused by gram-negative bacteria, are a major global health problem because of increasing mortality and antibiotic resistance. Therefore, this survey aimed to determine the gram-negative bacteria and antibiotic resistance patterns among patients admitted to Yas Hospital Complex.

MATERIALS AND METHODS: Clinical specimens were obtained from autumn to winter 1403. Bacterial isolates were identified and antibiotic susceptibility was described following the Clinical and Laboratory Standards Institute (CLSI) guidelines using the Kirby-Bauer disk diffusion method. For each isolate, the following antibiotics were tested: gentamicin, cefazolin, ciprofloxacin, cefoxitin, co-trimoxazole, cefepime, ceftazidime, cefotaxime, and piperacillin-tazobactam. Statistical analysis was performed using SPSS version 22.

RESULTS AND DISCUSSION: A total of 8,568 clinical samples were processed, with the distribution of clinical specimens as follows: 55.8% urine, 34% blood, 4.3% wound, 3.4% sputum, and 2.4% from other sources. From the samples, 560 gram-negative isolates were identified: Escherichia coli (34.8%), Klebsiella pneumoniae (33%), Pseudomonas aeruginosa (10.8%), Acinetobacter spp. (9.4%), and other species (11%). Interestingly, Acinetobacter spp. had 100% resistance to all tested antibiotics throughout both seasons. P. aeruginosa and K. pneumoniae also showed high resistance rates (approximately 60%). Seasonal fluctuations in both prevalence and resistance patterns were observed. The findings reveal an alarming prevalence of multidrug-resistant gram-negative bacteria. This highlights an urgent need for antimicrobial stewardship, infection control, and management practices. We advocate alternative therapeutic options to reduce resistance to nosocomial pathogens.

Keywords: Hospital-Acquired Infections, Antibiotic Resistance, Gram-Negative Bacteria, Multi-Drug Resistance

Comparing the anti-Listeria and cytotoxicity properties of the hydroethanolic extract of Golpar, as well as its nanoemulsion and nanocapsule

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BACKGROUND AND OBJECTIVES: Two appealing new techniques for adding active plant extracts to food preparations and medication formulations are nanoemulsions and nanocapsulations. Our goal of study was to examine the anti-listeria standard (LSTD) (ATCC 7466) and isolated from food (LIFF) and cytotoxicity activities of Heracleum persicum hydroethanolic extract (HPHE), along with their nanoemulsion (NEHP) and nanocapsule (NCHP).

MATERIALS AND METHODS: HPHE was prepared using maceration method. Subsequently, a high-energy emulsification approach was employed to enhance water dispersion, resulting in the creation of the nanomaterials. TEM and DLS were then used to evaluate shape and structure of the Nanomaterials preparations. The antibacterial activities of HPHE, NEHP, NCHP were measured using the minimum inhibitory concentration (MIC), minimum bactericidal concentration (MBC), zone of inhibition diameter, biofilm development inhibition against LSTD and LIFF. MTT test was used to assess cytotoxicity in the colon cancer (HCT116) and human dermal fibroblast (HDF) cell lines.

RESULTS AND DISCUSSION: The shape and structure of the Nanomaterials have been verified. The assessed average particle sizes of NEHP and NCHP were approximately 116.1 nm and 68.5 nm, respectively. The MIC values ranged from 7.8 to 250 mg/ml, while the MBC values ranged from 15.6 to 500 mg/ml. NCHP showed the greatest suppression of biofilm formation against LSTD. In all treatments, exposure to a high concentration of HPHE, NEHP, NCHP led to a noticeably decreased viability of HCT116 cells compared to HDF cells. According to our results, we suggest HPHE, NEHP, NCHP as sustainable food preservative agents in the food industry.

Keywords: Heracleum persicum, anti-listeria activity, cytotoxicity activity, extract, nanoemulsion, nanocapsule.

Comparison of Antibacterial Activity of Streptococcus salivarius K12 Supernatants from Two Culture Media against Streptococcus mutans

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BACKGROUND AND OBJECTIVES: Streptococcus salivarius K12 is a probiotic strain known for its potential to produce bacteriocins effective against oral pathogens such as Streptococcus mutans, a key contributor to dental caries. However, the synthesis of these antimicrobial compounds is highly dependent on the environmental and nutritional conditions under which the bacteria are cultivated. This study aimed to evaluate the antibacterial properties of cell-free supernatants obtained from S. salivarius K12 cultured in two different growth media: Tryptic Soy Broth (TSB) and Brain Heart Infusion (BHI).

MATERIALS AND METHODS: S. salivarius K12 was cultured in TSB and BHI media under appropriate conditions. After incubation, cultures were centrifuged to collect the resulting cell-free supernatants (CFSs), which were then sterilized by 0.22 µm filtration. The antibacterial activity of the CFSs against Streptococcus mutans was evaluated using the agar well diffusion assay.

RESULTS AND DISCUSSION: The CFS obtained from TSB medium showed no inhibition zone, indicating lack of antibacterial activity. In contrast, the BHI-derived CFS exhibited a clear inhibition zone of approximately 20 mm against S. mutans, demonstrating notable antibacterial potential. These findings indicate that the composition of the culture medium plays a key role in determining the antibacterial potential of S. salivarius K12-derived supernatants. The enhanced activity observed in the BHI media is likely due to the presence of nutrients or conditions that better support the production of inhibitory compounds. This highlights the importance of optimizing culture conditions to improve the antimicrobial properties of postbiotics such as CFS.

Keywords: K12,cell free supernatant, BHI, TSB, Agar well diffusion, Optimization, Mutans

Comparison of antibiotic resistance patterns and demographic characteristics of ICU patients caused by Pseudomonas aeruginosa using laboratory and molecular methods

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BACKGROUND AND OBJECTIVES: P. aeruginosa is a common cause of nosocomial infections. Studies have reported the high occurrence of P. aeruginosa isolated from ICU. WHO has warned about deaths caused by these bacteria. The goal of this study is to compare the antibiotic resistance patterns and demographic characteristics of ICU patients from two educational hospitals.

MATERIALS AND METHODS: 40 samples from the ICU of one educational hospital and a burn center were gathered. Isolates were identified by biochemical studies followed by PCR (existence of toxA gene with 390 kbp). Resistance patterns were examined by antibiogram test. demographic characteristics were gathered by Questionnaire.

RESULTS AND DISCUSSION: 14 (70%) and 11 (55%) of isolates were XDR in educational hospital and burnt center respectively. Other isolates in burnt center were MDR. For all of these XDR isolates colistin was prescribed. 54.54% and 66.66% of patients receiving colistin died because of sepsis. Rate of resistance in hospital was the highest for levofloxacin and trimethoprim-sulfamethoxazole (80%) and the lowest for cefepime (60%). For burnt center the highest resistance was seen in meropenem, cefepime, tobramycin, piperacillin-tazobactam and trimethoprim-sulfamethoxazole (100%) and the lowest was with ceftazidime- clavulanic acid (35%). High rate of death because of sepsis in patients with XDR isolates shows the danger of antibiotic resistance. High percentage of patients died during colistin treatment. Higher resistance rate in burn center was seen compared to the educational hospital. This could indicate the difference between P. aeruginosa strains in these two medical centers, which requires further study.

Keywords: antibiotic resistance, P. aeruginosa, multi drug resistance, sepsis, ICU

Comparison of Multiplex Quantitative Real-Time PCR and Culture Methods for the Diagnosis of Bacterial Meningitis in Patients with Suspected Meningitis

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BACKGROUND AND OBJECTIVES: Introduction: This study aimed to compare the diagnostic efficacy of the standard culture method with multiplex quantitative real-time polymerase chain reaction (qPCR) in examining cerebrospinal fluid (CSF) samples collected from patients with suspected meningitis.

MATERIALS AND METHODS: Methods: A retrospective evaluation was conducted on 166 patients with suspected meningitis, who were treated in Vali-Asr hospital in Birjand, Iran, between 2011 and 2020. Diagnosis of bacterial meningitis was based on CSF culture and multiplex qPCR results.

RESULTS AND DISCUSSION: Results: Among 166 patients, conventional methods identified causative pathogens in only 10.3% of cases, while multiplex qPCR detected pathogens in eight out of 25 culture-negative cases as well. The most common pathogens identified were enterovirus, Epstein-Barr virus, herpes simplex, Haemophilus influenzae, and Streptococcus pneumoniae. Conclusion: Multiplex qPCR appears to be a more effective method than conventional culture in identifying bacterial and viral pathogens that most commonly cause meningitis. The incorporation of qPCR as a routine diagnostic method for meningitis in clinical practice could significantly enhance clinical decision-making and patient care.

Keywords: Bacterial meningitis, Culture, Real time polymerase chain reaction

Comparison of some oral bacterial flora in smoker and non-smoker Patients

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BACKGROUND AND OBJECTIVES: The oral flora comprises various microorganisms, including bacteria, that are essential for maintaining oral health. Disruptive factors, such as smoking, may alter the microbial balance, potentially causing oral diseases. This study aimed to compare oral microbial flora between smokers and non-smokers in Sanandaj, western Iran.

MATERIALS AND METHODS: A total of 100 saliva samples (50 from smokers and 50 from non-smokers) were collected from patients referred to the Department of Oral and Dental Diseases, Faculty of Dentistry, Kurdistan University of Medical Sciences, Sanandaj. DNA was extracted from saliva specimens. Nine bacterial species (Aggregatibacter actinomycetemcomitans, Capnocytophaga ochracea, Eikenella corrodens, Fusobacterium nucleatum, Micromonas micros, Porphyromonas endodontalis, Prevotella intermedia, Porphyromonas gingivalis, and Treponema denticola) were identified using Nested PCR. Data were analyzed statistically, with significance set at p 0.05.

RESULTS AND DISCUSSION: A. actinomycetemcomitans (p = 0.004) and F. nucleatum (p = 0.046) were significantly more prevalent in non-smokers, whereas P. intermedia (p = 0.023) was more frequent in smokers. Age and gender were significantly associated with some bacteria. No significant association was found between daily cigarette consumption and bacterial presence (p 0.05), but smoking duration correlated positively with several bacteria (p 0.05). Smokers had a significantly higher DMFT (decayed, missing, and filled permanent teeth) index (p 0.05). Long-term smoking demonstrated a stronger association with the studied bacteria than other examined variables, potentially promoting colonization of pathogenic species. Considering the elevated DMFT index and the bacterial involvement in periodontitis and other oral diseases, smoking cessation is critical for maintaining oral health.

Keywords: Smoking, microflora, mouth, bacteria

Comparison of Two Lactobacillus acidophilus Postbiotics Against Staphylococcus aureus

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BACKGROUND AND OBJECTIVES: Lactobacillus acidophilus is an important probiotic known for producing lactic acid, bacteriocins, and other bioactive compounds. Besides live cells, its metabolic by-products called postbiotics have recently gained attention as novel agents to promote health and control pathogens. Staphylococcus aureus is an opportunistic pathogen responsible for various infections. This study aimed to compare the antimicrobial effects of two postbiotics derived from L. acidophilus: one obtained by UV inactivation and the other by filtration through a syringe filter.

MATERIALS AND METHODS: Cell-free supernatant (CFS) was prepared by centrifuging an overnight culture at 8000 rpm for 5 minutes followed by filtration through a 0.22 µm syringe filter. Sterility was confirmed by plating on MRS agar for 72 hours. For UV-inactivated postbiotic, a bacterial suspension (0.5 McFarland) was exposed to UV-C light for 15 minutes, and complete inactivation was verified by plating. Antimicrobial activity was tested using agar well diffusion against S. aureus. Wells were filled with MRS broth (control), CFS, and UV-inactivated suspension, and plates were incubated at 37°C for 24 hours.

RESULTS AND DISCUSSION: No bacterial growth occurred after 15 minutes of UV exposure and in the CFS. The UV-inactivated postbiotic showed a significantly larger inhibition zone (23.00 ± 3.56 mm) compared to CFS (8.75 ± 0.96 mm), demonstrating stronger antibacterial activity. As a result Both postbiotics inhibited S. aureus, but UV-inactivated postbiotic was more effective, indicating that inactivated cells with metabolites enhance antimicrobial effects. UV-inactivated postbiotics show promise as alternative agents against opportunistic pathogens.

Keywords: antimicrobial activity, Cell-free supernatant, Lactobacillus acidophilus, Postbiotics, Staphylococcus aureus, UV

Comprehensive Lipid Profiling of Escherichia coli BL21 by MALDI-TOF MS

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BACKGROUND AND OBJECTIVES: Escherichia coli BL21, a widely used strain in biotechnology and recombinant protein production, serves as a model for understanding bacterial membrane composition. Despite its frequent use, the detailed lipidomic profile of E. coli BL21 remains under-characterized.

MATERIALS AND METHODS: In this study, E. coli BL21 was cultured in nutrient broth for 24 hours at 37 °C with shaking at 150 rpm. Cells were harvested and subjected to lipid extraction using the Bligh and Dyer method. The resulting extracts were analyzed using a Waters Synapt G1 MALDI-TOF mass spectrometer with α-cyano-4-hydroxycinnamic acid as the matrix and calibrated to 20 ppm tolerance. The instrument operated with a mass accuracy tolerance of 20 ppm. Matrix-associated peaks were excluded, and lipid identification was performed by matching experimental m/z values to the LipidMaps database.

RESULTS AND DISCUSSION: Analysis by MALDI-MS revealed a dominance of phosphatidylethanolamines (PE) and phosphatidylserines (PS)—notably PE 35:5 and PS 33:5—with smaller signals for phosphatidic acid (PA) and phosphatidylinositol (PI). PE and PS predominate in E. coli membranes—PE as the principal zwitterionic lipid ensuring fluidity and permeability, and PS contributing to curvature and stability—while PA serves as a key biosynthetic precursor. The rare PI peaks likely reflect trace intermediates or slight database misassignments. This study on the lipidomics of E. coli BL21, confirming the abundance of key membrane lipids and demonstrating the utility of MALDI-TOF MS in rapid bacterial lipid profiling. These findings offer a foundation for future metabolic and membrane-targeted investigations

Keywords: Escherichia coli, Phospholipids, Lipidomics, Mass Spectrometry, MALDI, Phosphatidic Acids

Computational Design and screening of new Enterococcal Surface Protein Inhibitors

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BACKGROUND AND OBJECTIVES: Enterococcus faecalis is an opportunistic pathogen that plays a main role in urinary, wound, and endocarditis infections. Due to bacterium's antibiotic resistance, treating infections caused by it has become difficult. Enterococcal Surface Protein (Esp) is one of the important pathogenic proteins in Enterococcus faecalis that helps in adhesion of the bacterium to host cells and the establishment of infection. This study investigates the most potent inhibitory ligand candidates against Esp through molecular docking and pharmacological analysis.

MATERIALS AND METHODS: The three-dimensional structure of Esp Enterococcus faecalis was obtained from the RCSB PDB database (PDBID:6ori). The structure of two inhibitors,kojicacid (PubChemCID:3840) and parietin (PubChemCID:10639), and their analogs were filtered according to Lipinski's rules of five in Pubchem . Molecular docking was conducted using MVD program. Interactions and binding energy scores were analyzed by MVV program, and finally, pharmacological properties were evaluated through SwissADME server.

RESULTS AND DISCUSSION: The molecular docking analysis showed that PubchemCID:23275238 has the best interaction and binding energy of -111.506 kcal/mol with Esp. This ligand forms five hydrogen bonds with amino acids Ser223, Thr234, Tyr440, Gly261, and Ser262, and eleven steric bonds with amino acids Asn264, Glu232, Thr234, Ser233, Gln82, Gly261, His260, Gly441, Tyr440, Ser262, and Val263. In addition, SwissADME results demonstrated that this ligand has a molecular weight:291.35g/mol, LogP:-3.79, TPSA:111.87A, LogP: 2.49, H-bond acceptors:4, and H-bond donors:1. These results suggested that PubchemCID:23275238 is a good candidate for inhibiting Esp Enterococcus faecalis, and further studies should be conducted experimentally to investigate the potential of this therapeutic agent.

Keywords: Molecular Docking, Enterococcus faecalis, Enterococcal surface protein.

Computational Targeting of Fusobacterium nucleatum FadA by Sodium New Houttuyfonate and Analogs: A Novel Pathway to Colorectal Cancer Therapy

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BACKGROUND AND OBJECTIVES: Introduction Colorectal cancer (CRC) is a significant global health burden. The bacterium Fusobacterium nucleatum plays a crucial role in CRC development and progression. Since there are currently no specific antimicrobial therapies against F. nucleatum in CRC, identifying new therapeutic agents is necessary. Therefore, in this study, we explored a promising inhibitory candidate against Fusobacterium adhesin A (FadA), a key membrane protein for Fusobacterium pathogenicity, via a molecular docking study.

MATERIALS AND METHODS: Methods: The 3D structure of FadA (PDB ID: 3ETW) was retrieved from the RCSB PDB database. The structures of inhibitory ligand of Sodium New Houttuyfonate (SNH) and a total of 25 analogs were obtained from the PubChem database. Molecular docking was performed using Molegro Virtual Docker v.6., and the best ligand with the lowest energy binding was selected. The pharmacokinetic properties of the top ligand were then analyzed using the SwissADME database.

RESULTS AND DISCUSSION: Results: Our analysis identified 1-Hydroxy-3-oxohexadecane-2-sulfonic acid as the most potent inhibitor candidate. This ligand showed a binding energy of -88.4835kcal/mol, which is more favorable than SNH's binding energy of -83.2878 kcal/mol. The new ligand formed one hydrogen bond with Arg108 and six steric interactions. Its ADME profile indicated suitable properties for a drug candidate which that this ligand had LogS of -3.75, MLOGP of 2.24 and TPSA of 100.05. Conclusion: Our findings suggested that 1-Hydroxy-3-oxohexadecane-2-sulfonic acid is a promising inhibitor for the Fusobacterium nucleatum FadA protein. Further in vitro and in vivo studies are needed to confirm its efficacy.

Keywords: Fusobacterium nucleatum, Molecular Docking, Colorectal Cancer, 1-Hydroxy-3-oxohexadecane-2-sulfonic acid, Sodium NewHouttuyfonate.

Construction of adenovector based prophylactic and therapeutic vaccines

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BACKGROUND AND OBJECTIVES: Adenoviruses are highly versatile viral vectors that have gained significant attention for the development of both prophylactic and therapeutic vaccines. Their advantages stem from a number of key features, including a well-characterized genome that is easily manipulated, the capacity to carry large foreign DNA inserts, and the ability to induce robust and long-lasting humoral and cellular immune responses.

MATERIALS AND METHODS: The construction of these vectors typically involves the deletion of early viral genes, such as E1, which renders the vector replication-defective and enhances its safety profile. This deletion also creates space in the viral genome for the insertion of transgenes, such as those encoding foreign antigens or immunomodulatory molecules. Subsequent generations of adenoviral vectors, including "gutless" or high-capacity vectors, have further increased the safety and transgene capacity by removing additional viral genes.

RESULTS AND DISCUSSION: For prophylactic vaccines, the goal is to present an antigen to the immune system to generate protective immunity against a pathogen. For therapeutic applications, particularly in cancer immunotherapy, adenoviral vectors can be engineered to deliver tumor-associated antigens to stimulate an anti-tumor immune response. They can also be modified to express molecules that directly kill cancer cells or enhance the activity of other immunotherapies. Despite their immense potential, challenges such as pre-existing immunity to common adenovirus serotypes and the potential for a strong inflammatory response to the vector itself must be addressed.

Keywords: Adeno vector, prophylactic vaccines, therapeutic vaccines

Correlation Between Antibiotic Resistance and Exotoxin Genes in Multidrug-Resistant Pseudomonas aeruginosa Clinical Isolates

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BACKGROUND AND OBJECTIVES: Pseudomonas aeruginosa is one of the most important causative agents among the hospital acquired infections, especially in intensive care units. To increase the severity of the disease, Pseudomonas uses a type III secretion system to inject exotoxin proteins into the cytoplasm of eukaryotic cells. Four effector proteins have been described in Pseudomonas aeruginosa. The aim of this study was to investigate the relationship between antibiotic resistance and exotoxin genes among Pseudomonas aeruginosa isolates with multidrug resistance.

MATERIALS AND METHODS: A cross-sectional study was conducted on 150 P. aeruginosa isolates collected from five hospitals in Mashhad over six months. Isolates were identified by biochemical tests. Antibiotic resistance was evaluated by disk diffusion, and exotoxin genes (ExoS, ExoT, ExoU, ExoY) were detected using PCR.

RESULTS AND DISCUSSION: Imipenem and meropenem showed the highest resistance rates (84.8%), while ceftazidime had the lowest (60.6%). The prevalence of ExoS, ExoT, ExoU, and ExoY genes was 64.6%, 61.3%, 38.6%, and 15.3%, respectively. 20 (68.9%) of the isolates with exoS and exoT genotypes were resistant to gentamicin. A statistically significant association was observed between exotoxin gene presence and antibiotic resistance. The result of this study showed a high resistance rate to the most antibiotic classes and a specific relationship between the virulence genotype and antimicrobial resistance. The co-occurrence of multidrug resistance and virulence genes suggests a serious challenge in managing P. aeruginosa infections and underlines the need for molecular surveillance in clinical settings.

Keywords: Pseudomonas aeruginosa, antibiotic resistance, exotoxins, type III secretion system.

Correlation of pvl gene with biofilm strength and antimicrobial activity of vancomycin and ceftaroline in Staphylococcus aureus skin and soft tissue infections in Tehran, Iran

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BACKGROUND AND OBJECTIVES: Methicillin-resistant S. aureus (MRSA) strains with biofilm formation and Panton-Valentine leukocidin (PVL) production are linked to skin and soft tissue infections (SSTIs) and recurrent skin abscesses. A study will explore the correlation of pvl genes with biofilm strength, and assess vancomycin and ceftaroline efficacy against S. aureus SSTI.

MATERIALS AND METHODS: 134 S. aureus isolates were collected from SSTI patients in Razi Hospital. Identification was performed using microbiological standard tests. Vancomycin and ceftaroline susceptibilities were tested using agar dilution and disc diffusion, respectively. PCR assays detected nuc, mecA, and pvl genes. Biofilm formation was assessed using the tissue culture plate method. Statistical analysis employed the Chi-square test or Fisher's exact test with a significance level of p 0.05.

RESULTS AND DISCUSSION: 58.2% of SSTIs were MRSA-related, all S. aureus had biofilm production capability, from which 10.4% were highly positive and 89.5% low-grade positive. 16.4% of S. aureus causing SSTIs had pvl gene, 59% of PVL-positives were MRSA. Weak/moderate biofilm isolates mostly had pvl gene (P=0.03). 98.5% were susceptible to vancomycin, with MIC50 of 1 µg/L for 51.4%. 1.4% MRSA strains were moderately resistant, with MICs of 4-8 µg/L. 96.2% were susceptible to ceftaroline and 3.8% were dose-dependent isolates. Our study found a significant link between pvl gene and the strength of biofilm production. pvl gene related to lower biofilm strength, this result may provide a valuable perspective for future studies. Ceftaroline proposed as vancomycin alternative for MRSA SSTI to address the increasing resistance rate.

Keywords: Biofilm strength, Ceftaroline, pvl, S. aureus, SSTI.

Corynebacterium: An Emerging Platform for Recombinant Protein Production - Characteristics, Advantages, and Challenges

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BACKGROUND AND OBJECTIVES: Corynebacterium glutamicum has emerged as a safe and efficient host for recombinant protein production, gaining prominence in biopharmaceutical and industrial applications. Its ability to utilize alternative carbon sources, such as acetate, significantly reduces production costs. Moreover, its endotoxin-free nature, adaptability to large-scale conditions, and capacity for direct protein secretion enhance its appeal. However, challenges remain, including limited expression of certain proteins and its thick cell wall, which can hinder secretion efficiency. This study examines the key attributes that make C. glutamicum an effective host, while also addressing its limitations, aiming to provide insights into optimizing its use for industrial protein production.

MATERIALS AND METHODS: the present narrative review is based on published scientific articles from 1995 to 2024, in PubMed, Google Scholar, and ScienceDirect using key terms such as "Corynebacterium glutamicum", "Recombinant protein", and " Corynebacterium glutamicum AND Recombinant protein".

RESULTS AND DISCUSSION: Corynebacterium glutamicum is a promising host for recombinant protein production, offering non-pathogenic, endotoxin-free advantages and efficient protein secretion, reducing purification costs. Its low extracellular protease activity enhances protein stability, and its ability to utilize inexpensive carbon sources like acetate makes it ideal for industrial applications. However, limitations such as its thick cell wall and restricted protein secretion necessitate optimization. Strategies like strong promoters, engineered signal peptides, and Sec/Tat pathways have improved secretion efficiency. Additionally, its robust growth and stress tolerance ensure stable, scalable bioprocessing, reinforcing its potential as an optimized platform for industrial biotechnology.

Keywords: Corynebacterium glutamicium, Recombinant Protein, Protein Secretion, Gene Expression, Non-Pathogenic host

CRISPR-Cas Systems in Microbial Engineering: From Gene Editing to Biotechnological Innovations

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BACKGROUND AND OBJECTIVES: CRISPR-Cas systems were initially discovered as an adaptive immune mechanism in prokaryotes to defend against foreign genetic elements. Their transformation into genome editing tools has revolutionized microbial engineering due to their accuracy, efficiency, and programmability. These tools have enabled advancements in metabolic engineering, synthetic biology, antimicrobial strategies, and biosensor development. The objective of this review is to summarize the current understanding of CRISPR-Cas biology, highlight key microbial applications, and identify ongoing challenges and opportunities for innovation in biotechnology.

MATERIALS AND METHODS: This review is based on studies retrieved from PubMed, Scopus, and Web of Science using terms such as "CRISPR-Cas" and "microbial engineering". Articles from 2010–2025 were reviewed, focusing on original research and recent innovations.

RESULTS AND DISCUSSION: CRISPR tools have been widely used in bacteria and yeast for gene knockouts, metabolic pathway optimization, antimicrobial development, and biosensor design. Dead Cas9 (dCas9) allows transcriptional regulation without cutting DNA. Despite challenges like off-target effects and delivery barriers, newer Cas variants and delivery methods are improving efficiency. CRISPR-Cas systems have become essential in microbial biotechnology. As innovations continue, these tools promise advanced microbial platforms for sustainable industry, diagnostics, and therapeutics.

Keywords: CRISPR-Cas, Microbial Engineering, Gene Editing, Synthetic Biology, Biotechnology

Current status of Dengue fever in Iran

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BACKGROUND AND OBJECTIVES: Dengue fever is an acute febrile viral disease caused by viruses of the genus Flavivirus with four serotypes (DENV-1 to DENV-4) and transmitted mainly by Aedes aegypti and A. albopictus mosquitoes. The importance of this disease from a public health and epidemiological perspective highlights the need to establish a national diagnostic network and strengthen virological capacities

MATERIALS AND METHODS: Epidemiological data were obtained from reports of the Ministry of Health's syndromic surveillance system, review of clinical records, as well as laboratory diagnosis of the dengue fever diagnostic network consisting of the arbovirus reference laboratories of the Pasteur Institute of Iran and nine selected academic centers across the country.

RESULTS AND DISCUSSION: From the beginning to August 12, 2025, the total number of positive cases was 406 (390 locally transmitted and 16 imported cases). The epidemiological pattern indicates a concentration of indigenous cases in the southern regions and its high dependence on the presence of vectors and the density of international travel. Analysis of surveillance samples revealed the presence of two circulating serotypes (DENV-1,2). This is important from a virological and immunological perspective, as secondary infection with a different serotype increases the risk of severe dengue fever and dengue shock syndrome. Accurate identification of serotypes, in addition to clinical management, is crucial for predicting epidemic patterns and designing future vaccination strategies. In the meantime, the National Diagnostic Network plays a key role in containing the transmission cycle by providing rapid access to standardized tests and serotyping capacity.

Keywords: dengue, national diagnostic network, locally transmitted casese

Cytotoxic Activity of Cytoplasmic Extracts from Yogurt-Derived Lactobacillus Strains Against HT-29 Human Colorectal Cancer Cells

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BACKGROUND AND OBJECTIVES: This study investigated Lactobacillus strains isolated from traditional yogurt for their potential anticancer effects. Given their known probiotic properties and ability to produce bioactive metabolites, the cytotoxicity of their cytoplasmic extracts was evaluated against HT-29 colorectal cancer cells to explore safer therapeutic options for colorectal cancer.

MATERIALS AND METHODS: MATERIALS AND METHODS: Twenty-one traditional yogurt samples were collected, refrigerated, and processed immediately. Eight Lactobacillus isolates were identified as Gram-positive, catalase-negative rods based on morphology and biochemical tests. Molecular analysis via PCR and 16S rRNA sequencing confirmed two isolates as Lactobacillus casei and one as L. fermentum. For cytotoxicity assays, cytoplasmic extracts were prepared by culturing isolates in MRS broth, followed by sonication and freeze-thaw disruption, and filtration. HT-29 colorectal cancer cells were treated with extract concentrations of 0.5–2.0 mg/mL and incubated for 24 and 48 hours. Cell viability was assessed using the MTT assay with absorbance measured at 570 nm.

RESULTS AND DISCUSSION: Molecular identification confirmed two isolates as L. casei and one as L. fermentum (AGR1487), all showing probiotic traits like bile tolerance and acid resistance. Cytotoxicity assays demonstrated that these strains inhibited HT-29 cell viability in a concentration-dependent manner, with L. fermentum AGR1487 showing the strongest effect (~58% reduction at 2.0 mg/mL). Significant inhibition occurred at concentrations ≥1.0 mg/mL (p0.01). Apoptotic morphological changes were observed, particularly in cells treated with L. fermentum. These findings suggest that yogurt-derived Lactobacillus strains, especially L. fermentum AGR1487, possess intracellular bioactive compounds with potential anticancer properties, warranting further investigation.

Keywords: Lactobacillus, Yogurt, Cytotoxicity, Probiotic, Colorectal cancer

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 OBJECTIVES: Advances in the field of genome sequencing with the help of bioinformatics have opened up methods for reverse engineering vaccine design. The aim was to design and manufacture a single protein containing three dominant parts in stimulating the immune system, consisting of three bacteria: Corynebacterium diphtheria, Clostridium tetani and Bordetella pertussis.

MATERIALS AND METHODS: to select the dominant epitope type of the candidate regions of the triple vaccine. The best methods for analyzing immunogenic regions were performed by the PDB, DISCOTOPE, ELLIPRO and BCTOPE servers. The epitopes were linked together and ordered from a foreign company. Gene transfer and expression were performed at two temperatures and the purity of the recombinant protein was examined by SDS-PAGE in the weight range of 67 kDa and its presence was examined by Western blotting. Bradford, dialysis and LAL tests were performed. Eight groups of ten mice were injected intramuscularly. ELISA tests were designed and the toxicity of the sample on eukaryotic cells was examined.

RESULTS AND DISCUSSION: Modeling and validation of all three toxins were confirmed by Ramachandran plot. Transformation and expression were confirmed by SDS-PAGE and the presence of protein was confirmed by Western blotting. Endotoxin levels were reported within the permissible range. Statistically, the fever variable showed a significant difference on the third and fifth days between the first and second injections, but the weight variable did not have a significant difference.

Keywords: Toxin, Corynebacterium diphtheriae, Clostridium tetani, Bordetella pertussis

Design and Evaluation of a Gentamicin-Loaded Nanofibrous Composite with Antibacterial Properties

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BACKGROUND AND OBJECTIVES: Infections caused by opportunistic bacteria remain a major challenge in the treatment of chronic wounds. The use of bioactive scaffolds incorporating antibacterial agents offers a novel and effective approach for managing such wounds. In this study, a biocompatible nanofibrous composite based on cellulose nanofiber and gentamicin was designed and its properties were evaluated.

MATERIALS AND METHODS: The nanofibrous composite was prepared using cellulose nanofiber and gentamicin. Its antibacterial activity against Staphylococcus aureus and Escherichia coli was assessed using agar well diffusion, minimum inhibitory concentration (MIC), and minimum bactericidal concentration (MBC) methods. Biocompatibility was evaluated via the MTT assay on human fibroblast cell lines.

RESULTS AND DISCUSSION: Results: The fabricated nanofiber exhibited a uniform structure and suitable absorption capacity. Antibacterial assays demonstrated that the composite effectively inhibited the growth of both Gram-positive and Gram-negative bacteria. Furthermore, the cellulose nanofiber scaffold enabled the controlled release of gentamicin, allowing the drug to diffuse through the culture medium and exert its antibacterial effect even in areas where fiber penetration was limited. Discussion and Conclusion: The nanofibrous composite developed in this study, utilizing biocompatible polymers and a potent antibacterial agent, shows great potential as a bioactive wound dressing for the treatment of infected and resistant wounds. Owing to its strong antibacterial properties, controlled drug release, and favorable biocompatibility, this composite can be further explored for the development of advanced smart dressings for clinical applications. Additional in vivo studies and evaluations of long-term stability and efficacy may facilitate its future commercialization.

Keywords: nanofibers/ antibiotics resistance/ secondary infection/ antibacterial drugs

Design and Evaluation of Three Novel Antimicrobial Peptides Against Methicillin-Resistant Staphylococcus aureus (MRSA) Using In Silico Approaches

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BACKGROUND AND OBJECTIVES: The increasing resistance of Staphylococcus aureus to conventional antibiotics, particularly methicillin-resistant Staphylococcus aureus (MRSA), necessitates the development of new antimicrobial agents. This study aims to design novel antimicrobial peptides (AMPs) and assess their allergenicity.

MATERIALS AND METHODS: In this study, three antimicrobial peptides ranging from 18 to 19 amino acids in length were designed. Key characteristics considered in the design included amphipathicity, net positive charge (≥ +6), hydrophobicity, structural stability, allergenicity, and predicted anti-MRSA activity. These parameters were evaluated using the tools CAMP-R3, AntiBP2, AllerTOP, and AlgPred. The 3D structures of the peptides were predicted using the PEP-FOLD software.

RESULTS AND DISCUSSION: Three peptides with the following sequences were designed: A: RRWKWILGRKILRRWKLK, B: KLIKIRRWVKLLRWRRKV and C: WRRKKILRRWIRVKLKRK. All three peptides demonstrated high antimicrobial activity and exhibited promising anti-MRSA potential. Among them, peptide B showed superior performance due to its stable helical structure, high net positive charge (+7), amphipathic arrangement, and predicted non-allergenicity. Moreover, peptide B lacked known immunogenic epitopes and was predicted to have lower toxicity compared to the other two peptides. Based on the obtained results, peptide B is proposed as the most promising candidate for further experimental validation and potential development as an anti-MRSA therapeutic agent.

Keywords: Antimicrobial peptide, Allergenicity, MRSA

Design and Evaluation of Three Novel Antimicrobial Peptides Against Methicillin-Resistant Staphylococcus aureus (MRSA) Using In Silico Approaches

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Keywords: Antimicrobial peptide, Allergenicity, MRSA

Design and Simulation of a VanR Inhibitory Peptide to Counteract Vancomycin Resistance in Enterococcus faecalis

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BACKGROUND AND OBJECTIVES: Vancomycin resistance in Enterococcus faecalis is often mediated through activation of the VanR/VanS two-component regulatory system, leading to the expression of resistance genes such as vanHAX. This study aims to design an inhibitory peptide that binds to the DNA-binding domain of the VanR protein to prevent the transcription of resistance genes.

MATERIALS AND METHODS: The designed peptide sequence comprises a Tat cell-penetrating domain (YGRKKRRQRRR) and an inhibitory segment derived from the DNA-binding domain of VanR (RERIRKLLQR). The three-dimensional structure of VanR was retrieved from the AlphaFold database (UniProt ID: Q833X9) and processed in PDB format. The peptide structure was modeled using the PEP-FOLD3 server, and molecular docking was performed using AutoDock Vina on the C-terminal domain of VanR.

RESULTS AND DISCUSSION: Docking results indicated that the designed peptide specifically occupies the DNA-binding region of VanR and interacts with key residues such as Arg167, Lys170, and Gln174. The binding energy was measured in the range of −7.4 to −8.1 kcal/mol. The interactions were primarily composed of hydrogen bonds and electrostatic forces. By structurally mimicking DNA, the designed peptide acts as a competitive inhibitor, potentially preventing the activation of resistance genes. These findings suggest that the peptide may serve as a promising candidate for the development of peptide-based antimicrobial agents.

Keywords: Vancomycin, antibiotic resistance, Enterococcus faecalis, VanR, inhibitory peptide, molecular docking

Designing a multifactorial experiment to improve carotenoid production in Arthrobacter citreus

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BACKGROUND AND OBJECTIVES: Bacterial cells synthesize a vast array of biologically active compounds, including vitamins, pigments, antibiotics, and enzymes. Microbial production of pigments offers advantages over other sources due to the rapid growth rates of microorganisms, which can lead to high productivities.

MATERIALS AND METHODS: Optimization of biomass and pigment production by Arthrobacter citreus was performed using Design-Expert software. Incubation temperature, pH, and aeration were identified as the three primary factors influencing both biomass and pigment yield. Incubation temperatures were set at 20, 25, 30, 35, and 40 degrees Celsius. The pH was adjusted to five different values: 4, 6, 8, 10, and 12. Shaker speeds were maintained at 100, 130, 160, 190, and 220 revolutions per minute (rpm).

RESULTS AND DISCUSSION: Arthrobacter citreus is characterized as a mesophilic, neutrophilic, and aerobic microorganism, with oxygen being a critical factor for its growth. The software analysis indicated optimal efficiency at a pH of 7.76, a temperature of 28.34 degrees Celsius, and an aeration rate of 157.05 rpm. Under these optimized growth conditions, we achieved a cell biomass production of 1.753 g/l and a carotenoid pigment yield of 0.117 g/l. Given the acceptable yield of crude pigment obtained from cellular biomass, further investigations are recommended. These studies should explore additional optimization factors, such as the specific nutrients involved in growth, to further enhance production.

Keywords: Bacterial pigment , design of experiment , Arthrobacter citreus ,

Designing affibody in in silico medium using structure engineering and protein-protein docking approaches against adenylyl sulfate reductase in Desulfovibrio desulfuriacens bacteria as an effective factor in inducing atherosclerosis

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BACKGROUND AND OBJECTIVES: The proatherogenic effect of Desulfovibrio desulfuricans was demonstrated in an analytical study. Here, we designed a recombinant affibody—ZAASR—using in silico rational design methods to target the adenylyl sulfate reductase (AprA) enzyme in D. desulfuricans.

MATERIALS AND METHODS: AprA sequences from Desulfovibrio species were aligned, revealing a conserved GRGPIYMDT motif at positions 346–354. The crystal structure of Megalodesulfovibrio gigas AprA was used for 3D modeling. ElliPro was applied to the 3gyx structure to predict antigenic epitopes, identifying a major region (342–379) encompassing the conserved motif. Three affibody variants (V1–V3) were rationally designed via charged and polar substitutions, followed by molecular docking and scoring to assess binding affinity and stability.

RESULTS AND DISCUSSION: Sequence alignment confirmed strong conservation of the GRGPIYMDT motif within AprA. type affibody showed moderate affinity (docking score −189.85). Variant V3 demonstrated significantly improved binding (docking score −212.63) and the highest confidence coefficient (0.7777). Structural analysis revealed that V3's engineered positively charged residues form additional hydrogen bonds and electrostatic interactions with Asp and Thr in the motif, enhancing complex stability. The rationally engineered affibody variant V3 exhibits significantly improved binding affinity to the AprA enzyme's conserved GRGPIYMDT motif compared to the wild type. This study provides a promising foundation for developing protein-based diagnostic tools to detect or inhibit key enzymes involved in sulfate reduction, with potential applications in mitigating biocorrosion and anaerobic pathogenesis caused by Desulfovibrio species.ElliPro predicted a major surface-exposed epitope overlapping this motif. Docking of the wild-

Keywords: Affibody ZAASR, Protein engineering, Desulfovibrio spp., Adenylyl sulfate reductase, Atherosclerosis

Designing Next-Generation Probiotics for Targeted Bacterial Factor Modulation in Brain Function and Psychiatric Disorders

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BACKGROUND AND OBJECTIVES: Recent advances have highlighted the pivotal role of the gut microbiota in mental health via the gut-brain axis. Psychobiotics, a subclass of probiotics, modulate neural and immune pathways by producing bioactive bacterial metabolites such as SCFAs. These compounds influence neurotrophic and inflammatory gene expression, thereby impacting cognitive and emotional functions. The development of specifically designed probiotic strains with enhanced capacity to produce neuroactive metabolites presents a novel therapeutic approach for chronic psychiatric disorders.

MATERIALS AND METHODS: A modified Lactococcus lactis strain with increased expression of key enzymes involved in tryptophan was utilized. Male mice were divided into control, CRS-induced depression model, and CRS + psychobiotic treatment groups. Expression of IL-6 and BDNF was assessed by RT-qPCR. Behavioral assessments included Forced Swim Test (FST), Open Field Test (OFT), and Y-maze to evaluate depression-like behavior, anxiety, and working memory, respectively.

RESULTS AND DISCUSSION: Psychobiotic-treated mice exhibited significant increases in tryptophan in serum and (p 0.01). Expression levels of IL-6 decreased significantly, while BDNF were markedly upregulated (p 0.05). Behavioral tests demonstrated reduced depressive-like behavior (decreased immobility in FST), enhanced exploratory activity (OFT), and improved working memory (increased entries to novel arm in Y-maze).This study demonstrates that engineered probiotic strains capable of producing key bacterial metabolites modulate neuroimmune signaling and improve intestinal barrier integrity, resulting in neuroprotective effects and behavioral improvements in a depression model.

Keywords: Probiotics, bacterial metabolites, SCFAs, depression, BDNF, gut-brain

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Designing an RNAi Approach to Overcome a Multidrug-Resistant Pseudomonas aeruginosa

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BACKGROUND AND OBJECTIVES: Pseudomonas aeruginosa is a major cause of nosocomial infections and exhibits high levels of intrinsic and acquired resistance to a broad range of antibiotics. The emergence of multidrug-resistant (MDR) strains significantly limits treatment options and increases morbidity and mortality. Novel therapeutic approaches, such as RNA interference (RNAi), offer targeted strategies to silence resistance genes and restore antibiotic efficacy.

MATERIALS AND METHODS: In this study, key resistance-associated genes of MDR P. aeruginosa—including mexB, oprM, and genes involved in biofilm formation and β-lactamase production—were identified through in silico analysis. Synthetic antisense RNA molecules were designed to bind specifically to the target mRNAs, inhibiting their translation. RNA constructs were tested in vitro to evaluate their effects on gene expression and bacterial susceptibility to antibiotics.

RESULTS AND DISCUSSION: Treatment with the designed RNAi molecules led to a marked downregulation of target resistance genes. This gene silencing was associated with increased bacterial susceptibility to previously ineffective antibiotics and a notable reduction in bacterial growth and viability. The combined treatment of RNAi and antibiotics demonstrated a synergistic effect in combating MDR P. aeruginosa. RNAi-based gene silencing offers a promising and precise strategy to counteract multidrug resistance in P. aeruginosa. This approach could be developed as a novel adjunctive therapy to enhance antibiotic effectiveness and address the growing threat of antimicrobial resistance

Keywords: Pseudomonas aeruginosa, Multidrug resistance (MDR), RNA interference (RNAi), Antisense RNA,

Determining antibiotic resistance in bacteria isolated from traditional dairy products in Isfahan Province

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BACKGROUND AND OBJECTIVES: Antimicrobial resistance has emerged as a global public health concern, particularly in food sciences. Dairy products like traditional yogurt, which are not heat-treated before consumption, may carry antibiotic-resistant bacteria. Therefore, it is crucial to assess the antibiotic resistance properties of commonly consumed fermented dairy products.

MATERIALS AND METHODS: In this study, 21 samples of traditional dairy products (yogurt, curd, and buttermilk) were randomly collected and analyzed from the Isfahan province. Five grams of each sample were homogenized with 45 ml of peptone water. Serial dilutions were prepared, and 0.5 ml of each dilution was added to nutrient agar media. The plates were incubated for 48 hours at 37°C, and bacterial growth was monitored and identified using biochemical tests and microscopic analysis. The antimicrobial resistance profiles of the isolates were determined using the standard Kirby–Bauer disk diffusion method for nine antibiotics, including Ampicillin, Sulfamethoxazole/trimethoprim, Gentamicin, Tetracycline, Vancomycin, Ciprofloxacin, Rifampicin, Streptomycin, and Cefotaxime.

RESULTS AND DISCUSSION: The results revealed that 30 strains were isolated, most of which were gram-positive isolates from lactic acid bacteria, such as Lactobacillus species. Approximately 20% of the isolates were pathogenic, including Bacillus cereus and Enterobacteriaceae, commonly found in buttermilk and curd. The highest bacterial population was observed in the buttermilk samples. The highest antibiotic sensitivity and resistance were recorded for tetracycline (95%) and ampicillin (65%), respectively. The use of antibiotics in animal feed may contribute to antibiotic resistance among bacteria in dairy products, highlighting the importance of utilizing antibiotic-free starter cultures.

Keywords: Bacteria, Antibiotic, Resistance, Dairy product

Detection and Molecular Characterization of Hepatitis A Virus in Hospital Wastewater in Tehran, Iran

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BACKGROUND AND OBJECTIVES: Hepatitis A is a member of Picornaviridea family that can affect the liver and can be considered as a serious public health problem, especially in areas where sanitation is poor and clean water is not easily available. The virus mainly spreads to humans through the digestive system, often by consuming food or water that has been contaminated. The aim of this study was to detect hepatitis A virus genome in Tehran's hospitals wastewater samples and to determine the predominant genotype.

MATERIALS AND METHODS: In this study, six hospital wastewater samples were collected from six various hospitals in Tehran. The samples were concentrated, the viral RNA was extracted, cDNA was synthesized and HAV genome was detected using nested PCR. Positive sample was sequenced and phylogenetic analysis was performed to determine the genotype.

RESULTS AND DISCUSSION: Out of the 6 samples tested, 1 sample (16.6%) was positive for HAV genome. The positive sample was sequenced and phylogenetic analysis revealed that it belonged to IA genotype. The identification of genotype IA in wastewater can be considered as an indicator of this genotype of the virus circulation in the Iranian community. The relatively high percentage of this virus in hospital wastewater is also a warning of risk that requires further investigation of this virus in the community to control its spread of this virus.

Keywords: Hepatitis A, hospital wastewater, conventional PCR, public health

Detection of Cutaneous HPV in Tehran Hospitals Wastewater

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BACKGROUND AND OBJECTIVES: Cutaneous human papillomaviruses (HPVs), especially those from the beta and gamma genera, are common in the environment and can be found in water reservoirs. Hospital wastewater is a potential source of HPV release, contributing to viral dissemination and environmental exposure. Growing international interest in wastewater-based epidemiology highlights the need to monitor HPV presence in such settings. The aim of this study was to detect cutaneous HPV DNA in wastewater from five hospitals in Tehran.

MATERIALS AND METHODS: In this study, fifty wastewater samples were collected over a three-month period (October to December) from the influents and effluents of five hospitals in Tehran. HPV detection was performed using nested PCR, and Sanger sequencing was conducted to determine types of positive samples.

RESULTS AND DISCUSSION: Out of fifty wastewater samples, 6 tested positive for HPV DNA, representing a 12% positivity rate. Four of the positive samples were sequenced, identifying HPV types 15, 20, and 100. Monitoring pathogenic agents in wastewater is essential for environmental and public health, as it provides insight into virus circulation and potential community exposure. These results underscore the importance of routine environmental water system surveillance

Keywords: Papillomaviridae, Wastewater, Polymerase Chain Reaction, Environmental Monitoring, Hospitals, Water Pollution

Detection of Human Papillomavirus DNA in Fresh Colorectal Tissue Samples

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BACKGROUND AND OBJECTIVES: Colorectal cancer (CRC) represents a serious global health burden, ranking among the most diagnosed malignancies within the healthcare system. Despite several studies that have suggested a probable role for human papillomaviruses (HPV) in CRC, the evidence remains inconclusive, largely because of the wide variation in reported HPV genome in colorectal tumors. The goal of the present survey was to detect the HPV genome in fresh tissues of Iranian colorectal cancer patients in comparison with healthy individuals.

MATERIALS AND METHODS: Ten CRC patients' malignant tissues and adjacent normal tissues with confirmed pathological results, in addition to twenty tissue samples from individuals without malignant conditions were studied. Viral DNA was extracted and the extraction process quality was checked through PCR amplification of a human β-globin gene partial segment. HPV DNA was detected using Nested PCR method by amplifying a conserved region of the L1 HPV genome.

RESULTS AND DISCUSSION: The study included 40 samples from 11 (37%) male and 19 (63%) female. DNA samples positive for the β-globin gene were subsequently tested for HPV. Using the PCR method, none of the 40 tissue samples, including tumor tissues, adjacent normal tissues, and controls, tested positive for HPV DNA. The absence of HPV DNA in all the colorectal tissues indicates that HPV is unlikely to contribute to CRC development in the present study. Given the relatively small sample size, we recommend further research in larger populations to determine any probable association between HPV and CRC.

Keywords: Colorectal Neoplasms, Papillomavirus Infection, Fresh tissue samples, Oncogenic Viruses, Polymerase

Detection of human T-lymphotropic virus type 1 (HTLV-1) and Helicobacter pylori cagA gene in gastric cancer compared to control group in Northwest Iran

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BACKGROUND AND OBJECTIVES: Gastric cancer (GC) is one of the most prevalent and fatal cancers, influenced by multiple factors such as infection with Helicobacter pylori (H. pylori) and human T-lymphotropic virus type 1 (HTLV-1). This study aimed to investigate the presence of HTLV-1 and the cytotoxin-associated gene A (CagA) of H. pylori in cancerous tissue samples and controls in northwest Iran.

MATERIALS AND METHODS: In this descriptive cross-sectional study, 50 cancerous samples (blood samples along with paraffin-embedded tissue samples) and 50 control samples were collected from hospitals in East Azerbaijan Province over 11 months (May 2024 to April 2025). To detect the presence of HTLV-1 antibodies, enzyme-linked immunosorbent assay (ELISA) testing was used, and polymerase chain reaction (PCR) was employed to identify the presence of the cagA gene.

RESULTS AND DISCUSSION: Among 50 cancer samples, 5 tested positive for HTLV-1 antibodies by ELISA. Additionally, 10 samples were positive for the cagA gene by PCR. No positive cases for cagA gene or HTLV-1 antibodies were found in the control group. In this study, no significant association was observed between the presence of the cagA gene and HTLV-1 infection in patients with GC. This study demonstrated the presence of the cagA gene and HTLV-1 antibodies in GC patients, while no cases were detected in the control group. However, more extensive studies are required to validate these findings and investigate the precise underlying mechanisms.

Keywords: Helicobacter pylori, Human T Lymphotropic Virus 1, Bacterial infection, Gastric

Detection of Listeria monocytogenes in Ardabil's Milk Supply Using Molecular Method

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BACKGROUND AND OBJECTIVES: Listeria monocytogenes, a leading bacterial pathogen responsible for human listeriosis, is associated with sporadic foodborne outbreaks and contaminated food consumption, posing significant health risks, especially to vulnerable individuals. This cross-sectional study investigates the prevalence of L. monocytogenes in bulk milk samples obtained from Ardabil province, Iran.

MATERIALS AND METHODS: A total of 281 unpasteurized bulk milk samples were collected from cattle, sheep, and goats in Ardabil province, Iran, between April and August 2024. The samples were hygienically transported and kept at -20 °C. DNA extraction was conducted on 15 mL of milk, followed by pathogen identification using the polymerase chain reaction (PCR) and sequencing methods.

RESULTS AND DISCUSSION: Among 281 bulk milk samples, the overall prevalence of L. monocytogenes was recorded at 1%. Detection rates varied across different milk sources: 1.4% in cattle (2 out of 138 samples), 0.8% in sheep (1 out of 113 samples), and no presence detected in goat milk (0 out of 30 samples). Conclusion: This study highlights the presence of L. monocytogenes in unpasteurized bulk milk samples from Ardabil province, Iran. While the overall prevalence was relatively low, the detection of the pathogen in cattle and sheep milk underscores the potential risks associated with raw milk. The absence of L. monocytogenes in goat milk samples suggests possible species-specific differences in contamination susceptibility. These findings emphasize the importance of stringent hygiene practices and routine microbial monitoring in dairy production to mitigate public health risks and ensure food safety.

Keywords: Milk, Listeria monocytogenes, PCR

Detection of new polymorphisms in 23S rRNA and rfaF genes among clarithromycin-resistant Helicobacter pylori isolates in Iran

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BACKGROUND AND OBJECTIVES: Introduction: Several point mutations in the 23S rRNA gene are associated with antibiotic resistance to clarithromycin in Helicobacter pylori. Additionally, mutations in rfaF can induce amino acid changes in a protein involved in H. pylori cell wall formation, which increases drug resistance against several antibiotics, including clarithromycin. Detection of common mutations in each geographic area can help treatment regimens for H. pylori eradication.

MATERIALS AND METHODS: Methods: In this study, sequencing was performed on clarithromycin-resistant and -susceptible clinical isolates from symptomatic adults to detect common mutations in 23S rRNA and rfaF genes relative to a reference strain. Resistance of clinical H. pylori isolates to clarithromycin was assessed using the E-test method.

RESULTS AND DISCUSSION: Results: In total, 68% of clinical H. pylori isolates were resistant to clarithromycin. Sequencing of resistant isolates revealed an A2142C mutation in 12% and a novel mutation, A2056G, in 35% of the isolates, as common polymorphisms associated with the clarithromycin resistance phenotype. Other mutations, such as A2055G, T2095C, and A2213G, were also detected. A2056G mutation was significantly higher in the resistant isolates (35% vs 0% in susceptible isolates; p-value= 0.03). The majority of amino acid changes in rfaF were located in the C-terminal region of the resistant isolates, whereas in susceptible isolates, changes were frequently observed in the N-terminal region. Conclusion: High frequency of clarithromycin resistant strains and emergence of new mutations in the genes linked to the development of resistance phenotype in H. pylori is concerning in Iran.

Keywords: Keywords: Helicobacter pylori, mutation, clarithromycin-resistance, clarithromycin-susceptible, 23S rRNA, rfaF

Detection of shiga toxin coding gene in Escherichia coli isolates obtained from shrimp

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BACKGROUND AND OBJECTIVES: Shiga toxin-producing Escherichia coli (STEC) is one of the most significant foodborne pathogens, which inhibit protein synthesis in target cells, leading to severe damage in intestinal epithelial and vascular endothelial cells. This mechanism leads to diarrhea in both humans and animals; however, strains that produce stx2 are more strongly associated with severe complications such as hemolytic uremic syndrome (HUS). This study was conducted with the aim of identifying this virulence gene in Escherichia coli isolated from shrimp.

MATERIALS AND METHODS: In this study, 96 shrimp samples were collected from Kerman and processed within 24 hours under cold chain conditions. Homogenized samples were cultured on selective media, and purified colonies underwent DNA extraction via the boiling method and The Touchdown PCR technique was employed to detect the virulence gene.

RESULTS AND DISCUSSION: The results indicated that out of the 96 shrimp samples collected, 76 (79.17%) were confirmed positive for E. coli based on biochemical tests. Following PCR analysis The prevalence of the shiga toxin virulence gene, which encodes STEC pathotype was observed in 11 samples (14.47%) that Among these, 4 isolates (5.26%) carried the stx1 gene, while 7 isolates (9.21%) harbored the stx2 gene. Considering that the bacterium Escherichia coli is not naturally separated from shrimp and other aquatic organisms, but the results of the present study indicate a significant contamination with STEC pathotype. These measures, including thorough cooking and proper packaging of shrimp can significantly improve food safety and public health by minimizing the risk of E. coli contamination.

Keywords: E.coli, STEC, HUS, shrimp, foodborne pathogens.

Determination of ESBL producing Enteroaggregative Escherichia coli isolated from clinical samples in Bushehr

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BACKGROUND AND OBJECTIVES: Enteroaggregative Escherichia coli (EAEC) causes chronic intestinal inflammation in children, leading to malnutrition and growth retardation. EAEC is also the second leading cause of travelers' diarrhea after ETEC strains. Bacterial strains producing extended-spectrum beta-lactamases (ESBLs) inactivate beta-lactam drugs, and the widespread dissemination of plasmid-borne ESBLs among E. coli isolates is a global problem. Purpose of this study was to find out the incidence of ESBL producing EAEC strains from patients with diarrhea.

MATERIALS AND METHODS: A total of 12 EAEC isolates collected from stool samples of diarrheic patients by PCR for aggR and pCVD432 genes from November 2021 to April 2022 in Bushehr province. EAEC isolates were analyzed to detect ESBL producing through phenotypic combined disk test (CDT) according to CLSI recommendations and molecular identification of blaCTX-M, blaTEM and blaSHV genes.

RESULTS AND DISCUSSION: In total, 41.6% of isolates were found to be ESBL producers with CDT. PCR was performed for EAEC isolates, and 25%, 50%, 8.3% of the isolates showed blaCTX-M, blaTEM and blaCTX-M + blaTEM genes, respectively. None of the isolates carried the blaSHV gene. The most common beta-lactamase genes reported in ESBL-producing DEC isolates include blaCTX-M and blaTEM with the highest frequency of ESBL enzymes found in E. coli pathotypes. It is recommended that clinical laboratories use ESBL detection methods in gastrointestinal pathotypes of E. coli, as a helpful guide for empirically treating bacterial infections.

Keywords: Enteroaggregative Escherichia coli, Diarrhea, beta-lactamases, PCR.

Development of a Novel Aptamer for the Detection of Staphylococcal Enterotoxin Type D

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BACKGROUND AND OBJECTIVES: Staphylococcal food poisoning (SFP) is one of the most significant foodborne diseases caused by the ingestion of heat-resistant staphylococcal enterotoxins. Pasteurization of food kills staphylococci but usually does not affect the activity of exotoxins. Consequently, rapid, sensitive, and reliable detection methods are crucial for routine monitoring of SED. Aptamer technology is one of the newer approaches introduced into the field of molecular diagnostics. Aptamers are oligonucleotides composed of ssRNA or ssDNA molecules or peptide molecules that can bind to their targets with high specificity and affinity due to their unique three-dimensional structure.

MATERIALS AND METHODS: The current study aimed to isolate high-affinity single-stranded DNA (ssDNA) aptamers that target SED. In this study, we identified aptamers using the Systematic Evolution of Ligands by Exponential Enrichment (SELEX) approach, the Enzyme-Linked Apta-Sorbent Assay (ELASA), and Surface Plasmon Resonance (SPR).

RESULTS AND DISCUSSION: Several aptamers obtained via the SELEX procedure were examined. Aptamer 1, with a dissociation constant (KD) of 4.4 ± 2.26 nM, demonstrated favorable specificity for SED. The limit of detection (LOD) for SEC was 45 nM. Our results suggest that the design of the ELASA system, using the aptamer obtained from this research, can measure enterotoxin D in samples with higher specificity, sensitivity, and reproducibility.

Keywords: Staphylococcus aureus, staphylococcal enterotoxin D, SELEX, ssDNA-aptamer, ELASA, SPR.

Diagnostic Evaluation and Clinical Associations of Helicobacter pylori Infection in Gastrointestinal Patients from Southwest Iran

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BACKGROUND AND OBJECTIVES: Helicobacter pylori (H. pylori), a globally prevalent pathogen, is the primary cause of various gastrointestinal disorders, ranging from chronic gastritis to gastric cancer. Early and accurate detection of H. pylori infection is crucial for preventing disease progression. This study aimed to assess the prevalence of H. pylori in Khuzestan Province, southwest Iran, using the rapid urease test (RUT), histology, and PCR.

MATERIALS AND METHODS: In this cross-sectional study (2023–2024), 550 patients with gastrointestinal symptoms referred to the Endoscopy Unit of Imam Khomeini Hospital, Ahvaz, were evaluated. Gastric biopsy specimens were tested using RUT and histology. PCR (ureB gene) was performed on RUT-positive specimens to confirm infection. Associations between clinical symptoms, endoscopic findings, and H. pylori infection were analyzed using appropriate statistical tests.

RESULTS AND DISCUSSION: The overall prevalence of H. pylori infection in Khuzestan was 51.8% (285/550). RUT (PCR-confirmed) detected infection in 35.1% (193/550) of patients, while histology identified 234 positives (49.4%) among 474 patients with available results. The highest infection rates were observed in the eastern (58.9%), northern (55.9%), and central-western regions (52.0%), while the south had the lowest rate (41.4%). Significant associations were found between H. pylori infection and melena, antral nodularity, and duodenal ulcer. The high prevalence of H. pylori in Khuzestan underscores the need for effective screening and eradication programs, with regional variations calling for targeted interventions. Histology demonstrated higher sensitivity than RUT, and PCR improved diagnostic accuracy. Melena, antral nodularity, and duodenal ulcer may serve as important clinical predictors of infection.

Keywords: Helicobacter pylori, Gastrointestinal diseases, Urease test, Histological Examination, PCR

Discovery of Potent Inhibitors Targeting Pneumolysin of Streptococcus pneumoniae via Molecular Docking Analysis

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BACKGROUND AND OBJECTIVES: Streptococcus pneumoniae is a significant pathogen responsible for pneumonia, and meningitis. Pneumolysin, a key cholesterol-dependent cytolysin produced by S. pneumoniae, contributes to its virulence by disrupting host cell membranes and triggering immune responses. Inhibiting pneumolysin has emerged as a promising therapeutic strategy to reduce pneumococcal pathogenicity. This study evaluated the inhibitory potential of natural flavonoids, including epigallocatechin gallate (EGCG) and wogonin, along with their structural analogs, against pneumolysin using molecular docking.

MATERIALS AND METHODS: The crystal structure of pneumolysin was obtained from the RCSB PDB (PDB ID:5Cr6). EGCG (PubChemCID:65064) and wogonin (PubChemCID:5281703) and a total of 200 structural analogs were retrieved from PubChem database. Protein and ligand preparation were performed via 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. The pharmacokinetic properties of the best ligand were then evaluated using SwissADME server.

RESULTS AND DISCUSSION: Among All Ligands , [(2R,3R)-2-(3,4-dihydroxyphenyl)-5,7-dihydroxy-chroman-3-yl] octanoate (PubChemCID: 3009235; molecular weight 416.5g/mol) demonstrated the most energetically favorable binding (ΔGbind: -135.809kcal/mol) to pneumolysin. It formed six hydrogen bonds and eight steric interactions. Pharmacokinetic profiling revealed moderate water solubility (LogS -4.60), favorable lipophilicity (LogP 3.9), four hydrogen bond donors, and seven acceptors, with a polarity index of 116.45 $Å^2$. These findings highlight PubChemCID 3009235 as a promising pneumolysin inhibitor for future drug development against S. pneumoniae. Further experimental studies are recommended to validate these computational results.

Keywords: Streptococcus pneumoniae, Pneumolysin, Molecular Docking, Epigallocatechin gallate.

Distribution of Pathogenicity Islands and Antibiotic Resistance Patterns in Uropathogenic Escherichia coli Isolates

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BACKGROUND AND OBJECTIVES: Urinary tract infections (UTIs) are common bacterial infections primarily caused by Escherichia coli. Pathogenicity islands (PAIs) contribute to the virulence and antibiotic resistance of uropathogenic E. coli (UPEC). This study aimed to assess the distribution of PAIs and their association with antibiotic resistance in UPEC isolates.

MATERIALS AND METHODS: A total of 100 E. coli isolates were collected from UTI patients. The presence of PAIs (I–IV from strains 536, CFT073, and J96) was detected using PCR. Antibiotic susceptibility was tested by the disk diffusion method following CLSI guidelines.

RESULTS AND DISCUSSION: The most frequent PAIs were PAI IV 536 (23%), PAI III 536 (22%), PAI I 536 (17%), and PAI II CFT073 (17%). The highest resistance rates were observed for ampicillin (87%), trimethoprim-sulfamethoxazole (65%), and ciprofloxacin (57%). In contrast, imipenem (96%) and nitrofurantoin (92%) showed the highest effectiveness. A statistically significant association was found between certain PAIs and antibiotic resistance (p 0.05). These findings align with previous studies in Iran and globally. Our results highlight the role of PAIs in resistance development in UPEC, underscoring the need for molecular surveillance to guide appropriate antibiotic therapy.

Keywords: Uropathogenic Escherichia coli, Urinary tract infection, Pathogenicity islands, Antibiotic resistance

Diversity and identification of phytase-producing fungi from undisturbed Ecosystems of Delfan Region, Iran

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BACKGROUND AND OBJECTIVES: The global scarcity of inorganic phosphorus and environmental concerns arising from undigested phytate in agricultural and animal waste have underscored the importance of microbial phytases. Fungal-derived phytases have attracted interest due to their efficiency and adaptability. This study aimed to isolate and characterize phytase-producing fungal strains from natural habitats in Nurabad Delfan County, Lorestan Province, Iran.

MATERIALS AND METHODS: Samples were collected from ten sites across agricultural lands, poultry litter, mineral and hot springs, and surrounding soils in the villages of Darkoli, Cheshmeh Abe Garm, Alafsaneh, and Shahanabad. Fungal enrichment was carried out using a phytase screening medium (PSM) containing phytic acid as the sole phosphorus source. Strains exhibiting clear halos were selected as indicative of phytase activity. Morphological and microscopic characteristics were used for preliminary identification of isolates.

RESULTS AND DISCUSSION: Out of 29 isolated fungal strains, 13 showed detectable phytase activity. These isolates were affiliated with the genera Aspergillus, Penicillium, Mucor, and Rhizopus. Among them, isolates PN4-b (Aspergillus sp.) and PN4-g(Penicillium sp.), obtained from soil samples, respectively, exhibited the highest enzymatic activity. These two were selected for advanced molecular identification and quantitative phytase assays. The initial findings indicate both isolates are strong candidates for biotechnological exploitation. The Nurabad Delfan region supports a rich fungal diversity with notable phytase-producing potential. Selected native strains, particularly PN4-g and PN4-b, offer promising prospects for industrial applications such as eco-friendly phosphorus supplementation in poultry and aquaculture feed. Ongoing studies include optimization of enzyme production under solid-state fermentation and precise measurement of phytase yields.

Keywords: Delfan, Phytase, Enzymatic activity, Fungi

DNA Origami Nanostructures: A Novel Approach to Combat Antimicrobial Resistance

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BACKGROUND AND OBJECTIVES: Antimicrobial resistance represents one of the most urgent health issues worldwide, where pathogenic microorganisms no longer respond to conventional antimicrobial treatments. This crisis contributes to approximately 7.7 million deaths annually from bacterial infections, underlining the pressing demand for innovative therapeutic strategies (1). Recent advances in synthetic biology have emerged as promising solutions to combat antimicrobial resistance. DNA origami, a robust self-assembly technique giving rise to two- and three-dimensional DNA based nanostructures, offers novel opportunities for developing next-generation antimicrobial interventions.

MATERIALS AND METHODS: Herein, we review recent advances regarding the application of DNA origami in addressing antimicrobial resistance by searching on "Google Scholar" database for publications.

RESULTS AND DISCUSSION: DNA origami nanostructures are fabricated by folding a long single-stranded DNA scaffold with short staple strands, yielding structures with subnanometer precision (2). Such nanostructures hold significant potential in combating antimicrobial resistance through two key mechanisms. First, they could function as antimicrobial delivery systems (3). Their highly specific and efficient targeted antimicrobial delivery reduces off-target effects, leading to resistance development. Second, DNA origami-based nanocompartments successfully confined and organized chemical reactions, creating artificial nanofactories that eliminated the need for cellular environments (4). This approach tackles antimicrobial resistance by compartmentalizing biosynthetic enzymes to enhance antibiotic production. Additionally, these nanocompartments enable the development of novel antimicrobial pathways for synthesizing new antibiotic compounds. DNA origami represents a transformative approach in combating antimicrobial resistance, offering dual functionality as targeted delivery systems and artificial nanofactories with promising potential for next-generation antimicrobial interventions.

Keywords: Drug Resistance, Microbial, DNA, Nanotechnology, Synthetic Biology

Dual Targeting of Enzymatic and Efflux Resistance Mechanisms in Acinetobacter baumannii Using a Combined Drug Approach

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BACKGROUND AND OBJECTIVES: Acinetobacter baumannii is a major cause of carbapenem-resistant nosocomial infections. Two primary mechanisms underlying this resistance are the production of metallo-beta-lactamases (MBLs) and the overexpression of efflux pumps. This study aimed to inhibit MBL activity using the metal chelator ethylenediaminetetraacetic acid (EDTA) and to counteract drug efflux using doxepin, a lipophilic tricyclic compound with potential efflux pump-inhibitory properties. The objective was to evaluate the synergistic effects of these agents in combination with meropenem.

MATERIALS AND METHODS: Carbapenem-resistant A. baumannii isolates were collected and screened for MBL production using the imipenem/EDTA combination disk test. A checkerboard assay was then conducted to assess the synergistic interaction between meropenem and EDTA, and the fractional inhibitory concentration index (FICI) was calculated to determine synergy. Subsequently, doxepin was added to the synergistic combination to evaluate its effect on efflux pump inhibition and its impact on the minimum inhibitory concentration (MIC) of the regimen.

RESULTS AND DISCUSSION: The combination disk assay confirmed MBL production in the isolates. The meropenem–EDTA combination demonstrated a significant reduction in MIC compared to either agent alone, indicating a synergistic interaction. The addition of doxepin to this combination led to a further two-fold decrease in MIC, suggesting effective inhibition of efflux pump activity and enhanced antibacterial efficacy. The triple combination of meropenem, EDTA, and doxepin may offer a promising approach to overcoming multidrug resistance in A. baumannii. Further molecular studies are warranted to elucidate the exact role of doxepin as an efflux pump inhibitor.

Keywords: Acinetobacter baumannii, Drug Resistance, Metallo-Beta-Lactamase, Chelating Agents, Efflux Pumps, Doxepin

Dual-Function PEGylated ZIF-8-CIP Nanozymes for Targeted Quorum Sensing Disruption and Biofilm Eradication in Ciprofloxacin-Resistant Pseudomonas aeruginosa

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BACKGROUND AND OBJECTIVES: Ciprofloxacin-resistant Pseudomonas aeruginosa (CRP) poses a critical challenge in the treatment of burn wound infections due to its ability to form resilient biofilms and regulate virulence through the quorum sensing (QS) system. Targeting QS pathways has emerged as an effective strategy for disrupting biofilm-associated resistance. This study aimed to develop and evaluate ciprofloxacin-loaded PEGylated ZIF-8 nanozymes (PEG-ZIF-8-CIP) as a dual-function nanoplatform for enhanced antibacterial activity and QS inhibition.

MATERIALS AND METHODS: ZIF-8-based nanozymes were synthesized and characterized by FESEM, DLS, zeta potential, and FTIR analyses. Their antibacterial and antibiofilm activities were assessed via disk diffusion, MBEC assays, and time-dependent biofilm removal studies. Gene expression of QS regulators (lasI, lasR, rhlI, and rhlR) was evaluated using RT-PCR.

RESULTS AND DISCUSSION: PEG-ZIF-8-CIP nanozymes demonstrated significantly higher antimicrobial and antibiofilm activity compared to free CIP and other ZIF-8 formulations. The formulation effectively downregulated all four key QS genes, confirming its anti-virulence potential. PEGylation improved particle stability, reduced aggregation, and enhanced biofilm penetration. PEG-ZIF-8-CIP represents a promising nanotherapeutic candidate for treating CRP infections in burn wounds by combining controlled antibiotic delivery with quorum sensing inhibition. This dual-action strategy holds potential to overcome conventional antibiotic resistance.

Keywords: Pseudomonas aeruginosa, ZIF-8 Nanozyme, PEGylation, Ciprofloxacin, Quorum Sensing, Biofilm, Burn.

Dual-Gene PCR Assay for Rapid Identification of Uropathogenic Escherichia coli (UPEC)

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BACKGROUND AND OBJECTIVES: Uropathogenic Escherichia coli accounts for over 80% of E. coli caused urinary tract infections (UTI) which encompass around 80% of acute UTI and 33% of catheter associated UTI. The ability of E. coli in spreading and acquiring resistance genes, can lead to more complicated and hard-to-treat infections. Therefore, it is important to identify the different pathogenic groups for determining the best treatment approach and for purposes such as epidemiological, virulence factor, and antibiotic resistance studies. The goal of this study is to develop a rapid and reliable identification method of UPEC pathotypes.

MATERIALS AND METHODS: Forty two pathogenic E. coli, isolated from UTI patient urine samples in several hospitals and labs across the city, were used in UPEC identification. Through comparing various genotypic and epidemiologic data regarding UPEC bacteria, two genes with efficient characteristics to be used as identifiers in PCR were detected. chuA and c3509 are both frequently observed in UPEC isolates and are specific to this strain. Primers were designed for both genes and subsequently used in PCR analysis.

RESULTS AND DISCUSSION: Amongst these UTI causing E. coli, 83% (35/42) possess c3509, 23% (8/35) being only positive for c3509. Meanwhile, 73% (31/42) possess chuA, 16% (5/31) being only positive for chuA. Overall, 59% (25/42) of the total were positive for both genes. Considering the high phylogenetic coverage of the genes and the UTI origin of the tested isolates, it can be concluded that they can detect UPEC in approximately 90% of E. coli cases.

Keywords: Uropathogenic Escherichia coli, urinary tract infection, PCR, virulence factor

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 OBJECTIVES: 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.

MATERIALS 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 P0.05.

RESULTS AND DISCUSSION: The 20-ppm ozone and 1% CHX gels significantly decreased dental plaque compared to the control group (P0.05), and their effects were similar (P0.05). These gels significantly decreased the colonies and bacterial counts of S. mutans (P0.05).

Keywords: Chlorhexidine gel; Dental plaque; Ozone gel; Streptococcus mutans. ©2023

Effect of aqueous and alcoholic extracts of Marrubium anisodon on the growth and expression of the alpha hemolysin gene in Staphylococcus aureus

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BACKGROUND AND OBJECTIVES: : Staphylococcus aureus is a significant bacterial pathogen leading to serious human infections. Hence, This study aims to investigate the effects of aqueous and alcoholic extracts of the medicinal herb (Marrubium anisodon) on the growth and expression of the alpha hemolysin gene in the bacterium.

MATERIALS AND METHODS: In this study 100 suspected samples of Staphylococcus aureus were collected from medical centers in Shiraz. After conducting phenotypic tests, the antibiotic resistance patterns were evaluated using the disk diffusion method. Then the prevalence of the alpha hemolysin gene (Hla) was assessed using PCR. Finally, antibacterial properties of Marrubium anisodon were tested using the Minimum Inhibitory Concentration (MIC) method. Additionally, the expression levels of the gene were determined after treatment with the plant extracts using Real-Time PCR.

RESULTS AND DISCUSSION: in this project, out of 100 samples 19 were detected as Staphylococcus aureus. the results indicated that the organism showed different antibiotics susceptibility. the highest resistance belonged to penicillin (100%) and the lowest to gentamicin (36.84%). The antibacterial effects of aqueous extract had positively influenced on the expression of the Hla gene, Given the rising antibiotic resistance in Escherichia coli and Staphylococcus aureus, there is an urgent need for new strategies to control infections and prevent the spread of drug resistance. This study demonstrates the antimicrobial effects of Marrubium anisodon extracts on the examined bacteria and their influence on the expression of hemolysin genes.

Keywords: Staphylococcus aureus, α-hemolysin gene, Marrubium anisodon.

Effect of chitosan /Campylobacter jejuni secretome nanocomposite on the expression of CRC signaling pathway genes

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BACKGROUND AND OBJECTIVES: Colorectal cancer (CRC) is one of the most common cancer worldwide, with a high mortality rate; hence, the use of alternative therapeutic method 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 CRC.

MATERIALS 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 CRC signaling pathway genes on Caco-2 cell were evaluated via real-time PCR method.

RESULTS AND DISCUSSION: : The particle size and zeta potential were recorded 159.7± 5.0 nm and + 4.5 mV, respectively. 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. The nanoparticle also demonstrated the greatest efficacy in suppressing the expression of TGFα, Bcl2, TLR4, CEA, TGF-β, and PI-3K oncogenes by to 0.06 , 0.34 , 0.14 , 0.13 ,0.08 and 0.14-fold (p value.0001) .Despite, it led to a significant increase in the expression of the suppressor genes CASP9 and PTEN by to 55.7 and 1.8-fold (p value.0001). CS-Cj-sup NP with significant anticancer properties can be considered as an alternative option for CRC treatment.

Keywords: Colorectal cancer, Campylobacter jejuni, Oncogenes, Suppressor Genes

Effect of cytoplasmic extract of Lactobacillus leichmannii on Murine Colon Carcinoma Cell Line (CT26)

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BACKGROUND AND OBJECTIVES: Probiotics and their derived components have been shown in preclinical research, to be potential anti-cancer agents. In this study the effect of the cytoplasmic extract of Lactobacillus leichmannii was investigated on the viability of CT26 (colorectal cancer).

MATERIALS AND METHODS: CT26 cells were treated with the cytoplasmic extract of L. leichmannii at two different concentrations and incubated for 24, 48, and 72 hours. The viability of the cells were determined at each time point using the MTT assay.

RESULTS AND DISCUSSION: The cytoplasmic extract of L. leichmannii significantly reduced the viability of CT26 cells compared to the control group at all time points. This effect was dependent on both the concentration of the extract and the incubation time. After 24 hours, the higher concentration indicated a greater inhibitory effect than the lower concentration. After 48 hours, both concentrations led to the maximum reduction in cell viability. The lower concentration exhibited a more inhibitory effect than the higher concentration after 48 hours. This pattern indicated a non-linear, time and dose-dependent response. All of the changes were statistically significant ($P \leq 0.05$). The cytoplasmic extract of L. leichmannii significantly reduced the viability of CT26 cells in vitro. The observed effects were dependent on the concentration and duration of treatment, with the greatest inhibition after 48 hours. These results provide the basis for further studies underlying the anticancer effects of L. leichmannii extract by molecular mechanisms.

Keywords: Probiotic, Lactobacillus leichmannii, Antitumor effect, CT26, In Vitro Techniques

Effect of Galactose on Expression of Transferrin in Pichia pastoris

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BACKGROUND AND OBJECTIVES: Introduction: Transferrin, an iron-binding glycoprotein, has therapeutic applications, but its efficient production in microbial hosts remains a challenge. Pichia pastoris is a widely used expression system, typically induced by methanol, which poses safety and regulatory concerns. This study explores galactose as an alternative inducer for recombinant transferrin production.

MATERIALS AND METHODS: Materials and Methods: The study used Pichia pastoris X-33 strain transformed with a transferrin-expressing vector. Cultures were grown in buffered glycerol-complex medium (BMGY) and induced with galactose (0.5–2%) in methanol-free BMMY. Cell density (OD600) and protein expression were analyzed at 24, 48, and 72 hours. SDS-PAGE and anti-transferrin Western blotting quantified expression. Controls included methanol-induced cultures. Data were normalized to total protein (Bradford assay) and statistically analyzed (ANOVA, p 0.05).

RESULTS AND DISCUSSION: Results: Galactose successfully induced transferrin expression, with optimal yields at 1% concentration. Maximal protein production occurred at 48 hours post-induction. Compared to methanol-induced cultures, galactose showed comparable expression levels while eliminating methanol-associated toxicity risks. Conclusion: Galactose is a viable and safer alternative to methanol for transferrin expression in P. pastoris, offering potential for scalable biopharmaceutical production. Further optimization could enhance yield and cost-efficiency. Discussion: Galactose produced transferrin levels matching methanol, with faster growth and no toxicity. Peak expression occurred at 1% galactose, indicating optimal induction. Unlike methanol, galactose removes explosion hazards, facilitating scale-up. Reduced yields at 2% suggest carbon repression. Future work could explore mixed feed strategies or promoter modifications. Galactose emerges as a safer, practical inducer for Pichia-based bioproduction.

Keywords: Keywords: Pichia pastoris, galactose, transferrin, expression.

Effect of phenylalanine arginyl β-naphthylamide on the imipenem resistance, elastase production, and the expression of quorum sensing and virulence factor genes in Pseudomonas aeruginosa clinical isolates

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BACKGROUND AND OBJECTIVES: P. aeruginosa is one of the most important nosocomial pathogens that possess the ability to produce multiple antibiotic resistance and virulence factors. LasB is the major factor implicated in tissue invasion and damage during P. aeruginosa infections, whose synthesis is regulated by the quorum sensing system. Anti-virulence approach is now considered as potential therapeutic alternative and/or adjuvant to current antibiotics' failure. The aim of this study is primarily to find out the impact of the efflux pump inhibitor phenylalanine arginyl β-naphthylamide (PAβN) on the production of elastase B and the gene expression of lasI quorum sensing and lasB virulence factor in clinical isolates of P. aeruginosa.

MATERIALS AND METHODS: Five P. aeruginosa isolates recovered from patients with respiratory tract infections were examined in this study. Antimicrobial susceptibility of isolates was performed by the disk agar diffusion method. Effect of the PAβN on imipenem susceptibility, bacterial viability, and elastase production was evaluated. The expression of lasB and lasI genes was measured by quantitative real-time PCR in the presence of PAβN.

RESULTS AND DISCUSSION: All isolates showed resistance to carbapenem (MIC = 64–256 µg/mL). Susceptibility of isolates to imipenem was highly increased in the presence of efflux inhibitor. PAβN significantly reduced elastase activity in three isolates tested without affecting bacterial growth. In addition, the relative expression of both lasB and lasI genes was diminished in all isolates in the presence of inhibitor. Efflux inhibition by using the EPI PAβN could be a potential target for controlling the P. aeruginosa virulence and pathogenesis.

Keywords: Phenylalanine arginyl β-naphthylamide · P. aeruginosa

Effect of slvador persica on bacterial resistant in pressur ulcers

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BACKGROUND AND OBJECTIVES: Bedsores are common in immobile patients and often become infected with bacteria like Staphylococcus aureus and Pseudomonas aeruginosa, complicating treatment. This study evaluated the antibacterial effect of ethanolic extract of Salvadora persica on bacteria isolated from bedsores. Extracts at concentrations of 80, 150, 200, and 300 g/L were tested using the well diffusion method. Results showed no inhibitory effect at any concentration. Factors such as plant variety, extraction method, and test conditions may influence the outcome.

MATERIALS AND METHODS: Salvadora persica was collected from Sistan and Baluchestan, dried, and powdered. Fifty grams of powder was soaked in 96% ethanol for 72 hours at room temperature. Extracts were prepared at 80, 150, 200, and 300 g/L. Samples from 50 patients' bedsores were cultured on blood agar. Bacterial suspensions (2×10^8 CFU/mL) were prepared using the McFarland standard. Antibacterial activity was tested using the well diffusion method on Mueller-Hinton agar. Streptomycin and 70% ethanol served as positive and negative controls, respectively.

RESULTS AND DISCUSSION: The ethanolic extract of Salvadora persica at concentrations of 80, 150, 200, and 300 g/L showed no visible inhibition zones against bacteria isolated from bedsore samples. In contrast, streptomycin (positive control) produced clear zones of inhibition in all tested plates, while 70% ethanol (negative control) showed no antibacterial activity. These findings suggest that under the conditions used, the extract had no inhibitory effect on bacterial growth. Possible reasons include the plant species used, the solvent (ethanol), extraction conditions, or experimental variables such as well diameter and extract diffusion in the medium.

Keywords: Salvadora persica

Effect of Thymol on Beta-Lactamase Inhibition and Enhancement of Beta-Lactam Antibiotic Efficacy Against Multidrug-Resistant Clinical Isolates of Klebsiella pneumoniae

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BACKGROUND AND OBJECTIVES: One of the most important resistance mechanisms in Klebsiella pneumoniae against commonly used beta-lactam antibiotics is the production of beta-lactamase enzymes. The aim of this study was to investigate the effect of thymol on beta-lactamase inhibition and its potential to enhance the efficacy of beta-lactam antibiotics against multidrug-resistant clinical isolates of Klebsiella pneumoniae.

MATERIALS AND METHODS: Clinical isolates of Klebsiella pneumoniae were collected from urine samples in diagnostic laboratories in Rasht in 2024. Identification was confirmed by biochemical tests. Antibiotic resistance was assessed by disk diffusion, and beta-lactamase production detected by the combined disk method. Thymol's effect on beta-lactamase-producing isolates was evaluated by determining minimum inhibitory concentration (MIC) and using the nitrocefin disk test. Synergistic effects of thymol combined with ceftazidime, cefotaxime, and cefoxitin were assessed by the checkerboard method.

RESULTS AND DISCUSSION: Results. Inhibition zones by 1 mg thymol against ten multidrug-resistant, beta-lactamase-producing isolates ranged from 14 to 32 mm. MIC values ranged from 0.98 to 15.6 mg/mL. Thymol above 1 mg prevented nitrocefin hydrolysis and color change. Combined with cefotaxime, thymol showed an additive effect in 70% of isolates, reducing cefotaxime MIC 2- to 16-fold. For cefoxitin, thymol had additive effects in four isolates and synergistic effects in two, reducing MIC 2- to 8-fold. Conclusion. These findings indicate that thymol possesses antimicrobial and beta-lactamase inhibitory properties. In combination with beta-lactam antibiotics such as cefotaxime and cefoxitin, thymol offers a promising basis for developing new therapeutic strategies against beta-lactamase-producing bacteria.

Keywords: Klebsiella pneumoniae, beta-lactamase, antibiotic resistance, thymol effect

Effectiveness of Multimodal Infection Control Strategies Against Carbapenem-Resistant Acinetobacter baumannii and Klebsiella pneumoniae: Data from an Iranian Referral Center

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BACKGROUND AND OBJECTIVES: Carbapenem-resistant Gram-negative bacteria (CR-GNB), particularly CRAB and CRKP, have become increasingly prevalent worldwide. This study evaluates infection prevention and control (IPC) measures against these pathogens.

MATERIALS AND METHODS: We conducted a quasi-experimental study in a tertiary Iranian ICU from September 2018 to September 2021, divided into seven 6-month periods. Multimodal IPC interventions were implemented starting in Period 2, with a temporary suspension during Period 4 (March-September 2020) due to COVID-19 disruptions. We longitudinally compared CRKP/CRAB prevalence and antimicrobial resistance patterns across all periods.

RESULTS AND DISCUSSION: In total, 1,862 GNB isolates were identified across seven periods, with K. pneumoniae (41%) being the most prevalent pathogen, followed by Escherichia coli (24.6%) and A. baumannii (14%). The highest antibiotic resistance rates, including 65.5% for meropenem, were observed during the fourth period. From September 2019 to March 2022, 178 CRKP and 97 CRAB isolates were identified, with infection rates of 78.1% and 62.9%, respectively. Following IPC interventions, a significant reduction in CRKP and CRAB prevalence was noted in the second and third periods, although an increase occurred during the fourth period. By the seventh period, the lowest prevalence of CRKP (26 isolates) and CRAB (5 isolates) was observed. Finally, a moderate inverse correlation (-0.571) was found between hand hygiene compliance and mortality incidence. IPC bundles significantly decreased CRKP/CRAB rates, but pandemic disruptions revealed vulnerability. Sustained success requires: (1) real-time surveillance, (2) ongoing IPC training, and (3) protocol adherence.

Keywords: Keywords: Infection prevention and control (IPC), Carbapenem-resistant, Gram-negative bacteria

Effects of Lactobacillus fermentum FH5 and capecitabine on colon cancer management and related apoptosis and inflammatory markers expression in BALB/c model

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BACKGROUND AND OBJECTIVES: Colon cancer is one of the most common and dangerous types of cancer that 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 a colon cancer model.

MATERIALS AND METHODS: We used probiotic 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 before tumor implantation and 4 weeks after CRC induction. Also, capecitabine was orally added at the last week of treatment procedure. Their anticancer effects were evaluated by tumor size measurement, apoptotic (Bax, Bcl-2, Caspase-3) and inflammatory markers (TNF-α, IL-18, IL-1β) analysis.

RESULTS AND DISCUSSION: In the tumor groups treated with capecitabine, probiotic and the capecitabine + probiotic combination group, the volume of tumors decreased significantly compared to the cancer control group, and the smallest average tumor size was observed in the combination group. Western botting analysis showed that administration of capecitabine and probiotic in the tumor+probiotic and tumor+probiotic+capecitabine groups increased the level of Bax/Bcl-2 ratio and caspase-3 compared to the tumor group. Besides, TNF-α and IL-1β levels decreased significantly in probiotic and combination groups in comparison to tumor group. In contrast, Lf FH5 and capecitabine had no notable effects on IL-18 levels. Long term oral consumption of probiotics as an adjuvant treatment may play an important role in reducing cancer severity and modulating inflammation.

Keywords: Probiotic, Colon cancer, Apoptosis, Animal model, Inflammatory markers

Effects of NSAIDs and Corticosteroids on Biofilm Formation and Antimicrobial Activity Against Staphylococcus aureus

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BACKGROUND AND OBJECTIVES: Biofilm formation significantly contributes to antimicrobial resistance and persistent infections, particularly in pathogens such as Staphylococcus aureus. Although corticosteroids and non-steroidal anti-inflammatory drugs (NSAIDs) are widely used to control inflammation, their direct impact on bacterial growth and biofilm remains underexplored. This study investigated the in vitro antimicrobial and antibiofilm activities of selected corticosteroids and NSAIDs against clinical and standard bacterial strains.

MATERIALS AND METHODS: Five clinical S.aureus isolates and three reference strains (S. aureus ATCC 25923, Escherichia coli ATCC 25922, Staphylococcus epidermidis RP62A) were assessed. The antimicrobial activity of four corticosteroids (dexamethasone, betamethasone, hydrocortisone, prednisolone) and two NSAIDs (ibuprofen, ketoprofen) was evaluated by determining the Minimum Inhibitory Concentration (MIC) and Minimum Bactericidal Concentration (MBC) via microdilution broth.. The Minimum Biofilm Inhibitory Concentration (MBIC). To ensure repeatability, measurements were performed in triplicate.

RESULTS AND DISCUSSION: Corticosteroids exhibited no significant antibacterial activity (MIC/MBC ≥2048 µg/mL). Notably, these agents promoted biofilm formation at higher concentrations (MBIC ≥4096 µg/mL). Ibuprofen had moderate antimicrobial effects against standard strains and stronger anti-biofilm activity (MBIC: 250–500 µg/mL in clinical isolates; 1024 µg/mL in standard strains). Ketoprofen showed consistent antimicrobial activity (MIC = 1024 µg/mL) and strong anti-biofilm effects (MBIC = 250 µg/mL in most strains). Conclusion: Our findings suggest that corticosteroids may exacerbate biofilm-associated infections. Conversely, NSAIDs, particularly ketoprofen, possess promising antibiofilm capabilities. This highlights the potential of ketoprofen as an adjunctive therapy for managing chronic or biofilm-related infections, warranting further investigation.

Keywords: Staphylococcus aureus, Biofilms, Anti-Inflammatory Drugs

Efficacy of Anti-PIA/PNAG Antibodies in Inhibiting Escherichia coli Biofilm Formation

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BACKGROUND AND OBJECTIVES: 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.

MATERIALS 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 AND DISCUSSION: The extracted polysaccharide was confirmed using FTIR, NMR, and colorimetric methods, and the results showed that the purified PIA induced protective antibodies with 40.48% opsonization properties in E. coli. The sera of the PIA-immunized groups showed a significant increase in antibody production and protective IgG titer levels compared to the control group. Also, the antibodies produced showed a substantial difference in inhibiting biofilm production in vitro compared to non-immunized serum. Antibodies produced against PIA with a lethality of 40.48% showed a significant effect on the absence of biofilm formation in E. coli. Despite the opsonic properties of the antibodies for E. coli, the simultaneous effect of these antibodies on infections caused by S. epidermidis and E. coli may have a role that requires further investigation and studies in animal models.

Keywords: Escherichia coli, Staphylococcus epidermidis, Immunization, PIA, PNAG

Effect of Lactobacillus gasseri probiotic supernatant on apoptosis and expression of Bax and Bcl-2 genes in HeLa cervical cancer cells

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BACKGROUND AND OBJECTIVES: Abstract: Cervical cancer is among the most common cancers in women worldwide and remains a major cause of mortality, particularly in developing countries. In recent years, natural compounds with anticancer properties—especially probiotics—have gained increasing attention. Probiotic bacteria can modulate immune responses, regulate microbial flora, and induce apoptosis, contributing to tumor growth suppression. This study aimed to evaluate the apoptotic effects of the cell-free supernatant (CFS) of Lactobacillus gasseri on cell viability and the expression of apoptosis-related genes, Bax and Bcl-2, in HeLa cervical cancer cells.

MATERIALS AND METHODS: Methods: A native strain of L. gasseri was cultured in MRS broth, and the CFS was prepared. HeLa cells were treated with various concentrations of the CFS. Cell viability was assessed by MTT assay, and IC_{50} values were calculated. Apoptosis was evaluated through DAPI staining, and gene expression analysis for Bax and Bcl-2 was performed using Real-Time PCR. Additionally, antibacterial activity was assessed via MIC and MBC assays.

RESULTS AND DISCUSSION: Results: CFS of L. gasseri significantly reduced HeLa cell viability in a dose-dependent manner. A notable upregulation of Bax and downregulation of Bcl-2 were observed, indicating the induction of apoptosis in the treated cells. Conclusion: The findings suggest that Lactobacillus gasseri exerts potential anticancer effects by triggering apoptotic pathways in HeLa cells. This probiotic strain may be considered a promising complementary agent in cervical cancer therapy.

Keywords: Keywords: Lactobacillus gasseri, apoptosis, Bax, Bcl-2, HeLa cells, MTT.

Effect of methyl methacrylate on the biofilm–forming activity of microorganisms

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BACKGROUND AND OBJECTIVES: In dentistry, synthetic polymeric materials are often used to treat patients. It is known that when using such materials, one can observe the monomer release, that affects the functional activity of oral microorganisms. The aim of the research was to evaluate the effect of methyl methacrylate for basic dental plastics on the microorganisms biofilm–forming activity.

MATERIALS AND METHODS: Staphylococcus aureus ATCC 25923, Staphylococcus epidermidis 28922, Escherichia coli M-17, Enterococcus faecalis ATCC 29212 and methyl methacrylate as a monomer for basic plastics (Russia) were used. Microorganisms were cultured in the presence of methyl methacrylate in concentrations of 0,001; 0,05; 0,1; 0,2; 0,3; 1 µg/ml, which corresponds to the concentrations of monomer in saliva in prosthetic patients with different clinical conditions. At the end of incubation, biofilms were stained with crystalline violet, and their thickness was assessed by dye extraction according to O'Toole (2011). Statistical analysis of the results was performed using the Duncan criterion and the Pearson correlation coefficient.

RESULTS AND DISCUSSION: It was found that methyl methacrylate in all concentrations has no significant effect on the biofilm-forming activity of S. aureus ATCC 25923, S. epidermidis 28922, E. coli M-17, E. faecalis ATCC 29212. Correlation analysis showed that there is a positive relationship of average severity between the concentration of methyl methacrylate in the culture medium and the level of biofilm-forming activity (r=0.34;p0.05). Thus, it can be assumed that methyl methacrylate released from removable dental plate prostheses does not have a significant effect on the biofilm-forming activity of bacteria.

Keywords: synthetic polymeric materials; oral microorganisms; biofilm–forming activity

Efficacy of ceftazidime/avibactam against third- and fourth-generation cephalosporin-resistant Enterobacterales: A study on maternal and neonatal colonization

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BACKGROUND AND OBJECTIVES: Ceftazidime/avibactam is crucial for treating infections caused by third- and fourth-generation cephalosporin-resistant Enterobacterales, a critical concern, especially in preterm neonates. This study assessed ceftazidime/avibactam efficacy against these resistant Enterobacterales colonizing preterm mothers and their neonates.

MATERIALS AND METHODS: Fifty mothers with gestational ages below 37 weeks, experiencing labor pain, were included. Vaginal and rectal swabs were collected from mothers pre-labor. From their 50 preterm neonates admitted to the NICU, rectal and skin swabs were obtained at day zero, 48-72 hours post-admission, and weekly thereafter for up to 30 days or discharge. Enterobacterales were isolated from samples, and antibiotic susceptibility testing was performed using the disk diffusion method. For isolates resistant to third- or fourth-generation cephalosporins, additional susceptibility testing to ceftazidime/avibactam was conducted using the same method.

RESULTS AND DISCUSSION: Neonatal isolates exhibited significantly higher third- or fourth-generation cephalosporin resistance (81%) than maternal isolates (38.2%) (p 0.0001). Ceftazidime/avibactam was highly effective against maternal isolates (96.2% susceptible) but notably less effective in neonates (51.9% resistant, p 0.0001). Klebsiella pneumoniae and Escherichia coli were predominant, with K. pneumoniae and K. aerogenes showing the highest ceftazidime/avibactam resistance among resistant strains (46.5% and 75% respectively). Our findings highlight significant colonization by third- or fourth-generation cephalosporin resistant Enterobacterales in preterm labor, with reduced ceftazidime/avibactam efficacy in preterm neonates, particularly for K. pneumoniae and K. aerogenes. This underscores the critical need for improved infection control and antibiotic stewardship in NICUs.

Keywords: Ceftazidime/avibactam, Third- and fourth-generation cephalosporins resistant Enterobacterales, Preterm labor, Colonization

Emergence of Extensively Drug-Resistant and Biofilm-Producing Acinetobacter baumannii in Isfahan Healthcare Facilities: A Molecular Typing Study

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BACKGROUND AND OBJECTIVES: Acinetobacter baumannii is an opportunistic pathogen frequently associated with hospital-acquired infections and multidrug resistance. This study aimed to evaluate biofilm formation, antimicrobial resistance profiles, and genetic diversity of A. baumannii clinical isolates using repetitive-element PCR (Rep-PCR).

MATERIALS AND METHODS: Sixty clinical A. baumannii isolates were collected from hospitalized patients. Initial identification was performed using biochemical tests and confirmed by PCR amplification of the blaOXA-51 gene. Antimicrobial susceptibility was determined by the Kirby-Bauer disk diffusion method, and biofilm formation was assessed using a crystal violet microtiter plate assay. Genetic relatedness was analyzed by $(GTG)_5$-PCR fingerprinting.

RESULTS AND DISCUSSION: The mean patient age was 36 years (26.6% female, 73.4% male). Most isolates (66.6%) were obtained from wound specimens. Antibiotic susceptibility testing revealed that 98.3% of isolates were extensively drug-resistant (XDR). The highest resistance rates were observed against piperacillin, cefepime, and imipenem (100%), while the lowest resistance was reported for doxycycline (13.3%) and tobramycin (11.7%). Biofilm analysis demonstrated that 50% of isolates were strong producers, 18.3% moderate, and 26.6% weak. $(GTG)_5$-PCR typing of the 60 isolates revealed high genetic diversity, with all isolates exhibiting unique banding patterns (3–13 bands; 300 bp to 1500 bp). The discriminatory index (D) was 100%. The A. baumannii isolates in this study exhibited high biofilm-forming capacity and extreme antibiotic resistance, underscoring the need for continuous surveillance and stringent infection control measures. Rep-PCR demonstrated exceptional discriminatory power, which could aid in tracking infection sources.

Keywords: Acinetobacter baumannii, Biofilm, Antibiotic resistance, Rep-PCR

Emerging functions and clinical applications of exosomes as an antimicrobial weapon for oral pathogens

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BACKGROUND AND OBJECTIVES: Exosomes, nanosized extracellular vesicles secreted by various cell types, have recently emerged as pivotal mediators in the oral cavity's defense against microbial pathogens. The oral microbiome comprises diverse microorganisms whose imbalance can lead to infectious diseases such as periodontitis, dental caries, and oral candidiasis. Exosomes derived from mesenchymal stromal/stem cells (MSCs) exhibit potent antimicrobial and immunomodulatory properties, making them promising candidates for novel therapeutic interventions in orodental infections.

MATERIALS AND METHODS: These vesicles carry bioactive molecules—including proteins, lipids, and nucleic acids—that modulate host immune responses by enhancing antigen presentation, regulating inflammation, and promoting tissue regeneration. Unlike conventional antibiotics, MSC-derived exosomes offer a cell-free therapy that can overcome challenges such as antimicrobial resistance and excessive inflammatory damage. Recent studies have demonstrated their efficacy in controlling oral pathogens by directly inhibiting microbial growth and by modulating the host's immunoinflammatory environment. Furthermore, engineered exosomes can be tailored for targeted drug delivery, increasing therapeutic specificity and minimizing side effects.

RESULTS AND DISCUSSION: Recent studies have demonstrated the efficacy of MSC-derived exosomes in controlling oral pathogens both by direct antimicrobial effects and by modulating the host immune response. Engineered exosomes show enhanced potential for targeted delivery, improving therapeutic outcomes while reducing adverse effects. Despite promising preclinical and early clinical data, challenges remain in standardizing exosome isolation, characterization, and clinical application protocols. Continued research into the molecular mechanisms and optimization of exosome-based therapies is essential to fully harness their potential as an innovative antimicrobial weapon against oral pathogens, ultimately improving outcomes in oral infectious diseases.

Keywords: Mesenchymal stem cells, Exosome, Oral microbiome

Emerging Therapeutic Approaches in Bacterial Prostatitis Infections: Can Phage Therapy Replace Current Treatments?

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BACKGROUND AND OBJECTIVES: Bacterial prostatitis is an inflammatory infection of the prostate that can significantly affect the quality of life. This condition may present acutely or chronically and is associated with symptoms such as pain during urination, urinary frequency and urgency, and pain in various regions. Treatment challenges include the limited penetration of antibiotics into prostate tissue and the presence of multidrug-resistant bacteria. This resistance arises due to the formation of biofilms in the prostate, which renders bacteria resistant to treatment. Consequently, in light of the failure of antibiotic therapy, novel therapeutic approaches such as bacteriophages and probiotics are being explored as alternative options for treating these infections. The aim of this research is to evaluate the efficacy of bacteriophage therapy in treating prostatitis.

MATERIALS AND METHODS: This study is a systematic review conducted using the PRISMA checklist. Databases including PubMed, Scopus, and ScienceDirect were searched on June 13, 2025, The retrieved articles were imported into EndNote software and assessed based on inclusion and exclusion criteria. Relevant and credible documents were selected with no restrictions regarding nationality, ethnicity, or gender, while irrelevant and duplicate articles were excluded

RESULTS AND DISCUSSION: Among the six patients studied, all underwent treatment with bacteriophages after encountering antibiotic resistance for their prostatitis infections. Of these, four patients were completely treated with monophage therapy, and two patients were treated with phage cocktails, reporting no adverse effects from the bacteriophages. Therefore, phage therapy can be considered an effective method for treating antibiotic-resistant prostatitis infections.

Keywords: Bacterial prostatitis, bacteriophage, phage therapy, bacteriophage therapy, antibiotic resistance.

Endolysin as a Complementary Tool in Phage Therapy: A Novel Approach to Combat Antibiotic Resistance

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BACKGROUND AND OBJECTIVES: The rapid emergence of antibiotic-resistant bacterial strains has become a critical global health challenge, necessitating the development of innovative antimicrobial strategies. Endolysins, bacteriophage-derived peptidoglycan hydrolases, have shown promising potential as alternative therapeutics due to their ability to selectively degrade bacterial cell walls. Advances in protein engineering have enabled the modification and optimization of endolysins to enhance their stability, specificity, and efficacy against multidrug-resistant (MDR) pathogens. Engineered endolysins can overcome limitations of traditional antibiotics by targeting a broad spectrum of bacteria, disrupting biofilms, and minimizing the development of resistance.

MATERIALS AND METHODS: Advantages of endolysins: Rapid bactericidal activity: Endolysins can degrade bacterial cell walls within minutes, leading to swift bacterial death, in contrast to many antibiotics that require hours or even days to exert their effects (18) . Effectiveness against resistant strains: By directly targeting the bacterial cell wall, endolysins remain active against drug-resistant bacteria, including strains such as MRSA (19) . High specificity: Most endolysins act selectively on particular bacterial species, minimizing disruption to beneficial microbiota, unlike broad-spectrum antibiotics (20) .Low likelihood of resistance development: The direct mechanism of action on the cell wall reduces the probability that bacteria will rapidly develop resistance compared to conventional antibiotics (21)

RESULTS AND DISCUSSION: With the rapid rise of antibiotic-resistant bacteria, the need for alternative and effective antimicrobial strategies has become increasingly urgent. Endolysins, which are cell wall-degrading enzymes derived from bacteriophages, have shown great potential in combating drug-resistant bacterial infections.

Keywords: Endolysin,Antibiotic Resistance

Engineering Recombinant Phytogenic Antimicrobials Using Plant-Based Synthetic Biology Approaches: A Review

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BACKGROUND AND OBJECTIVES: The emergence of antibiotic-resistant pathogens is a mounting global health concern. In recent years, plant-based synthetic biology has gained attention as a sustainable and innovative approach to producing phytogenic antimicrobial agents by leveraging plants' natural biosynthetic capabilities.

MATERIALS AND METHODS: This review summarizes studies published between 2015-2025, retrieved from databases such as PubMed, Scopus, and Web of Science, using keywords including "plant-based antimicrobials", "synthetic biology", "CRISPR", and "phytogenic antimicrobial peptides". Emphasis was placed on articles describing engineered metabolic pathways, gene editing tools, and production platforms in model plant systems.

RESULTS AND DISCUSSION: Recent literature highlights successful engineering of plants like Nicotiana benthamiana to produce antimicrobial peptides and secondary metabolites with potent activity against multidrug-resistant bacteria and fungi. These studies demonstrate how synthetic biology tools — such as modular cloning, CRISPR/Cas, and inducible gene circuits — enhance the specificity, yield, and biosafety of antimicrobial production in planta. The integration of plant metabolic engineering with synthetic biology offers a promising frontier in developing next-generation antimicrobials. While technical and regulatory hurdles remain, the approach presents a sustainable alternative to traditional antibiotic development and aligns with global efforts to combat antimicrobial resistance.

Keywords: Antimicrobial Agents, Synthetic Biology, Phytotherapy, Genetic Engineering, Drug Resistance

Enhanced Antibacterial Efficacy of Thymol Combined with Cefotaxime Against Escherichia coli

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BACKGROUND AND OBJECTIVES: This study examined the antibacterial synergy of thymol and cefotaxime against Escherichia coli (E. coli) bacteria.

MATERIALS AND METHODS: The MIC-MBC method was used to evaluate the antimicrobial effects of thymol and cefotaxime, both separately and in combination, against E. coli ATCC25922. This method highlighted a compound with synergistic effects on twenty clinical strains of E. coli. Additionally, FTIR analysis was conducted to examine molecular interactions, while cytotoxicity was assessed using various techniques, including the checkered method, time-killing curve, biofilm inhibition, hemolysis, and the MTT assay on human skin fibroblast cells (Ffk) and red blood cells (RBCs). The A3 compound demonstrated a synergistic effect.

RESULTS AND DISCUSSION: The study found that thymol, cefotaxime, and the combined compound (A3) exhibited antimicrobial activities against E. coli at 256 µg/ml, 32 µg/ml, and 128/16 µg/ml (FICI: 1 µg/ml), respectively. The A3 compound showed antibacterial activity against clinical strains of E. coli, with efficacy ranging from 1024 µg/ml to 16 µg/ml. The combined treatment proved more effective at eliminating E. coli compared to individual treatments. These compounds interacted with various chemical groups, while thymol and cefotaxime were linked through C=C conjugated compounds. The biofilm inhibition rates were 29.69% for thymol, 16.28% for cefotaxime, and 39.28% for A3. Regarding toxicity, thymol, cefotaxime, and A3 had RBC toxicity values of 36.12, 8.33, and 8.38, respectively, and Ffk toxicity values of 19.66, 7.08, and 9.03. The results emphasized the strong antibacterial and anti-biofilm properties of the thymol/cefotaxime combination, warranting further investigation despite cefotaxime's resistance in E. coli infections.

Keywords: Escherichia coli, Thymol, Cefotaxime, Synergistic

Enhancement of Covid-19 Candidate Vaccine-Induced Immunity by Probiotics and Micronutrients: Investigating the Role of TLR5 in Adult Female BALB/c Mice

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BACKGROUND AND OBJECTIVES: It has been reported that probiotic-based vaccines may provide effective protection against COVID-19. Comprehensive micronutrient interventions have been associated with slower progression of COVID-19 and improved immune function. Frequent vitamins and trace minerals exhibit immunomodulatory effects, and their levels or supplementation have been associated with the incidence and severity of infections. Moreover, plentiful evidence indicates that maintaining sufficient micronutrient levels or supplementing with micronutrients is associated with enhanced vaccine responses and immunogenicity, including responses to COVID-19 vaccinations. This study assessed the protective effects of two different regimens of multiple dietary supplements on the subunit protein.

MATERIALS AND METHODS: Methods: The probiotic supplement BioBoost® and PastoCovac® vaccine, which contains six expressed receptor-binding domain (RBD) and conjugated with tetanus toxin, were administered concurrently. The safety and efficacy were assessed by determining IgG antibody titers to RBD and cytokines, mRNA expression of TLR5, and clinical symptoms.

RESULTS AND DISCUSSION: Results: Results showed that both single and multi-dose treatment groups receiving the probiotic supplement had significantly increased IL-4, TNF-alpha, IFN-gamma, and IgG antibody titers compared to the control group, with the multi-dose treatment group showing highest levels. Moreover, the multi-dose treatment group showed significantly increased expression of TLR5 when compared to the other groups. Conclusion: This comprehensive approach provided insights into the immune responses and demonstrated the efficacy of probiotic supplementation on the subunit protein vaccine platform.

Keywords: Probiotic; Micronutrients; Immunogenicity; PastoCovac® vaccine; COVID-19.

Enteric-Borne Sepsis: Gut Microbiota Dysbiosis and Its Causal Link to Sepsis Pathogenesis

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BACKGROUND AND OBJECTIVES: Sepsis constitutes a major clinical challenge worldwide, accounting for significant mortality rates among hospitalized patients. This condition emerges from uncontrolled host immune reactions to infectious agents, creating a complex physiological state marked by concurrent inflammatory activation and immune dysfunction. recent researches have identified the gut microbiota as a pivotal factor in sepsis development and outcomes. Microbial imbalance, termed dysbiosis, fundamentally alters the host-microbe equilibrium. Consequently, gut barrier integrity becomes compromised, facilitating bacterial translocation into systemic circulation and triggering widespread inflammatory cascades.

MATERIALS AND METHODS: We searched PubMed, Scopus, Google Scholar, and Medline databases using the keywords: "gut microbiota AND sepsis", "dysbiosis AND sepsis", "sepsis AND microbial metabolites".

RESULTS AND DISCUSSION: Recent studies indicate that septic patients exhibit characteristic microbial patterns, notably elevated Proteobacteria levels alongside reduced diversity of beneficial genera including Bacteroides and Bifidobacterium. These changes correlate with impaired production of short-chain fatty acids and metabolic dysfunction, which influence immune cell behavior and organ function. These microbial alterations have been linked to heightened susceptibility to secondary infections and poor clinical outcomes. Also, therapeutic interventions targeting the microbiome-sepsis axis show encouraging clinical potential. The therapeutic intervention targeting gut microbiota such as microbiota modulation, probiotic, metabolite-based treatments for restoring microbial homeostasis, microRNA-targeted therapies for enhanced sepsis prevention and management through microbial restoration and strengthened host immunity, could potentially alleviate inflammation and organ injuries associated with sepsis, highlighting the crucial role of dysbiosis and gut inflammation in the disease's pathogenesis

Keywords: Sepsis, gut microbiota, dysbiosis, leaky gut

Enzootic Bovine Leukosis and BLV: A Comprehensive Review of Its Biology, Transmission, Diagnosis, and Control Strategies

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BACKGROUND AND OBJECTIVES: Bovine leukemia virus (BLV) is an oncogenic deltaretrovirus infecting cattle worldwide and causing enzootic bovine leukosis (EBL). It is mainly transmitted through blood, vertical transmission, or arthropod vectors such as *Tabanus*, *Stomoxys*, and *Simulium* species. BLV prevalence varies globally; while some countries have eradicated the virus, others still face high infection rates, particularly in dairy herds. Given its economic impact and potential association with human retroviruses, BLV continues to receive significant research attention.

MATERIALS AND METHODS: The present review is based on a literature search conducted in databases such as PubMed, Scopus, and Web of Science, including the keywords "Bovine Leukemia Virus", "Retroviridae Infections", and "Cattle Diseases". Inclusion criteria were English publications between 2000 and 2025. Articles examined included original research, reviews, and epidemiological studies related to the structure, transmission, diagnosis, and control of BLV.

RESULTS AND DISCUSSION: BLV is a positive-sense, single-stranded RNA virus that infects B-lymphocytes and integrates into the host genome, leading to lymphocyte proliferation. Most infections are subclinical, though about 30% of cases develop persistent lymphocytosis, and fewer than 5% progress to lymphosarcoma. Diagnosis is typically based on ELISA or PCR. Control measures include test-and-slaughter, improved herd management, and selective breeding. A major challenge is early detection, as the infection often remains silent. The lack of an effective vaccine or treatment also limits control efforts. Future research should focus on rapid diagnostics, vaccine development, and potential zoonotic risks.

Keywords: Bovine Leukemia Virus, Enzootic Bovine Leukosis, Retroviridae Infections, Cattle Diseases

Epidemiological Analysis of Human Brucellosis in North Khorasan Province, Iran (2018–2023)

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BACKGROUND AND OBJECTIVES: Brucellosis is a bacterial zoonotic disease that poses significant threats to public health and animal food production worldwide. Its endemic nature in Iran is largely due to its geographical location and the presence of neighboring countries where brucellosis is common and incidence of this disease in both humans and animals remains high in Iran.

MATERIALS AND METHODS: This study utilized data from the Zoonotic Disease Department (Deputy Minister of Health and Medical Education) to examine the epidemiological characteristics of brucellosis in North Khorasan province, northeast Iran, over a six-year period. The patients' data were analyzed using SPSS software.

RESULTS AND DISCUSSION: Between 2018 and 2023, there were 1,877 confirmed cases of brucellosis through serological testing, representing 7.7% of the tested population. Among these cases, 55.9% were male, and 44.1% were female. Additionally, 81.5% of the patients lived in rural areas, while 17.5% resided in urban areas. Notably, 85.3% of the patients consumed non-pasteurized dairy products. Several factors have contributed to the challenges in controlling brucellosis, including dietary habits related to the consumption of non-pasteurized dairy and raw meat, a lack of awareness about the disease, the absence of a regular livestock vaccination program, and the unavailability of vaccines for humans.

Keywords: Epidemiological, Human Brucellosis, North Khorasan, Iran

Epidemiological study of covid-19 in certain areas of Kohgiluyeh and Boyer-Ahmad Province

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BACKGROUND AND OBJECTIVES: Introduction & Objective: Since the identification of the SARS-CoV-2 virus, a large number of individuals have been infected with COVID-19, exhibiting a wide range of clinical symptoms. Various factors such as age, gender, underlying diseases, occupation, place of residence, travel history to endemic areas, and vaccination status have been studied in relation to disease severity and mortality rates. This study aimed to investigate the prevalence of SARS-CoV-2 and its association with gender, age, occupation, place of residence, and vaccination history among patients in Kohgiluyeh and Boyer-Ahmad Province

MATERIALS AND METHODS: Materials & Methods: This cross-sectional study was conducted on individuals suspected of having COVID-19 from April 2021 to February 2023. A total of 8,101 individuals participated in the study. Nasopharyngeal swab samples were collected from all patients and transported under cold chain conditions in viral transport media to a molecular diagnostic laboratory for SARS-CoV-2 testing. Viral genome extraction was performed using the Genova kit, and real-time PCR tests were conducted on all samples. Additionally, demographic information was collected at the time of sample collection

RESULTS AND DISCUSSION: Results: Among the 8,101 suspected COVID-19 cases, 4,561 (59.3%) were male, and 3,460 (40.7%) were female. The results indicated that 765 individuals (9.5%) tested positive for COVID-19. Hypertension (42%) was the most common underlying condition among COVID-19 patients, followed by cardiovascular diseases (38%) and neurological disorders (14%).

Keywords: Keywords: SARS-CoV-2, COVID-19, Clinical Symptoms, Underlying Diseases

Epigenetic Mechanisms in Acinetobacter baumannii Drug Resistance: A New Horizon for Hospital Infection Control

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BACKGROUND AND OBJECTIVES: Acinetobacter baumannii is a critical hospital-acquired pathogen known for rapid emergence of multidrug resistance (MDR). Traditional approaches targeting genomic mutations have shown limited long-term efficacy, underscoring the need to explore alternative regulatory pathways. Emerging data show differential DNA methylation (e.g., m5C, m6A) can modulate transcription of key resistance genes (such as OXA family) under antibiotic stress. RNA-mediated regulatory networks, including small RNAs and nucleoid-associated proteins, further tune drug efflux and stress responses. Notably, preliminary translational studies highlight the potential of DNA methyltransferase inhibitors ("epidrugs") and incorporation of epigenetic profiling for outbreak surveillance. However, challenges remain in standardizing assays and linking epigenetic markers to actionable infection control protocols across hospital settings.

MATERIALS AND METHODS: We conducted a systematic review of literature (2020–2025) via PubMed and Scopus, focusing on epigenetic mechanisms—primarily DNA methylation and RNA-based regulation—in drug-resistant A. baumannii human clinical isolates. Selection emphasized translational insights and infection control perspectives.

RESULTS AND DISCUSSION: Emerging data show differential DNA methylation (e.g., m5C, m6A) can modulate transcription of key resistance genes (such as OXA family) under antibiotic stress. RNA-mediated regulatory networks, including small RNAs and nucleoid-associated proteins, further tune drug efflux and stress responses. Notably, preliminary translational studies highlight the potential of DNA methyltransferase inhibitors ("epidrugs") and incorporation of epigenetic profiling for outbreak surveillance. However, challenges remain in standardizing assays and linking epigenetic markers to actionable infection control protocols across hospital settings.

Keywords: Acinetobacter baumannii,Drug Resistance,Bacterial,Epigenetics,DNA Methylation, RNA, Hospital Infection Control

Epigenetic Mechanisms in Radiation Resistance of Deinococcus radiodurans: A Review of Multi-Omics Integration and Machine Learning Approaches

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BACKGROUND AND OBJECTIVES: Deinococcus radiodurans is renowned for its extraordinary resistance to ionizing radiation and oxidative stress. While genetic mechanisms behind this resilience have been widely studied, emerging evidence suggests a potential role for epigenetic regulation in orchestrating stress responses. This review aims to explore how multi-omics data integration—particularly epigenomics, transcriptomics, and proteomics—combined with machine learning algorithms, may reveal novel survival strategies in D. radiodurans.

MATERIALS AND METHODS: We reviewed and synthesized recent findings from publicly available datasets, published literature, and experimental studies focusing on epigenetic modifications (e.g., DNA methylation, histone-like protein modulation), and assessed their interplay with radiation tolerance. Additionally, we examined the role of machine learning techniques, such as Random Forests and graph neural networks, in identifying predictive epigenetic biomarkers.

RESULTS AND DISCUSSION: The evidence suggests that epigenetic modifications may dynamically regulate DNA repair, oxidative stress response, and membrane stability in D. radiodurans. Machine learning methods, when applied to integrative omics datasets, have demonstrated increased accuracy in predicting candidate genes and regulatory regions associated with radiation resistance. Importantly, theoretical frameworks such as "anticipatory epigenetics" are proposed to explain how the bacterium might prime itself for survival. Epigenetic mechanisms likely represent an underexplored but critical layer in the adaptive strategy of D. radiodurans. The synergy of multi-omics and machine learning not only enhances our understanding of microbial stress biology but also opens new possibilities in synthetic biology and space microbiology for engineering robust microbial lifeforms.

Keywords: Deinococcus radiodurans, Epigenesis, Genetic, Radiation Tolerance, Machine Learning, Multiomics

Escalating Antimicrobial Resistance in ICU Respiratory Pathogens: A Five-Year Surveillance of Ventilator-Associated Infections in a Trauma Referral Hospital (2019–2023)

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BACKGROUND AND OBJECTIVES: Ventilator-associated pneumonia (VAP) is a major complication in ICU patients, particularly among those with prolonged mechanical ventilation. The emergence of multidrug-resistant (MDR) Gram-negative bacteria poses a significant treatment challenge. To assess five-year trends in prevalence and antibiotic resistance patterns of respiratory pathogens in ICU patients, with a focus on carbapenem resistance.

MATERIALS AND METHODS: This retrospective study analyzed respiratory specimens from ICU patients in a trauma referral hospital in Iran between 2019 and 2023. Pathogens were identified by standard microbiological methods. Antimicrobial susceptibility was determined through routine antibiograms, focusing on carbapenems, aminoglycosides, and fluoroquinolones.

RESULTS AND DISCUSSION: Acinetobacter baumannii and Klebsiella pneumoniae were the most common pathogens in ICU respiratory cultures. Carbapenem resistance in A. baumannii increased from 45% in 2019 to over 75% in 2023. More than 70% of isolates demonstrated MDR profiles in the final year. K. pneumoniae also showed rising resistance to aminoglycosides and third-generation cephalosporins. The increase in resistant isolates paralleled a higher incidence of VAP over time. The growing resistance of key respiratory pathogens to life-saving antibiotics, especially in ICU settings, underscores the urgent need for enhanced infection control, targeted antibiotic stewardship, and continuous resistance monitoring.

Keywords: VAP, ICU, Acinetobacter baumannii, Klebsiella pneumoniae, carbapenem resistance, multidrug resistance

Essential oil composition and Antibacterial activities of Verbena, Lemon grass, and Balm mint grown in Sistan region climate

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BACKGROUND AND OBJECTIVES: This study was designed to investigate the chemical composition and antibacterial activities of essential oils extracted from aerial parts of three medicinal plants, Verbena, Lemon grass, and Balm mint cultivated in Sistan and Baluchestan province.

MATERIALS AND METHODS: This study was done in a factorial experiment based on the complete randomized design in 3 replications in Research Institute of Zabol, 2021 May to 2022 October. Melissa Officinalis, Cymbopogon citratus, and Aloysia citrodora's leaves were collected during spring. Collected samples were dried in shade and airflow conditions. 100 g of dried leaves were crushed into smaller pieces with electric mills, and hydrodistilled in a Clevenger system for 3h. The essential oils were analyzed on a 6890 N Agilent gas chromatograph coupled with a 5975 C Agilent mass selective detector. Antibacterial activities assay was performed by Minimal Inhibitory Concentration (MIC) and Minimal Inhibitory Concentration (MBC) tests against 3 gram-negative bacteria Escherichia coli (), Pseudomonas aeruginosa (), Salmonella typhi (), and 4 gram-positive bacteria Listeria monocytogenes (), Staphylococcus aureus (), and Bacillus cereus .

RESULTS AND DISCUSSION: 19 components accounting to 96.24 % of the total oil were identified in Melissa officinalis; 23 components accounting to 98.9 % of the total oil were detected in Aloysia citriodora and 15 components accounting to 89.35 % of the total oil were observed in Cymbopogon citratus. Aloysia citriodora had more bioactive compounds and the best antibacterial activity. The monoterpenes and sesquiterpenes confer the chemical profile of the analyzed essential oil of these samples causing antibacterial effects.

Keywords: antimicrobialproperties, essential oil, GC/MS, Herbal Tea.

Evaluation of carbapenemase genes in imipenem resistant Pseudomonas aeruginosa strains isolated from urinary tract infections

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BACKGROUND AND OBJECTIVES: Carbapenem resistant Pseudomonas aeruginosa is a serious cause of nosocomial infections.The main purpose of the study is to determine the prevalence rate of imipenem resistant Pseudomonas aeruginosa carrying carbapenemase genes.

MATERIALS AND METHODS: In this study, 100 Pseudomonas aeruginosa isolates were collected from teaching hospitals of Tehran and sanandaj University of Medical Sciences during a period of 9 months in 2024- 2025 years. These strains were identified using conventional microbiological tests. The susceptibility of isolates to antibiotics were assessed using disk diffusion test. The Modified hodge test was performed for detection of carbapenemase producing strains. Finally, polymerase chain reaction (PCR) was performed to detect carbapenemase genes, blaIMP, blaVIM, blaSPM,blaNDM and blaOXA-48 in imipenem resistant strains

RESULTS AND DISCUSSION: Out of 100 examined isolates, 48 isolates (48%) were resistant to imipenem. The MHT showed that among 48 imipenem resistant strains, 38 strains (79.1%) were phenotipically Carbapenemase producers. Additionally, the results of PCR method showed that 21 strains (43.7%), 12 strains(25%), 4 strains(8.3) and 3 strains(6.2%) of imipenem resistant Pseudomonas aeruginosa isolates contained blaVIM, blaOXA-48, blaIMP and blaNDM genes respectively. No blaSPM gene was found in the examined samples. In conclusion, Resistance of P. aeruginosa isolates to imipenem due to carbapenemase enzymes is increasing in Tehran and sanandaj. Because of clinical significance of this kind of resistance, rapid detection of carbapenemase producing strains and followed by appropriate treatment is necessary to prevent the spreading of these organisms

Keywords: Pseudomonas aeruginosa, Urinary tract infection, MHT, PCR

Evaluating the Repurposing Potential of a Pneumolysin Inhibitor against Streptolysin O: An In Silico Study

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BACKGROUND AND OBJECTIVES: Pneumolysin from Streptococcus pneumoniae and streptolysin O from Streptococcus pyogenes are cholesterol-dependent cytolysins (CDCs) that play crucial roles in bacterial pathogenicity. Building upon our previous research that identified compound 3009235 (PubChem CID) as a potential inhibitor of pneumolysin through molecular docking, this study explored the feasibility of repurposing the same compound to inhibit streptolysin O, given the high sequence and structural similarity (90%) between these toxins.

MATERIALS AND METHODS: The 3D structures of pneumococcal pneumolysin (PDB ID: 5CR6) and S. pyogenes streptolysin O (PDB ID: 4HSC) were retrieved from the RCSB PDB database. Using UCSF Chimera, both proteins were preprocessed by removing ligands and water molecules. Sequence alignment and structural comparison were performed using ClustalW and TM-align servers. Molecular docking of compound 3009235 (PubChem CID) with streptolysin O was conducted through Molegro Virtual Docker v.6.

RESULTS AND DISCUSSION: Docking results revealed that compound 3009235 ([(2R,3R)-2-(3,4-dihydroxyphenyl)-5,7-dihydroxy-chroman-3-yl]octanoate) with a molecular weight of 416.5g/mol, could bind to streptolysin O with a favorable binding energy (ΔGbind = -115.68 kcal/mol). This ligand formed three hydrogen bonds and five steric interactions with streptolysin O. Its pharmacokinetic properties, including LogS (-4.60), LogP (3.9), four hydrogen bond donors, seven acceptors, and a polarity index (TPSA) of 116.45Å², support its drug-like nature.These findings suggested that compound 3009235 has dual inhibitory potential against pneumolysin and streptolysin O. Further experimental validation is recommended to confirm these computational results.

Keywords: Streptococcus pneumoniae, Pneumolysin, Molecular Docking, Streptococcus pyogenes, Streptolysin O

Evaluation of Antibacterial and Anti-Motility Effects of Thymus vulgaris and Trachyspermum ammi Essential Oil against Salmonella Typhi, Paratyphi A, B and arizonae

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BACKGROUND AND OBJECTIVES: Salmonella enterica is a pathogenic bacterium with multiple serovars, including S. Typhi, S. Paratyphi A & B, and subspecies like S. arizonae, which are responsible for typhoid fever, paratyphoid, and gastroenteritis. Salmonella is an important zoonotic pathogen, posing a serious threat to human health and safety. The increasing multidrug resistance (MDR) has encouraged exploration of alternative therapies, such as plant-based essential oils as a common antibacterial product. This study investigates the antibacterial and anti-motility activity of Thyme (Thymus vulgaris) and ajwain (Trachyspermum ammi) essential oils on four significant Salmonella enterica.

MATERIALS AND METHODS: Minimum inhibitory concentration (MIC) was determined using the microdilution method. Ultimately, motility tests using soft agar confirmed inhibition of swarming in all tested serovars. For this purpose, anti-swarming test were conducted on soft agar with sub-MIC concentrations for all serovars. Motility radius was subsequently measured.

RESULTS AND DISCUSSION: The results support the potential application of natural oils as antimicrobial and anti-motility agents. Accordingly, both essential oils at 1% stock concentration demonstrated inhibitory activity, with the MIC observed at lower concentrations. It's indicating strong inhibitory potential at low concentration. The findings show that both essential oils had considerable antimicrobial activity. The anti-motility effects observed probably support their potential in disrupting bacterial colonization and virulence. This also suggests that anti-motility strategies may differentially impact serovars depending on their pathogenic pathways. Thyme and ajwain oils, are promising antimicrobial and anti-swarming agents against Salmonella serovars. Further studies, including in vivo models and synergism with antibiotics, are recommended.

Keywords: Salmonella enterica, Essential Oil, Antibacterial, Swimming, Serovar, Multidrug Resistance, Subspecies.

Evaluation of antibacterial property of TiO_2 Nanoparticles against MDR S. aureus and K. pneumoniae from ICU Patients

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BACKGROUND AND OBJECTIVES: Staphylococcus aureus and Klebsiella pneumoniae are among the most common causes of hospital-acquired infections. The increasing resistance of these pathogens to antibiotics, particularly in ICU settings, has become a serious threat to public health. In the face of this growing antibiotic resistance crisis, exploring alternative antimicrobial strategies—especially using nanoparticles—appears essential. In this study, the antimicrobial potential of titanium dioxide (TiO_2) nanoparticles, known for their strong oxidative power, chemical stability, and low toxicity, was evaluated as a possible alternative to conventional disinfectants.

MATERIALS AND METHODS: Multidrug-resistant (MDR) isolates of S. aureus and K. pneumoniae were obtained from ICU patients in a tertiary care hospita. TiO_2 nanoparticles were synthesized via chemical precipitation, and their physicochemical properties were characterized. Antimicrobial efficacy was then assessed through minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) tests.

RESULTS AND DISCUSSION: The MIC and MBC values of TiO_2 nanoparticles against both resistant strains were determined to be 0.75 mg/mL, indicating a significant antibacterial effect. The findings suggest that TiO_2 nanoparticles exhibit effective antimicrobial activity against resistant hospital pathogens. Although not a replacement for antibiotics, they may serve as a complementary approach in infection control practices. This, in turn, could help reduce antibiotic dependency and slow the spread of drug-resistant infections.

Keywords: Titanium dioxide nanoparticles, Staphylococcus aureus, Klebsiella pneumoniae, antibacterial, tertiary hospital

Evaluation of drug resistance patterns and virulence factors in Klebsiella pneumoniae isolated from intubated the teaching hospitals of Babol University of Medical Sciences

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BACKGROUND AND OBJECTIVES: Currently, hospital-acquired infections are the most common complications affecting hospitalized patients. Klebsiella pneumoniae is a gram-negative bacillus that is abundantly collected from patients on ventilators. Therefore, the objective of the present study was to assess the Evaluation of drug resistance patterns and virulence factors in Klebsiella pneumoniae isolated from intubated caught from the teaching hospitals of Babol University of Medical Sciences.

MATERIALS AND METHODS: In this descriptive-cross-sectional study, 20 Klebsiella pneumoniae isolates were isolated from bronchial lavage samples from intubated patients. Antibiotic susceptibility testing was performed using the Kirby-Bauer methods. Molecular PCR test was conducted using to identify the iutA, iroN, iucB and allS genes by the use of a polymerase chain reaction (PCR) method.

RESULTS AND DISCUSSION: According to the Antibiogram test findings. showed that the highest and lowest resistance rates were to cefotaxime (84.1%) and amikacin (12.7%), respectively. based on the PCR results, the frequencies of the genes iutA, iroN, iucB and allS were 53%, 20%, 13% and 7%, respectively. These findings demonstrate that showed a high level of antibiotic resistance in the isolates under study. Therefore, awareness of the resistance pattern of the region and continuous and continuous monitoring and surveillance are recommended for monitoring resistance.

Keywords: Klebsiella pneumoniae, Virulence factors, Polymerase chain reaction

Evaluation of Fungal Contamination in Traumatic Skin Wounds of Domestic Cats in Mashhad, Iran

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BACKGROUND AND OBJECTIVES: Fungal colonization of traumatic skin wounds has been under recognized in veterinary medicine despite its potential to delay healing. This study aimed to determine the prevalence, species diversity, and clinical correlates of fungal contamination in feline traumatic wounds.

MATERIALS AND METHODS: Fifty-four cats presenting with acute or chronic traumatic skin injuries at the Veterinary Hospital of Ferdowsi University of Mashhad were sampled over a 13-month period. Sterile swabs were cultured on Sabouraud Dextrose Agar with chloramphenicol, and the isolates were identified by both macroscopic/microscopic morphology, as well as biochemical tests. Associations between fungal presence and host factors (age, sex, weight, breed), wound characteristics (depth, etiology, contamination grade), underlying disease, and vaccination status were evaluated using Cramer's V (P0.05).

RESULTS AND DISCUSSION: Nine of 54 wounds (19%) yielded fungal growth. Identified genera included Aspergillus (n=3), Cladosporium (n=2), Cryptococcus (n=1), Prototheca (n=1), and Penicillium (n=2). No statistically significant associations were found between fungal contamination and any demographic or clinical variables (all P0.05). Fungal contamination occurred in approximately 19% of feline traumatic wounds, encompassing both yeast and filamentous genera. The absence of clear risk factors underscores the need for routine fungal screening, especially in wounds refractory to standard therapy. Further molecular studies and longitudinal follow-up are warranted to elucidate the impact of fungal biofilms on feline wound healing and to guide targeted antifungal interventions.

Keywords: Cats, Fungal Contamination, Wound Healing, Veterinary Mycology

Evaluation of Helium Atmospheric Cold Plasma (CAP) Potential on Elimination of Pseudomonas aeruginosa Infections in Burn Wounds

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BACKGROUND AND OBJECTIVES: Introduction: Pseudomonas aeruginosa is a gram-negative bacterium that can cause serious wound infections. The infections can be difficult to treat due to the bacterium's ability to survive in biofilms and develop antibiotic resistance. Cold atmospheric plasma (CAP) exhibits significant antimicrobial potential, offering a promising alternative to traditional antibiotics, particularly against antibiotic-resistant bacteria.

MATERIALS AND METHODS: Materials and Methods: In this study, we developed a helium-based CAP device and investigated its potential in eliminating zoonotic bacterial strains of P. aeruginosa. P. aeruginosa was derived from livestock cow dung. After isolation and identification, the antibiotic resistance profile was determined. The wound infection model was developed in Wistar rats using isolated P. aeruginosa. The direct helium plasma treatment was performed in the presence and absence of the immune system.

RESULTS AND DISCUSSION: Results: The results confirm the synergic effects of immune system and helium plasma without the use of antibiotics, while CAP cannot eradicate infections solitary. In the third week of therapy, the infections were abolished through a combination of immune response with physical and chemical effects of CAP, including the generation of reactive oxygen and nitrogen species to disrupt bacterial membranes, damage DNA, and ultimately lead to antibacterial effects. Conclusion: These results suggest that a combined effect of the immune response and helium plasma therapy, leading to a beneficial outcome, and this effect was achieved without the use of antibiotics. This could potentially be applied in various medical contexts.

Keywords: Pseudomonas aeruginosa, Biofilms, Cold atmospheric plasma, Reactive oxygen and nitrogen

Evaluation of Immunogenicity of Quadrivalent Inactivated Enterotoxemia Vaccine with with Different Alum Concentrations

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BACKGROUND AND OBJECTIVES: Clostridium perfringens is a significant pathogenic bacterium affecting livestocks and Vaccination remains the most effective method of prevention. Adjuvants such as aluminum hydroxide play a vital role in enhancing vaccine efficacy. This study aimed to evaluate the immunogenicity and protective efficacy of a polyvalent bacterin- toxoid Clostridium perfringens vaccine that formulated with different concentrations of aluminum hydroxide adjuvant

MATERIALS AND METHODS: Vaccines were prepared using standardized fermentation and formalin inactivation protocols. Monovalent cultures of C. perfringens types B, C, and D were combined according to specific proportions. Aluminum hydroxide adjuvant (1.65%) was incorporated at concentrations of 0.6, 1.2, 2.4 mg/ml while a non-adjuvanted group served as the control. Initial quality control assessments, including pH measurement, residual formalin testing, sterility, toxicity were conducted on all formulations. Rabbits were immunized in two stages Beta and epsilon antitoxin levels were determined to assess immune responses

RESULTS AND DISCUSSION: The formulations containing aluminum hydroxide demonstrated significantly enhanced immunogenicity compared to the non-adjuvanted group. Among the tested concentrations, the 1.2 mg/ml aluminum hydroxide group exhibited the highest titers of beta and epsilon antitoxins, indicating a strong and durable immune response. Aluminum hydroxide remains an effective adjuvant for clostridial vaccines, significantly boosting both the magnitude and duration of immune responses. Optimizing adjuvant concentration is essential for achieving maximal vaccine efficacy while minimizing adverse effects. These findings support the continued use of aluminum-based adjuvants as the standard benchmark in veterinary vaccine development but It is important to choose the right concentration Because may cause side effects and reduce immunogenicity

Keywords: Clostridium perfringens, Vaccine, Adjuvant,

Evaluation of microbial analysis of chicken samples collected from Bavanat city and determination of antibiotic pattern of the isolates

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BACKGROUND AND OBJECTIVES: The microbial study of bacterial diversity and interaction with other organisms, along with their drug resistance, has always been challenging due to the significant variations that can occur between samples. Although a wide variety of species can be hosted by meat products, the research aimed to evaluate on the presence of isolated microorganisms and the antibiotic resistance of culturable isolates from packaged and unpackaged chicken distributed in Bavanat County.

MATERIALS AND METHODS: A total of 100 chicken samples, both fresh and frozen, were prepared using rinsing, swabbing, and tissue scraping methods. Subsequently, the bacteria were identified using biochemical tests and molecular assays based on the 16S rRNA universal primer sequencing. Mueller-Hinton agar was used to determine the antibiotic susceptibility patterns of the isolates.

RESULTS AND DISCUSSION: The results indicate that Gram-negative isolates, compared to Gram-positive ones, exhibit a more diverse and greater resistance pattern to antibiotics. In Gram-negative isolates, the highest drug resistance was observed against erythromycin, nalidixic acid, and tetracycline, and in Gram-positive isolates, the highest drug resistance was observed against erythromycin and tetracycline. Research indicates that approximately 64% of the isolates showed MDR. According to the present study, the most resistant bacteria were Escherichia coli, Pseudomonas, and Staphylococcus aureus, while the most sensitive bacteria were Enterobacter and Klebsiella. Conclusion: To reduce the spread of resistant bacteria and maintain health, accurate systems for monitoring antibiotic consumption and bacterial resistance in farms should be established, and modern health management practices should be improved.

Keywords: Microbial Sensitivity Tests, Drug Resistance, Multidrug-Resistant, Culturable Bacteria

Evaluation of Pathogenic Genes in Escherichia coli in Patients Referred to Gonabad Hospitals, Iran

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BACKGROUND AND OBJECTIVES: Urinary tract infection (UTI) is one of the common bacterial infections. Escherichia coli is the most common cause of UTI. In this research, the prevalence of several virulence factors and beta-lactam resistance genes was investigated.

MATERIALS AND METHODS: One hundred E. coli isolates were collected from patients' specimens with UTI referred to Allame-Bohlol Gonabadi hospital. Polymerase chain reaction (PCR) was performed to identify five pathogenic genes fimH, aer, pap, hly, traT.

RESULTS AND DISCUSSION: The study identified the following frequencies of pathogenic genes in 100 UPEC isolates: traT (94%), fimH (90%), pap (91%), aer (82%), and hly (21%). These results highlight the high prevalence of adhesion and iron acquisition genes, emphasizing their critical role in UPEC pathogenicity and the need for targeted therapeutic strategies. Conclusion: Pathogenic genes may also increase the severity, progression, and expansion of urinary tract infections. Therefore, identifying these genes as critical controllers of illness can use for better manage the treatment.

Keywords: Antibiotic resistance genes, E. coli, Pathogenic genes, Polymerase chain reaction

Evaluation of postbiotic extracts from L. rhamnosus and L. casei in inhibiting biofilm formation of E. faecium strains

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BACKGROUND AND OBJECTIVES: One of the new approaches developed in the control of pathogens is the use of cellular structures and bioactive metabolites derived from probiotics as postbiotic compounds. Given that the severity of pathogenicity and drug resistance of pathogens is closely related to their ability to form biofilms, the use of postbiotics for biofilm control is of great importance. In this study, the postbiotic potential of cell-free supernatant of probiotic bacteria L. rhamnosus PTCC 1607 and L. casei PTCC 1608 in inhibiting biofilm formation of E. faecium strains was evaluated.

MATERIALS AND METHODS: To evaluate the biofilm formation by bacteria, the 96-well microplate method and crystal violet staining were used. Cell-free supernatant was obtained by centrifugation and filtration of L. rhamnosus and L. casei cultures in MRS broth. Inhibition of biofilm formation and removal of pre-formed biofilm were evaluated by different dilutions of cell-free supernatant.

RESULTS AND DISCUSSION: In this study, all E. faecium strains were able to form biofilm. No significant difference was observed between the percentages of inhibition of biofilm formation in these strains ($p<0.05$). In examining the effect of the cell free supernatant on the inhibition of biofilm formation, the supernatant obtained from L. rhamnosus and L. casei culture at a concentration of 1000 µg/ml could largely inhibit biofilm formation. However, the percentage of biofilm inhibition decreased at lower concentrations.

Keywords: Virulence, Biofilms, Probiotics, Drug Resistance

Evaluation of Probiotic Traits and Antifungal Activity in Lactobacillus Isolates from Rural Dairy Sources

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BACKGROUND AND OBJECTIVES: Lactobacillus species are among the most extensively studied probiotic microorganisms, widely recognized for their therapeutic qualities as well as their antifungal capabilities. Due to their diverse functional and technological attributes, these bacteria are regarded as beneficial microbes with significant applications in food biotechnology. This study aims to evaluate the probiotic potential and antifungal activity of indigenous Lactobacillus strains isolated from traditional dairy products.

MATERIALS AND METHODS: Microbial samples were collected from traditional dairy products from Yazd villages specifically Moghestan and Mohammad Abad in 2024. Lactobacillus strains were isolated using standard microbiological methods with MRS broth. Preliminary identification was conducted via Gram staining, catalase activity assays, evaluation of salt and temperature tolerance, and species-level characterization through biochemical profiling and fermentation analysis. The strains were further evaluated for acid resistance and antifungal activity. Molecular identification was conducted through DNA extraction and sequencing.

RESULTS AND DISCUSSION: After isolating and removing duplicates, three distinct isolates were identified by Molecular sequencing: SK1 (Streptobacter tropicalis, MK (Lactobacillus plantarum) KK0 (Lactobacillus delbrueckii). All isolates showed strong environmental resilience. Lactobacillus delbrueckii displayed in the most potent antifungal activity, effectively suppressing Aspergillus flavus growth. Indigenous Lactobacillus isolates, showed strong probiotic and antifungal properties, especially L. delbrueckii against Aspergillus flavus. Their resilience highlights their potential for improving safety and quality in fermented dairy applications.

Keywords: Probiotics, Antifungal activity, Acid tolerance, Traditional dairy products, Lactobacillus delbrueckii

Evaluation of the Antibacterial Effect of Anethole on Resistant and Susceptible Strains of Pseudomonas aeruginosa

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BACKGROUND AND OBJECTIVES: Pseudomonas aeruginosa is a Gram-negative opportunistic pathogen associated with persistent infections and notable antibiotic resistance, leading to its classification as a critical priority by the WHO. Its ability to form strong biofilms further complicates treatment. Therefore, developing new antibacterial strategies is crucial. This study investigates the antibacterial effects of anethole against resistant and susceptible clinical strains of P.aeruginosa, with a particular focus on mechanisms involving membrane permeability alteration.

MATERIALS AND METHODS: In this study, seven clinical isolates of Pseudomonas aeruginosa were identified through biochemical tests and PCR detection of the oprL gene. Genomic DNA quality and quantity were assessed using NanoDrop and agarose gel electrophoresis. Antimicrobial susceptibility was determined by disk diffusion. The antibacterial activity of anethole was evaluated by MIC and MBC assays, and its effect on membrane permeability was assessed using the crystal violet uptake method. Data were analyzed with SPSS version 8.

RESULTS AND DISCUSSION: Antimicrobial susceptibility testing showed multidrug resistance among the isolates; however, most remained sensitive to gentamicin, neomycin, and colistin. For isolate P3, the MIC and MBC were 1.25 µg/mL and 2.5 µg/mL, respectively, while for P4, they were 0.625 µg/mL and 1.25 µg/mL. Crystal violet uptake assays, supported by t-test analysis, revealed a significant increase in membrane permeability at MIC, ½MIC, and ¼MIC concentrations compared to the control (p 0.05). These results suggest that anethole exerts strong inhibitory and bactericidal effects against Pseudomonas aeruginosa by enhancing membrane permeability, highlighting its potential as a promising antimicrobial agent.

Keywords: P.aeruginosa, Antimicrobial resistance, Anethole, Minimum inhibitory concentration, Crystal violet uptake

Evaluation of the Antibacterial Effect of the Synthetic Antimicrobial Peptide AMP-X on Antibiotic-Resistant Pseudomonas aeruginosain a Mouse Model

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BACKGROUND AND OBJECTIVES: The rise of antibiotic-resistant Pseudomonasaeruginosa presents significant challenges in treating infections.Antimicrobial peptides (AMPs), like AMP-X, show potential due to their ability to disrupt bacterial membranes and lower resistance development.While AMP-X has demonstrated strong antibacterial effects in lab models, its effectiveness in living organisms remains unclear. This study aims to evaluate the efficacy of AMP-X in reducing the bacterial load of multi-drug resistant Pseudomonas aeruginosa and its impact on immune response and survival in a murine model.

MATERIALS AND METHODS: In this study, 30 BALB/c mice were randomly divided into three groups: the AMP-X treatment group, the antibiotic group (ciprofloxacin), and the control group.Following intraperitoneal injection of antibiotic-resistant Pseudomonas aeruginosai,treatments were administered for three consecutive days. Bacterial load (CFU), levels of inflammatory cytokines (IL-6 and TNF-α), and survival rates up to day seven were measured. Data were analyzed using appropriate statistical tests

RESULTS AND DISCUSSION: In the AMP-X-treated group, the bacterial load in blood and tissues was significantly lower compared to both the control and antibiotic groups. Additionally, levels of inflammatory cytokines IL-6 and TNF-α were elevated in this group, indicating activation of the innate immune response. The survival rate in the AMP-X group was also higher (90%) than in the other groups. These findings suggest that AMP-X not only directly inhibits the growth of resistant Pseudomonas aeruginosa, but may also enhance immune function to better control the infection. Compared to the reference antibiotic,AMP-X demonstrated greater efficac under resistant conditions, indicating its potential as a promising alternative or adjunct therapy in the treatment of multidrug-resistant infections.

Keywords: Antimicrobialpeptide,AMP-X,Pseudomonasaeruginosa

Evaluation of the Antimicrobial Activity Rind of Citrus Sinensis Extracts Against Pseudomonas aeruginosa Induced Burn Infections in a Murine Model

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BACKGROUND AND OBJECTIVES: Pseudomonas aeruginosa is a common opportunistic pathogen responsible for hospital-acquired infections, particularly in burn wounds. In recent years, plant extracts and essential oils have gained attention due to their broad-spectrum antimicrobial properties. This study investigates the antimicrobial effects of ethanolic and acetonic rind of extracts of orange (Citrus sinensis). P.Aeruginosa induced burn infections in mice.

MATERIALS AND METHODS: Rind of orange were collected, identified, and extracted using ethanol and acetone solvents. Minimum Inhibitory Concentration (MIC) and Minimum Bactericidal Concentration (MBC) were determined using serial dilution in nutrient broth within 24-well microplates. Burn wounds in mice were inoculated with a pseudomonas aeruginosa suspension (5×10^5CFU/ml) , and treatments were applied using the extracts at their respective MBC concentrations.

RESULTS AND DISCUSSION: Following extraction and testing, the results demonstrated the antimicrobial effects of ethanolic and acetonic extracts of orange rind. Based on the prepared serial dilutions, the minimum inhibitory concentration (MIC) of both the ethanolic and acetonic extracts against Pseudomonas aeruginosa was 3.2 mg/ml. Moreover, the minimum bactericidal concentration (MBC) of both extracts against Pseudomonas aeruginosa was found to be 7.8 mg/ml.

Keywords: Nosocomial infections, antimicrobial resistance, microbial resistance

Evaluation of the Antimicrobial Effects of Nisin and the Presence of the Colistin-Resistant Gene *mcr-1* in Klebsiella pneumoniae Clinical Isolates from Patients in Bonab City in 2023

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BACKGROUND AND OBJECTIVES: Klebsiella pneumoniae, particularly antibiotic-resistant strains, is a major cause of nosocomial infections. This study aimed to investigate the biochemical characteristics, antibiotic resistance patterns, and the effects of alternative antimicrobial agents such as nisin and colistin on Klebsiella pneumoniae.

MATERIALS AND METHODS: From June to October 2023, 16 Klebsiella pneumoniae isolates were collected from various clinical samples, including urine, stool, nasal mucus, and throat swabs. Biochemical tests confirmed their identity, and antibiotic susceptibility testing was performed for ciprofloxacin, cefixime, meropenem, and gentamicin. The antimicrobial effects of nisin and colistin were assessed at different concentrations using MIC and well diffusion assays. Additionally, PCR was used to detect the presence of the *mcr-1* gene, responsible for colistin resistance.

RESULTS AND DISCUSSION: Biochemical results confirmed the metabolic characteristics of Klebsiella pneumoniae, consistent with established scientific reports. Antibiotic susceptibility testing revealed increased resistance to ciprofloxacin, ceftriaxone, and cefixime, while meropenem and gentamicin remained effective. Both nisin and colistin inhibited bacterial growth at low concentrations. The *mcr-1* gene was not detected, indicating susceptibility to colistin in these isolates. This study highlights the rising resistance of Klebsiella pneumoniae to common antibiotics, while demonstrating that alternative antimicrobials like nisin and colistin remain effective. Further research is needed to explore their therapeutic potential.

Keywords: Klebsiella pneumoniae, antibiotic resistance, nisin, colistin, *mcr-1* gene.

Evaluation of the combination effect of Lactobacillus acidophilus and garlic extract against Salmonella enterica

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BACKGROUND AND OBJECTIVES: Salmonella enterica is a major enteropathogenic agent. It is also listed by the WHO as one of the antibiotic-resistant priority pathogens, which requires new strategies for infection management. This study aims to evaluate the effect of Lactobacillus acidophilus ATCC 4356 and garlic extract against S. enterica ATCC 14028 as a potential therapeutic alternative.

MATERIALS AND METHODS: Bacterial strains were obtained from ATCC (USA) via Iresco Life Science Co. (Iran). Garlic extract was prepared using the percolation method. Inactivation of L. acidophilus carried out by UVC-LED irradiation, and the efficiency of the process was evaluated at 5 different time intervals from 0 to 30 minutes. The postbiotic formulation was prepared by mixing 1:1 (v/v) of inactivated L. acidophilus and garlic extract. Antimicrobial activity against S. enterica was assessed using the agar well diffusion and broth microdilution methods.

RESULTS AND DISCUSSION: In the agar well diffusion assay, the combination of garlic extract and inactivated probiotic bacteria demonstrated a larger zone of inhibition (17 ± 1 mm) compared to either the inactivated bacterium (15 ± 1 mm) or garlic extract (12 ± 1 mm). However, the inhibition zone was smaller than that observed with oxacillin (22 ± 1 mm). which was used as a control antibiotic. Additionally, the antimicrobial activity of the combination of garlic extract and postbiotic showed a similar pattern, with minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) values of 3.2% and 6.25% (v/v), respectively. The developed formulation could be a promising alternative for controlling S. enterica infections.

Keywords: Garlic extract, Lactobacillus acidophilus, Postbiotic, Salmonella enterica,

Evaluation of the Effect of Bacteroides fragilis as a novel treatment against IBD

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BACKGROUND AND OBJECTIVES: Inflammatory bowel disease (IBD), as a group of chronic intestinal disorders, is associated with persistent inflammation and damage to intestinal tissue. The intestinal microbiome plays a key role in regulating immune and inflammatory responses. Bacteroides fragilis as a probiotic can have positive effects on the microbiome and inflammatory responses in IBD patients. The aim of this study is to evaluate the effect of Bacteroides fragilis on the expression of inflammatory cytokine genes in an in vitro model of IBD.

MATERIALS AND METHODS: First, the cancer cell line -29HT was obtained from the Pasteur Institute of Iran, and then Bacteroides fragilis was cultured. To investigate the toxicity of bacteria on cancer cells and the percentage of cell line viability under bacterial extract treatment, the MTT test was used for a period of 24 hours. Then, to investigate the expression of related cytokines, after RNA extraction, Reverse Transcription reaction was performed and the cDNA produced was used to perform Real-time PCR reaction.

RESULTS AND DISCUSSION: By analyzing the effect of Bacteroides fragilis on the expression of inflammatory cytokine genes in a simulated model of inflammatory bowel disease (IBD), it was shown that Bacteroides fragilis significantly increases the expression of IL-1B, IL-2, IL-8 cytokines compared to the control group. In an in vitro model of IBD, Bacteroides fragilis significantly increased the expression of inflammatory cytokine genes compared to the control group. This suggests that Bacteroides fragilis could be a promising new probiotic for the treatment of IBD.

Keywords: Bacteroides fragilis, cytokine, IBD, inflammation, probiotic

Evaluation of the effect of chitosan nanoparticle incorporated with Bifidobacterium bifidum secretome on colorectal cancer mitigation

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BACKGROUND AND OBJECTIVES: Colorectal cancer (CRC) is the second leading cause of cancer-related mortality rate in the world. The purpose of this study is to evaluate the impact of chitosan nanoparticles (CTNP) conjugated with Bifidobacterium bifidum (B. bifidum) secretome (CTNP/B.b-sec) on the expression of genes associated with CRC signaling pathways.

MATERIALS AND METHODS: CTNP/B.b-sec was fabricated via an ionic gelation technique. Dynamic light scattering (DLS), zeta potential (ZP), and scanning electron microscopy (SEM) analysis were employed for the characterization of nanoparticles. The cytotoxic effect of CTNP/B.b-sec on human colon adenocarcinoma (Caco-2) cells was evaluated using MTT assay. The effect of CTNP/B.b-sec on the expression of genes related to CRC signaling pathways was evaluated using real-time PCR.

RESULTS AND DISCUSSION: The particle size and zeta potential of CTNP/B.b-sec were 453.1 nm and 9.11 mV, respectively, with a suitable SEM morphology. CTNP/B.b-sec can cause a significant decrease in the expression of β-Catenin, PI3K, TGF-α, Bcl2, TLR4, CEA, and TGF-β oncogenes by 0.96, 0.37, 0.03, 0.41, 0.88, 0.69, and 0.71-fold, respectively. The nanoparticle led to a significant 73.4-fold increase in the expression of the caspase-9 suppressor. In conclusion, the use of B. bifidum secretome, combined with CTNP, presents a promising strategy for preventing the progression of colon cancer through molecular mechanisms. Therefore, after further studies in mouse models, it can be used as a novel approach to inhibit cancer and increase the survival of cancer patients.

Keywords: Bifidobacterium bifidum, Colorectal cancer, Chitosan nanoparticles

Evaluation of the Inhibitory Effect of the Antifungal Peptide Cliotide U1 on the Expression of Biofilm-Associated Genes in Clinical Isolates of Candida albicans Using Real-Time PCR

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BACKGROUND AND OBJECTIVES: Candida albicans is a major opportunistic fungal pathogen with high adaptability,As antifungal resistance continues to raise, alternative therapies such as antimicrobial peptides (AMPs) are being explored. This study investigates the effect of Cliotide U1, a natural antifungal peptide, on the expression of ALS3, HWP1, and ECE1 genes in clinical isolates of C. albicans.

MATERIALS AND METHODS: Gene expression analyses were performed using quantitative real-time PCR (qRT-PCR) to assess transcriptional changes in ALS3, HWP1, and ECE1. ACT1 was used as the reference gene. Untreated isolates served as controls. Expression levels were compared using the ΔΔCt method to evaluate the relative fold changes. No statistical modeling or numerical analysis is included in this abstract, per congress requirements.

RESULTS AND DISCUSSION: Cliotide U1 led to notable changes in the expression of all three target genes. ALS3, a gene involved in adhesion and the initial steps of biofilm formation, showed consistent downregulation in most strains, particularly among fluconazole-sensitive isolates. HWP1, essential for hyphal formation and structural integrity of the biofilm, was also downregulated upon treatment. This is consistent with phenotypic observations showing reduced hyphal development. The suppression of HWP1 may inhibit the yeast-to-hyphae transition, which is a critical virulence trait. ECE1, a gene associated with hyphal elongation and epithelial invasion, demonstrated marked transcriptional repression in several isolates. . The observed effects were present in both sensitive and resistant strains, although the magnitude varied, indicating that Cliotide U1 may exert its influence

Keywords: Antifungal Peptide Cliotide U1 Real-Time PCR Biofilm Candida albicans

Evaluation of the patterns of EPIYA motifs in the cagA gene of Helicobacter pylori isolated from patients with gastritis, peptic ulcer and gastric cancer in Ghaem Hospital, Mashhad

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BACKGROUND AND OBJECTIVES: Helicobacter pylori is associated with gastric cancer and MALT lymphoma. The virulence factor CagA plays a critical role in the pathogenesis of these diseases. The pathogenic activity of CagA is modulated by the tyrosine phosphorylation of EPIYA motifs in host cells. This study aimed to evaluate the patterns of EPIYA motifs in the cagA gene of H. pylori obtained from patients with gastritis, peptic ulcers, and gastric cancer at Ghaem Hospital in Mashhad.

MATERIALS AND METHODS: The study analyzed 67 DNA samples of Helicobacter pylori from previous research. The samples were categorized into three groups: gastritis, gastric ulcer, and gastric cancer. A PCR molecular test was performed to determine the EPIYA motif type for each sample.

RESULTS AND DISCUSSION: In a study involving 67 samples, typographic variation was identified in 52 samples, while 15 samples produced no interpretable results. Among the typed samples, 31 were classified as ABC type, 5 as ABD type, and 16 as AB type. Specifically, in gastritis-related samples, there were 20 classified as ABC, 2 as ABD, and 13 as AB types. For peptic ulcer samples, 10 were classified as ABC, 3 as AB, and 1 as ABD. In gastric cancer samples, 2 were classified as ABD and 1 as ABC. Statistical analysis revealed no significant relationship between the prevalence of ABC and ABD patterns and clinical symptoms.Our results showed that the common motif pattern observed among all samples was ABC. Therefore, ABC type was more prevalent in patients with peptic ulcers than in other patients.

Keywords: Helicobacter pylori, cagA gene, peptic ulcers

Evaluation of the synergistic effect of mesenchymal stem cells secretome and chitosan nanocomposite against MDR V. cholerae

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BACKGROUND AND OBJECTIVES: The purpose of this research is evaluation of the synergistic effect of mesenchymal stem cells secretome and chitosan nanocomposite (MSCsS/CSNPs) against V. cholerae using disk diffusion method.

MATERIALS AND METHODS: Ionic gelation procedure was employed to prepare MSCsS/CSNPs. Using DLS method nanoparticle was characterized. Antimicrobial susceptibility testing was done by disk diffusion method according to CLSI standard protocol. Briefly, 108 colony forming unit (CFU/mL) of V. cholerae was cultured on Muller Hinton agar. Next, blank disks were placed on the culture plate, and then 100 µL of MSCsS (1000µg), 100 µL of chitosan nanocomposite (0.05%), and 100 µL of MSCsS/CSNPs (1000 µg + 0.05%) were added to the blank discs. Finally, the plates incubated at 37 °C for 24 h, the inhibitory zone was then measured.

RESULTS AND DISCUSSION: The morphological properties, size, charge, entrapment efficiency, and protein release (after 72h at pH~7.2) of the novel nanocomposite were spherical shape, 312.4, +5.95, 75%, and 79%, respectively. The inhibition zone of MSCsS, CSNPs, and MSCsS/CSNPs were 15mm, 22mm, and 28mm, respectively. Our findings showed that the inhibition zone of MSCsS/CSNPs is larger than MSCsS and CSNPs. After 200 µL of CSNPs and 200 µL of MSCsS/CSNPs were separately added to blank disks, the inhibition zone moved towards each other and a synergistic effect was observed. Considering that genetic transmission does not lead to the emergence of antimicrobial resistance to MSCsS/CSNPs, it can be considered as a complementary strategy in modulating cholera disease.

Keywords: Keyword: Chitosan nanocomposite, Mesenchymal stem cells, Synergistic, Secretome; V. cholerae

Evaluation the antimicrobial effects of Actinobacteria strains isolated from soil samples in Kerman district, Iran

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BACKGROUND AND OBJECTIVES: The most interesting property of Actinobacteria is the ability to produce bioactive secondary metabolites, such as antibiotics with ability for inhibition or killing of human pathogens. So, the purpose of this research was the isolation of Actinobacteria strains and evaluation of their antimicrobial effects.

MATERIALS AND METHODS: Serial dilution method was used for soil samples to isolate Actinobacteria strains on ISP media. The morphological, physiological, and biochemical tests were used for identification of the isolates. Antimicrobial activity was also investigated by Cross Streak and Disk Diffusion methods against selected pathogens such as Escherichia coli, Pseudomonas aeruginosa, Staphylococcus aureus and Enterococcus faecalis.

RESULTS AND DISCUSSION: Twelve Actinobacteria strains were isolated on ISP media and identified by morphological characteristics such as unique colony appearance, spore formation, and pigmentation. Under microscope, they appeared as Gram-positive, filamentous with a branched, thread-like structures. All isolates were non-motile, positive for catalase, MR test and positive for H2S production and nitrate reduction, but negative for urease test, oxidase and VP test. The results of Cross streak and disc diffusion method were observed by clear inhibition zones related to each Actinobacteria at the intersection of the test pathogens and accordingly, two isolates with best interactions were also selected for further In Vivo tests. Actinobacteria has made a massive contribution to the field of medicine specially through antibiotics. Accordingly, two selected Actinobacteria isolates in this research may have the potential source of antibiotics, especially for suppressing of human pathogenic bacteria and they are good candidates for further In vivo tests.

Keywords: Actinobacteria, antimicrobial activity, novel antibiotics

Exploring microbial diversity in Kermanshah province's Kermanshahi oil through DGGE and sequencing analysis

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BACKGROUND AND OBJECTIVES: Ghee, known as "roghane heiwâni," or "Kermanshahi oil," is a traditional fermented butter-like product highly esteemed for its nutritional value. Ghee has substantial potential as a reservoir of probiotic microorganisms. Previous research delved into isolating and identifying lactic acid bacteria (LAB) in Kermanshahi through culture and PCR sequencing. This study seeks to elucidate the microbial profiles and diversity within Kermanshahi using culture, Denaturing Gradient Gel Electrophoresis (DGGE), and sequencing methodologies.

MATERIALS AND METHODS: Twenty samples of Kermanshahi oil were meticulously gathered from diverse locales across Kermanshah province. These samples were cultivated under specialized conditions in MRS and M17 environments spanning 24 to 72 h. After DNA extraction, the 16S rRNA gene sequences were amplified, culminating in sequencing for conclusive identification of the isolates. Furthermore, the DGGE technique was directly employed to separate and identify various species present in the oil samples utilizing bioinformatics software.

RESULTS AND DISCUSSION: Sequencing outcomes revealed a diverse array of microorganisms among the isolates, with Lactobacillus constituting 43%, Streptococcus comprising 27.6%, Enterococcus at 4.61%, and yeasts at 7.6%. Other species exhibited lower frequencies, encompassing Rhizobium, Bacillus coagulans, and Staphylococcus hominis. The isolation of a diverse spectrum of probiotic microorganisms underscores their potential utility in industrial dairy product production. These findings suggest the possibility of integrating these valuable microorganisms into the contemporary dairy industry. As consumer interest in probiotic-enriched products surges, the insights gained from this study pave the way for harnessing the benefits of Kermanshahi-derived probiotics.

Keywords: Probiotic, Kermanshahi oil, Lactobacillus, Streptococcus, Denaturing gradient gel electrophoresis

Exploring Novel Anti-TB Therapeutics: Molecular Docking and SwissADME Analysis of Pretomanid, Thiacetazone, and Isoniazid against CmaA3

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BACKGROUND AND OBJECTIVES: Tuberculosis (TB), caused by Mycobacterium tuberculosis, remains a drug-resistant challenge. Cyclopropane mycolic acid synthase A3 (CmaA3) is vital for methylating mycolic acid, which strengthens cell wall integrity and contributes to drug resistance. Inhibiting CmaA3 offers a potential approach for developing new anti-TB drugs. This study employs molecular docking to compare potential of three compounds, pretomanid, thiacetazone, and isoniazid, as CmaA3 inhibitors for novel anti-TB therapies.

MATERIALS AND METHODS: The 3D structure of CmaA3 was retrieved from the Protein Data Bank (PDB ID: 1L1E). Pretomanid (DB05154), thiacetazone, and isoniazid were obtained from PubChem databases in SDF format. CmaA3 and ligands were prepared and docked together using Molegro Virtual Docker v0.6. Molecular interactions and binding energies were analyzed with Molegro Molecular Viewer. Finally, pharmacokinetic properties were evaluated using SwissADME.

RESULTS AND DISCUSSION: Molecular docking revealed that pretomanid exhibited the strongest binding affinity with the lowest energy (-109.353kcal/mol) and the highest number of hydrogen bond acceptors (9), a polarity(TPSA: 91.33 Å²), despite having no hydrogen donors. Thiacetazone showed moderate binding energy (-100.87kcal/mol), three hydrogen bond donors, but a higher TPSA (111.6 Å²), possibly reducing permeability. Isoniazid had the weakest binding energy (-70.41kcal/mol), lowest TPSA (68.01 Å²), yet it violated Lipinski's rule and had zero oral bioavailability. SwissADME analysis identified pretomanid as the most balanced lipophilicity candidate for drug-likeness with optimal lipophilicity(LogP: 2.52).Pretomanid exhibited enhanced docking performance and favorable pharmacokinetic properties compared to thiacetazone and isoniazid, suggesting it as a more promising inhibitor for the CmaA3 protein. Further experimental analysis is required.

Keywords: Mycobacterium tuberculosis, CmaA3, Pretomanid, Thiacetazone, Isoniazid, Molecular Docking

Exploring Postbiotic Metabolites as a Solution to MRSA Resistance: Antimicrobial and Anti-Biofilm Effects of Pediococcus Strains

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BACKGROUND AND OBJECTIVES: Methicillin-resistant Staphylococcus aureus (MRSA) presents a significant challenge in both healthcare and industrial settings, causing severe infections and complicating treatment due to its resistance to antibiotics. In healthcare, MRSA leads to complicated infections, especially in immunocompromised individuals. In industrial settings, it can contaminate food products and affect animal health. The rise in antibiotic resistance highlights the need for alternative treatment approaches. We propose the use of Pediococcus-derived postbiotics as a promising solution for combating MRSA, given their strong antibacterial and anti-biofilm properties.

MATERIALS AND METHODS: Antimicrobial susceptibility testing was conducted on MRSA strains using postbiotics from three Pediococcus acidilactici strains: A.P 6(3), D.M II (6), and Y.L III (7), preserved as IBRC-M 11447, IBRC-M 11476, and IBRC-M 11450. The probiotic properties of these strains were confirmed by the Iranian Biological Resource Center (IBRC). Postbiotics were produced by culturing the strains under optimized conditions, followed by centrifugation and filtration. Antimicrobial activity was assessed by agar diffusion, while the minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) were determined through microdilution methods. Antibiofilm effects were evaluated using Crystal Violet staining and absorbance measurement at 595 nm.

RESULTS AND DISCUSSION: Inhibition zones ranged from 20 to 34 mm, with the MIC at 0.015 mg/ml and MBC at 0.5 mg/ml. The antibiofilm assay showed inhibition rates from 15% to 65%, with the highest inhibition at 1 mg/ml. These findings highlight the potential of Pediococcus-derived postbiotics as effective agents against MRSA, particularly in clinical settings dealing with antibiotic resistance.

Keywords: MRSA, Pediococcus acidilactici, postbiotics, antimicrobial, biofilm inhibition, MIC, MBC, resistance.

Exploring Prostate Health: Insights into Infections and Inflammation in Prostate Cancer Development and Management

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BACKGROUND AND OBJECTIVES: Prostate cancer (PCa) is a leading cause of male mortality worldwide, with increasing incidence linked to aging, genetics, and lifestyle. Emerging evidence highlights the significant role of infections and inflammation—such as prostatitis, benign prostatic hyperplasia (BPH), urinary tract infections (UTIs), sexually transmitted infections (STIs), and prostate microbiome alterations—in prostate tumorigenesis. This study aims to elucidate the epidemiological and molecular links between infections, inflammatory pathways, and PCa development and management, providing insights into potential preventive and therapeutic strategies.

MATERIALS AND METHODS: A comprehensive literature review was conducted, synthesizing data from epidemiological studies, molecular and microbiome analyses, and clinical trials. The review focuses on infection-related risk factors, specific inflammatory signaling pathways (e.g., NF-κB, STAT3, COX-2/PGE_2, IL-6/IL-8, TLR, NLRP3 inflammasome), and emerging therapeutic targets. Sources include peer-reviewed articles, meta-analyses, and current clinical guidelines.

RESULTS AND DISCUSSION: The review reveals a consistent association between prostatic infections and increased PCa risk, mediated through chronic inflammation and activation of oncogenic pathways. Key inflammatory mediators such as NF-κB and STAT3 promote tumor progression, while the prostate microbiome exhibits both tumor-promoting and protective bacterial signatures. Evidence also suggests that STIs like high-risk HPV, gonorrhea, HSV-2, and T. vaginalis may influence carcinogenesis via persistent immune activation. Furthermore, inflammatory pathways represent promising targets for novel therapies, with agents inhibiting NF-κB, COX-2, IL-6/IL-8, and NLRP3 showing potential in preclinical and clinical settings. Addressing detection bias and standardizing diagnostic criteria are essential steps toward integrating infection and inflammation management into PCa prevention and treatment paradigms.

Keywords: Prostate cancer, Prostatitis, Benign prostatic hyperplasia (BPH), Urinary tract infections

Exploring Toxoplasma gondii-Astrocyte Crosstalk in Schizophrenia Pathogenesis: From Parasitic Infection to Synaptic Disruption

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BACKGROUND AND OBJECTIVES: Toxoplasma gondii (T. gondii) invades astrocytes and other brain cells during the acute phase. The parasite is implicated as an environmental factor in neuropathophysiology by disrupting glutamate homeostasis, increasing neuroinflammation, and altering synaptic pruning. Schizophrenia (SCZ) is a genetically based psychiatric disorder in which astrocytes and abnormal immune responses may act as modulating risk factors. The precise molecular mechanisms and the influence of the timing of infection (particularly during the embryonic and pubertal periods) require further investigation. This review analyzes the available evidence and identifies research gaps.

MATERIALS AND METHODS: This review examined the T. gondii-SCZ association with astrocyte focus. We systematically searched PubMed, SJR, and Sage Journals (2016-2025). Only Q1/Q2 studies meeting inclusion criteria were analyzed: (1) T. gondii's astrocyte mechanisms in SCZ pathophysiology, (2) controlled designs, (3) defined samples. Exclusions: case reports, unclear methods, or uncontrolled studies. Quality was assessed via the Newcastle-Ottawa Scale (NOS≥7 = high quality).

RESULTS AND DISCUSSION: T. gondii infects astrocytes, triggering IL-6/TNF-α secretion and TGF-β dysregulation, which disrupts glutamate/GABA homeostasis. Astrocytes show dual roles: inhibiting parasite proliferation via IFN-γ/STAT1 while reducing GLT-1 expression and impairing synaptic pruning. In SCZ, this leads to CSPG depletion and PNN degradation, altering neural connectivity. Epidemiological data highlight increased T. gondii antibodies in SCZ patients, especially after fetal exposure or winter infections, suggesting critical timing effects. Although parasite-induced dopamine synthesis via tyrosine hydroxylase may contribute, the exact molecular mechanisms remain unclear, warranting further longitudinal studies. Most studies are cross-sectional; causal inferences require prospective designs.

Keywords: Toxoplasma gondii, Schizophrenia, Astrocytes

Expression, purification of recombinant bFGF from E.coli: cellular study

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BACKGROUND AND OBJECTIVES: Fibroblast growth factors (FGFs) develop a large family of polypeptide growth factors that are found in a wide range of organisms, from nematodes to humans. In humans, 22 members of the FGF family have been identified. Basic fibroblast growth factor (bFGF) is one of the key members of the FGF family. bFGF is a potent angiogenic molecule in the body and, under laboratory conditions, stimulates the growth of smooth muscle cells, wound healing, and tissue repair. Furthermore, bFGF is a strong mitogen and chemoattractant for endothelial cells in vitro and is an essential component of serum-free cell culture media.

MATERIALS AND METHODS: Considering pivotal role of fibroblast growth factor in stem cells media, the importance of FGF-2 purification emerges. This study concentrates on the expression, purification, and cellular studies of bFGF and interacted bFGF with gold nanoparticle. Therefore, bFGF_SUMO gene was transferred to E. coli strain BL21 in pET_21a vector, and protein expression was done under optimal conditions. Purification was carried out by nickel-agarose affinity column technique and purification of protein improved from 0.8 mg per ml to 1 and 1,5 mg per ml. Conformation of each step was done by SDS-PAGE gel. In order to investigate protein activity, wound healing test and MTT assay was used once with bFGF alone, also, with bFGF interacted with gold nano particle.

RESULTS AND DISCUSSION: The results depicted that gold nanoparticle can enhance the repair ability of FGF-2. Moreover, the toxicity of FGF-2 decreased after interaction with gold nano particle.

Keywords: Basic fibroblast growth factor, Wound healing, purification, expression, nanoparticle

Extracellular Vesicles in Oncogenic Virus Pathogenesis and Their Emerging Role in Prophylactic and Therapeutic Vaccine Development

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BACKGROUND AND OBJECTIVES: Oncogenic viruses, including human papillomavirus (HPV), Epstein-Barr virus (EBV), hepatitis B virus (HBV), and human T-cell lymphotropic virus-1 (HTLV-1), are etiologically linked to approximately 15–20% of global cancer cases. Recent advances in extracellular vesicle (EV) research have uncovered their critical involvement in oncovirus pathogenesis, where they serve as key mediators of intercellular communication, immune modulation, and tumor microenvironment remodeling. EVs-encompassing exosomes, microvesicles, and other membrane-bound nanoparticles-facilitate the transfer of viral oncoproteins, nucleic acids, and immunosuppressive molecules, thereby promoting viral persistence, cellular transformation, and metastatic progression.

MATERIALS AND METHODS: This review delves into the dual role of EVs in oncovirus-associated cancers, highlighting their contributions to disease mechanisms while exploring their potential as innovative vaccine platforms. How oncovirus-infected cells exploit EVs to disseminate oncogenic cargo, evade host immunity, and prime pre-metastatic niches. The promise of EV-derived biomarkers (e.g., non-coding RNAs, viral antigens) for early cancer detection and monitoring. Engineering strategies for EV-based vaccines, including cargo loading (viral antigens, adjuvants), surface modification for targeted delivery, and their advantages over conventional platforms (e.g., biocompatibility, cross-presentation efficiency).

RESULTS AND DISCUSSION: EVs are critical in oncovirus persistence but also offer unparalleled advantages as vaccine carriers due to their biocompatibility and cross-presentation capacity. Clinical translation requires standardization of EV isolation, scalable production, and trials comparing EV vaccines to existing platforms (e.g., mRNA-based).

Keywords: Extracellular vesicles, exosomes, oncogenic viruses, cancer vaccines, immunotherapy

Extraction of Umbilical Cord-Derived Mesenchymal Stem Cells and Evaluation of Their Antibacterial Properties Against Pseudomonas aeruginosa Wound Infections

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BACKGROUND AND OBJECTIVES: Mesenchymal stem cells (MSCs) derived from umbilical cord tissue have gained attention for their regenerative properties and potential therapeutic applications. This study aims to extract MSCs from umbilical cord tissue, confirm their identity using flow cytometry, and evaluate their antibacterial properties against Pseudomonas aeruginosa, a common pathogen in wound infections.

MATERIALS AND METHODS: Umbilical cord tissue was collected and processed to isolate MSCs using enzymatic digestion and standard cell culture techniques. Flow cytometry was employed to analyze the expression of specific surface markers (CD73, CD90, CD105, and CD34) to confirm the MSC phenotype. Additionally, differentiation assays were conducted by culturing MSCs in specific media for adipogenic, osteogenic, and chondrogenic differentiation. The antibacterial activity of the extracted MSCs was assessed through disk diffusion assays and minimum inhibitory concentration (MIC) tests against various strains of Pseudomonas aeruginosa.

RESULTS AND DISCUSSION: The results demonstrated that umbilical cord-derived MSCs exhibited significant antibacterial activity against Pseudomonas aeruginosa. Flow cytometry analysis confirmed the expression of positive markers (CD73, CD90, CD105) and the absence of hematopoietic markers (CD34), validating their identity as mesenchymal stem cells. Furthermore, the differentiation assays indicated successful adipogenic, osteogenic, and chondrogenic differentiation, showcasing the multipotent nature of the MSCs. This study highlights the potential of umbilical cord-derived MSCs as a promising source for antibacterial therapy and regenerative medicine.The successful characterization and differentiation of these cells support their application in treating bacterial infections and enhancing wound healing processes. Further research is warranted to explore their functional capabilities in clinical settings.

Keywords: Mesenchymal stem cells (MSCs); Umbilical cord; Pseudomonas aeruginosa; Wound infection

Fact or Fiction? AI-Based Methods' Hegemony in Protein Structure Prediction

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BACKGROUND AND OBJECTIVES: S-ribosylhomocysteine lyase, AKA LuxS, is one of the essential enzymes in biofilm formation and quorum sensing (QS) processes in K. pneumoniae (KP). So, it is potentially a promising drug target for discovering new anti-microbial agents. In the lack of the three-dimensional (3D) model of this enzyme of KP in the Protein Data Bank (PDB), we tried to predict the model using both homology modeling (HM) and AI-based prediction methods.

MATERIALS AND METHODS: FASTA sequence was obtained from UniProtKB, entry code B5XVC4. YASARA Structure version 25.1.19 was used as a tool for HM method, and AlphaFoldDB was utilized to obtain an AI-based constructed model.

RESULTS AND DISCUSSION: Results showed that HM method released more reliable results. HM method predicted the homodimer state of the enzyme. Also, nonetheless Zn++ was predicted instead of Fe++ according to the template structure, the presence of a metal ion in each monomer was predicted by HM method. AlphaFoldDB also provided a reliable 3D structure of the monomer state. However, it failed to predict the oligomerization state and the presence of a metal ion in the structure. The AlphaFoldDB models are integrated in protein-knowledge databases such as UniProtKB. Noteworthy, the models are predicted by the AlphaFold v2.0. There are reports that this version is capable to predict oligomerization states. As a conclusion, it is recommended to accompany an HM-based model along with the models obtained by AI-based methods, including AlphaFold method, to reach a more accurate and reliable insight on the 3D structure of an unknown protein.

Keywords: AlphaFoldDB, LuxS, Klebsiella pneumoniae, Homology modeling

Factors influencing the prevalence of Brucella abortus in canine populations

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BACKGROUND AND OBJECTIVES: This study investigates the epidemiological transmission of Brucella abortus to canines through the consumption of contaminated bovine placentas. It seeks to define the transmission mechanism and scope, aiming to inform the development of targeted biosecurity strategies that prevent pathogen spread in farm environments, thus safeguarding animal and public health.

MATERIALS AND METHODS: This study investigated a case of Brucella abortus transmission in a female farm dog post-abortion due to ingesting a contaminated bovine placenta. Diagnostic procedures commenced with culturing specimens on Brucella agar, confirmed via subtractive broth technique, followed by serological testing with the Rose Bengal, Wright's agglutination, and 2-Mercaptoethanol (2ME) tests. All serological tests indicated active infection, with both the 2ME and Wright tests yielding elevated titers of 1/80. Polymerase chain reaction (PCR) was performed last to detect Brucella abortus DNA, providing molecular confirmation of the pathogen. To complement the laboratory findings, detailed interviews were conducted with farm personnel to ascertain the dog's exposure and evaluate the farm's biosecurity protocols.

RESULTS AND DISCUSSION: Culture and subtractive broth tests identified Brucella abortus, with serological and PCR analyses confirming active infection and transmission via ingestion of infected bovine placentas. These findings underscore the need for robust biosecurity and waste management practices on farms to reduce zoonotic risk. Future research should investigate the chronic impact of brucellosis in canines and improve prevention strategies to limit interspecies transmission and safeguard public health.

Keywords: Brucella abortus, Polymerase Chain Reaction, Zoonoses, Rose Bengal, Wright's agglutination

Farm evaluation of a newly drinking water stabilizer on the titer stability of Newcastle disease and Infectious bronchitis vaccines

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BACKGROUND AND OBJECTIVES: Through vaccine administration via drinking water, stabilizers can protect live viral vaccines post-reconstitution. This study evaluated the efficacy of Vac-Stab Blue® ,a newly introduced poultry vaccine stabilizer, on the titer persistency of live Newcastle disease and infectious bronchitis vaccines administered via drinking water under farm conditions.

MATERIALS AND METHODS: The study compared Vac-Stab Blue® with Cevamune, a commercial vaccine stabilizer, across three experimental groups: Farm water (FW), FW treated with Cevamune® (Cevamune), and FW treated with Vac-Stab Blue®(VSB). Vaccine vials were dissolved in each diluent to provide one dose/mL and administered through distinct 70-meter-long water pipes in a broiler house. Samples collected from the pipe ends at 0 and 2hours post-administration were filtered (0.45µm and 0.2µm syringe filters), serially diluted, and titrated to determine the EID50 (50% Egg Infectious Dose).

RESULTS AND DISCUSSION: No significant differences were observed within ND and IB vaccine groups at 0hours post-reconstitution (ND: 5.7, 5.7, 5.9 log10EID50/dose for FW, VSB, Cevamune; IB: 3.1, 3.5, 3.5 log10EID50/dose for FW, Cevamune, VSB, respectively; (P<0.05). At 2hours, ND titers in FW was significantly lower than that of the Cevamune group (4.9 vs. 5.5; P>0.05). However, no significant difference was found between VSB and Cevamune (5.1 vs. 5.5; (P<0.05)). For IB at 2h post-reconstitution, the Cevamune and VSB groups showed significantly higher vaccine titers compared to the FW (2.9 vs 0.9; (P>0.05)). In conclusion, under farm conditions, Vac-Stab Blue® demonstrated comparable performance to Cevamune® in maintaining live poultry vaccine titer when administered via drinking water.

Keywords: Vaccine stabilizer, Newcastle disease, Infectious bronchitis, Titer persistency, Drinking water

First Case of Canine Wound Infection Caused by Corynascus verrucosus: Molecular Identification and Phylogenetic Insights

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BACKGROUND AND OBJECTIVES: Fungal infections are a common cause of skin disorders in companion animals. Here, we report the genetic characterization of a rare fungal isolate obtained from a wound infection in a canine patient.

MATERIALS AND METHODS: Skin scrapings were aseptically collected from a 4-year-old female Shih Tzu presenting with pruritus, alopecia, and scaling lesions. Direct microscopy and fungal culture were performed. Due to inconclusive morphological identification, the ITS genomic region (ITS1-5.8S-ITS2) was amplified using universal primers ITS1/ITS4. The PCR product was sequenced, and the consensus sequence was analyzed using BLASTn (NCBI) and aligned with related taxa. Phylogenetic reconstruction was conducted in MEGA7 via maximum likelihood.

RESULTS AND DISCUSSION: The fungal isolate exhibited 99.2% sequence identity with Corynascus verrucosus (GenBank accession PV082530). Phylogenetic analysis placed the isolate within a well-supported clade (bootstrap value = 98%) alongside C. verrucosus reference strains, confirming its taxonomic assignment. No closely related dermatophytes were identified, underscoring the rarity of this infection. To our knowledge, this is the first report of C. verrucosus causing infection in a canine host. The isolate's phylogenetic position within Chaetomiaceae aligns with recent taxonomic revisions but contrasts with earlier classifications of similar environmental fungi. While Corynascus spp. are typically saprophytic, this case highlights their potential as opportunistic pathogens in immunocompromised animals. Traditional culture-based methods failed to identify the isolate, reinforcing the necessity of ITS sequencing for accurate diagnosis of atypical fungal infections. Further studies should investigate the prevalence of Corynascus in veterinary samples and its antifungal susceptibility profile.

Keywords: Non-Dermatophyte, fungal Infection, Corynascus verrucosus, veterinary mycology, opportunistic fungal infection.

Formulation and Characterization of Nanoemulsion using Nasturtium officinale L. Extract and its Antibacterial Activities

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BACKGROUND AND OBJECTIVES: Nanoemulsions (NEs) are clear or opaque liquid mixtures of oil and water, often stabilized by a surfactant or a surfactant-cosurfactant combination. Due to their high surface area, long shelf life, transparent appearance, and tunable rheology, NEs have been used for decades in various fields such as drug delivery and food industry. Hence, the aim of the present project is to formulation and characterization of NEs using Nasturtium officinale L. extract and investigation of its antibacterial properties.

MATERIALS AND METHODS: The structure and morphology of the prepared nano-emulsion were evaluated using dynamic light scattering (DLS), zeta potential, and transmission electron microscopy (TEM). Then, the antibacterial activity of the prepared formulation was assessed by determining the minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) against Staphylococcus aureus and Escherichia coli.

RESULTS AND DISCUSSION: The results of the present study showed that the particle size of the NEs varied between 80 and 100 nm. Additionally, the zeta potential value was reported to be -30 mV. The MIC values ranged from 12.5 to 3.12 µg/mL, and the MBC values ranged from 50 to 12.5 µg/mL. The synthesized NEs demonstrated significant antibacterial activity and could potentially be used in the food and pharmaceutical industries.

Keywords: Nasturtium officinale L., Nano-emulsions (NEs), DLS, Escherichia coli, pharmaceutical industries.

Frequency and Antimicrobial Resistance of Uropathogens in urine samples of patients referred to Shahid Beheshti Hospital, Zanjan, Iran

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BACKGROUND AND OBJECTIVES: Urinary tract infections (UTIs) lead to antibiotic resistance. This study evaluates the frequency of urinary pathogens and antibiotic resistance patterns to guide effective treatment.

MATERIALS AND METHODS: : A total of 2,219 midstream urine samples were collected from outpatient and hospitalized patients between June 2024 and the end of June 2025. The midstream urine samples were cultured on EMB and blood agar. Positive isolates were tested using the disk diffusion method on Mueller-Hinton agar, and the sensitivity, intermediate, and resistance of the isolates were determined.

RESULTS AND DISCUSSION: Out of 2,219 midstream urine samples, 195 (8.78%) samples were positive. The most frequent agent of UTI was Escherichia coli (90.25%), followed by Staphylococcus saprophyticus (5.12%), Staphylococcus epidermidis (1.53%), Klebsiella pneumoniae (1.02%), Proteus mirabilis (0.51%), Staphylococcus aureus (0.51%), beta-hemolytic Streptococcus spp (0.51%), and Streptococcus spp. viridans group (0.51%). E. coli had the highest resistance to ampicillin (91%) and lowest to meropenem (24%). S. saprophyticus was most resistant to trimethoprim (50%) and least to ciprofloxacin (25%). S. epidermidis showed (66.7%) resistance to ciprofloxacin but only 33% to clindamycin. Klebsiella was most resistant to ampicillin (100%) and 50% resistant to ceftazidime, cefotaxime, ciprofloxacin, levofloxacin, and trimethoprim-sulfamethoxazole. Proteus was most resistant to nitrofurantoin and trimethoprim-sulfamethoxazole(100%). S. aureus showed 100% resistance to ciprofloxacin and clindamycin. Beta-hemolytic Streptococcus had no resistance, while Streptococcus spp viridans group was most resistant to ampicillin(100%).DISCUSSION: Duo to antibiotic resistance accurate diagnosis and treatment are essential.

Keywords: Antibiotic resistance, Disk diffusion, Uropathogen, Urinary tract infection

Frequency and determination of antibiotic resistance of diarrheagenic Escherichia coli pathotypes (EPEC, EHEC, ETEC, EAEC, EIEC) in raw milk samples collected from Zanjan

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BACKGROUND AND OBJECTIVES: Gastroenteritis caused by Escherichia coli is one of the most important and common food-borne diseases. Also, Escherichia coli diarrheal pathotypes, which include ETEC,EHEC, EPEC, EAEC, EIEC strains, are recognized as important factors associated with gastroenteritis and acute diarrhea. Therefore, considering the clinical significance of Escherichia coli diarrheal pathotypes and gastrointestinal diseases caused by raw and unpasteurized dairy consumption, the aim of this study was to investigate the frequency and pattern of antibiotic resistance of diarrheal pathotypes Escherichia coli in raw Milk samples.

MATERIALS AND METHODS: In this descriptive cross-sectional study, 200 raw milk samples were collected over two months from supplier stores and livestock. The samples were analyzed using standard culture methods and biochemical tests. Antibiotic resistance patterns were determined using the conventional disk diffusion method on agar. To identify and assess the frequency of diarrheagenic Escherichia coli pathotypes, genomic DNA was extracted from isolates, and pathogen-specific genes were detected using rapid PCR diagnostic techniques.

RESULTS AND DISCUSSION: Out of 200 raw milk samples, Escherichia coli was isolated in 43 cases (21.5%). In the antibiotic resistance test against 11 common antibiotics, the highest resistance was observed to polymyxin B (95.3%), while the lowest was to cotrimoxazole (2.3%). Among the isolates, 18 strains (41.8%) were identified as multidrug-resistant (MDR). The prevalence of E. coli pathotypes was as follows: enterohemorrhagic (58.1%), enterotoxigenic (58.1%), enteroaggregative (51.1%), enteropathogenic (18.6%), and enteroinvasive (13.9%). Commensal E. coli strains were also reported

Keywords: Escherichia coli,multidrug resistant bacteria,PCR

Frequency of blaTEM gene in Pseudomonas aeruginosa isolated from hospitals of Sanandaj 1403

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BACKGROUND AND OBJECTIVES: Pseudomonas aeruginosa is a prominent pathogen associated with hospital-acquired infections. Its clinical importance is increasing, attributed to its resistance to various antimicrobials and its capacity for developing high-level multidrug resistance (MDR), which is influenced by numerous virulence factors present in its genome. Here, we investigate frequency of blaTEM gene.

MATERIALS AND METHODS: This cross-sectional study was conducted in the Department of Microbiology in Kurdistan university of medical sciences. In this descriptive study, all P. aeruginosa isolates which referred to hospitals of Sanandaj in summer of 1403 were collected. The samples were identified by conventional tests. The DNA of isolates were tested by boiling method. Molecular identification for blaTEM gene was performed using specific primers and polymerase chain reaction (PCR) method. The following primer used in this study: "forward: ATGAGTATTCAACATTTCCGTG and reverse: TTACCAATGCTTAATCAGTGAG"

RESULTS AND DISCUSSION: in this study 54 isolates were confirmed as P. aeruginosa. The prevalence of blaTEM gene in these isolates were 25 (46.3%). At here more than half of our isolates have this gene. The rising resistance of bacteria to cephalosporins is primarily due to the production of beta-lactamase enzymes, which degrade the efficacy of beta-lactam antibiotics, such as penicillins and cephalosporins. blaTEM is one of the well-known gene related to beta-lactamase enzymes.

Keywords: blaTEM, Antibiotic resistance, Pseudomonas aeruginosa

Frequency of qnrB, qnrS Genes and Antibiotic Susceptibility Profiles of Escherichia coli Isolated from Urinary Tract Infections, Al-Anbar, Iraq 2024-2025

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BACKGROUND AND OBJECTIVES: In 1998s, the quinolone resistance gene qnr was initially recognized. The qnr determinants have been discovered on plasmids or the bacterial chromosome. Our study investigation attempted to detect fluroquinolone resistant cases and monitored the qnrB, and qnrS genes in E. coli using a molecular method.

MATERIALS AND METHODS: 135 urine samples were collected from patients who referred health institutions and government hospitals in the city of Al-Anbar from 1 June to 30 September, 2024, suffering from UTIs. 47 samples were diagnosed as E. coli bacteria. The Kirby-Bauer disk diffusion method was used to detect QNR phenotypes using antibiotic disks. PCR was used to investigate and detect the frequency of resistance genes qnrB and qnrS in E. coli isolates.

RESULTS AND DISCUSSION: 47 isolates were positive for E. coli. Frequency of UTI in females with E. coli was 28 cases (59.58%), compared to 19 cases (40.42%) in males. The age group of 21 to 30 years had the highest frequency of E.coli infections (29.78%).The highest resistance rate of E.coli isolates was nalidixic acid (91.48%), ciprofloxacin (85.10%) and ofloxacin (80.85%). The highest sensitivity belonged to amoxicillin and nitrofurantoin, which were recorded in 42 isolates (89.36%) for each. The qnrB gene was detected in most bacterial isolates at a rate of 75 and the frequency of qnrS gene was in 73% of isolates. It seems very important to pay attention to the management of hospital infections and to examine the pattern of antibiotic resistance at specific time intervals in the hospitals and the community.

Keywords: E.coli, qnrB, qnrS, antibiogram

From colonization to infection: PFGE-based analysis of MDR-GNB transmission in the NICU

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BACKGROUND AND OBJECTIVES: Multidrug-resistant Gram-negative bacteria (MDR-GNB) pose a critical threat in neonatal intensive care units (NICUs) especially for preterm neonates. Colonization serves as a potential reservoir for invasive infections. This study investigated MDR-GNB colonization in preterm neonates, mothers, healthcare workers (HCWs), and the NICU environment, aiming to assess potential transmission to preterm neonates who developed MDR-GNB sepsis.

MATERIALS AND METHODS: We included 150 mothers (gestational age 37 weeks) and their preterm neonates. Rectal and vaginal swabs were collected from mothers before labor. Neonates had rectal and skin swabs at admission, 48–72 hours later, and weekly until discharge or day 30. Environmental samples were obtained from NICU surfaces, equipment, air, and HCWs' hands. Gram-negative bacteria were isolated, and antimicrobial susceptibility testing identified MDR strains. If a neonate developed sepsis with an MDR-GNB, pulsed-field gel electrophoresis (PFGE) was used to compare isolates from the neonate, mother, and environment. Identical PFGE patterns (100% similarity) indicated possible transmission.

RESULTS AND DISCUSSION: Seven neonates developed MDR-GNB sepsis (six Klebsiella pneumoniae, one Escherichia coli). Three cases showed 100% identical PFGE pulsotypes, and all involved sepsis caused by MDR K. pneumoniae. Two cases had identical pulsotypes between blood isolates and rectal samples: one at 48 hours post-birth, and another between a second twin's blood and a rectal sample during the fourth hospitalization week. In the third case, the blood isolate differed from the maternal vaginal sample. These results support possible transmission from colonization sources to invasive infection and highlight the need for improved surveillance and infection control.

Keywords: MDR-GNB, Preterm labor, NICU, colonization, infection, PFGE

From Dysbiosis to Early Detection: Diagnostic Potential of the Microbiome in Cancer Development

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BACKGROUND AND OBJECTIVES: Growing evidence suggests that dysbiosis in the human microbiome are closely associated with cancer initiation and progression. Dysbiosis contributes to tumorigenesis through genotoxin production, immune dysregulation, and disruption of signaling pathways. Additionally, specific microbial signatures are being explored as non-invasive biomarkers for early cancer detection and prognosis. This study aims to review the role of microbiome dysbiosis in carcinogenesis and its diagnostic potential.

MATERIALS AND METHODS: A systematic search of PubMed, Scopus, and Web of Science was performed for studies published from 2015 to 2025. Inclusion criteria encompassed original and review articles addressing microbiome alterations in human cancers with emphasis on diagnostic applications. Studies lacking sufficient data, and non-English articles were excluded.

RESULTS AND DISCUSSION: Dysbiosis contributes to cancer through genotoxin production (e.g., colibactin from E. coli, CDT from C. jejuni), oxidative stress, chronic inflammation, and disruption of signaling pathways such as NF-κB and Wnt/β-catenin. Key oncogenic microbes include Fusobacterium nucleatum, Bacteroides fragilis, Peptostreptococcus anaerobius (colorectal cancer), Porphyromonas gingivalis (oral cancer), Helicobacter pylori, and Malassezia (pancreatic cancer). Microbiota like Akkermansia muciniphila and Bifidobacterium longum enhance response to immunotherapy, while Gammaproteobacteria mediate chemoresistance via drug inactivation. Diagnostic potential is shown by specific microbial signatures in saliva, stool, and plasma, for example, Flavonifractor plautii in young-onset CRC and Parvimonas micra in advanced disease, demonstrating superior sensitivity and specificity compared to conventional methods. Microbiome dysbiosis plays a pivotal role in cancer biology and offers novel avenues for early, non-invasive diagnosis. Future studies should prioritize longitudinal validation and standardization to translate microbiome-based diagnostics into clinical oncology.

Keywords: Microbiota, Dysbiosis, Biomarkers, Tumor

From Genes to Microbiome: Can Probiotics Rewrite Thiopurine Drug Response in IBD Patients with TPMT and NUDT15 Variants?

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BACKGROUND AND OBJECTIVES: Thiopurines, including azathioprine and 6-mercaptopurine, are widely used immunosuppressants in the management of inflammatory bowel disease (IBD). Polymorphisms in thiopurine S-methyltransferase (TPMT) and nudix hydrolase 15 (NUDT15) are established predictors of thiopurine metabolism and toxicity, enabling genotype-guided dosing. However, a considerable number of wild-type patients still experience adverse reactions or therapeutic failure, indicating that additional factors—particularly gut microbial metabolism—may play a significant role. This study investigates whether modulation of gut microbiota through probiotics could influence thiopurine response and toxicity.

MATERIALS AND METHODS: A focused literature review (2018–2025) was conducted using PubMed, Scopus, and EMBASE. Selected studies examined the enzymatic biotransformation of thiopurines by gut microbes and evaluated the impact of probiotic interventions on drug metabolism, safety, and efficacy in IBD.

RESULTS AND DISCUSSION: Recent evidence shows that specific gut bacteria can activate or inactivate thiopurines, thereby altering the ratio of therapeutic 6-thioguanine nucleotides (6-TGN) to hepatotoxic 6-methylmercaptopurine (6-MMP). Certain probiotic strains may restore microbial balance, promoting favorable drug metabolism—especially in genetically predisposed or microbiome-disrupted patients. This integrative pharmacogenomic–pharmacomicrobiomic approach could advance precision medicine in IBD.

Keywords: Inflammatory Bowel Disease; Thiopurines; TPMT; NUDT15; Gut Microbiota; Probiotics; Pharmacomicrobiomics;

From Infection to Inflammation: Revisiting the Bacterial Role in Carotid Plaque Pathogenesis

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BACKGROUND AND OBJECTIVES: Atherosclerosis of the carotid arteries is a major contributor to ischemic stroke. Increasingly, microbial pathogens are implicated in plaque formation through chronic inflammation and immune activation. This systematic review aimed to evaluate the prevalence and potential mechanisms of bacterial involvement in carotid atherosclerosis, with a focus on methodological quality and microbiological data.

MATERIALS AND METHODS: A total of 84 articles were screened; 81 met inclusion criteria after deduplication. Studies were assessed using a standardized checklist evaluating sample types, bacterial species identified, presence of inflammatory markers, molecular data, and analytical rigor. Descriptive and quantitative synthesis was performed.

RESULTS AND DISCUSSION: Of the included studies, 98% involved human, animal, or laboratory models. Porphyromonas gingivalis was the most frequently reported species (n=12), followed by Chlamydia pneumoniae (n=9) and Helicobacter pylori (n=7). Although 56.1% of studies found an association between bacterial presence and plaque development, only 4.9% included molecular-level data, and fewer than 10% examined systemic inflammatory markers such as IL-6 or CRP. Notably, none of the studies applied bioinformatics or omics approaches. Overall, 100% of studies used reliable methods and clearly addressed their research questions, but only 39% disclosed conflicts of interest. Our findings indicate consistent associations between certain bacterial pathogens and carotid atherosclerotic plaques. However, there is a critical lack of molecular and mechanistic evidence. Future studies should prioritize microbial genomics, host-pathogen interaction models, and integration of inflammatory profiling to better define causality and identify potential therapeutic targets. Incorporating advanced omics technologies and bioinformatics will be essential to bridge existing

Keywords: Carotid Atherosclerosis Bacterial Pathogens Systematic Review Inflammation Plaque

From Particle to Cure: Antibacterial Potential of MgO Nanoparticles Against S. aureus and K. pneumoniae

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BACKGROUND AND OBJECTIVES: Nosocomial infections remain a major clinical concern, resulting in increased patient mortality, longer hospital stays, and rising healthcare costs. Particularly concerning is their prevalence with antibacterial resistance. Among the key pathogens, are opportunistic bacteria like S. aureus (Gram-positive) and K. pneumoniae (Gram-negative). Recently, magnesium oxide nanoparticles have attracted attention as promising antimicrobial agents due to their strong bactericidal activity, stability, and biocompatibility. This study investigates the potential of MgO NPs to inhibit the growth of these two pathogens, aiming to support infection control strategies in healthcare.

MATERIALS AND METHODS: MgO NPs were synthesized via Chemical Deposition, and their physical properties were examined through DLS and SEM tests. The S. aureus and K. pneumoniae strains were obtained from the ATCC. Antibiotic susceptibility was determined using the antibiogram test. the antibacterial activity of the MgO NPs was evaluated using MIC and MBC test.

RESULTS AND DISCUSSION: The Minimum Inhibitory Concentration (MIC) and Minimum Bactericidal Concentration (MBC) of the MgO NPs were found to be 2 mg/mL for the K. pneumoniae, and 1 mg/mL for the S. aureus. The size of the synthesized nanoparticles, according to SEM test, was below 100 nm. MgO NPs, with strong special properties, represent a reliable option for combating pathogenic bacteria, including multidrug-resistant (MDR) strains. They hold significant potential in the control of nosocomial infections. The results of this study on standard strains provide strong evidence of the nanoparticle's effectiveness and clinical importance, providing a strong basis for future laboratory and applied research.

Keywords: Antibacterial, Magnesium oxide nanoparticles, Nosocomial infections

Future Trends, Challenges, and Opportunities in Medical Parasitology in Iran by 2035: A Foresight Study

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BACKGROUND AND OBJECTIVES: Parasitic diseases continue to pose a significant public health burden in Iran, disproportionately affecting vulnerable populations in rural and low-resource settings. The epidemiology of these infections is anticipated to undergo substantial shifts over the next decade, driven by rapid socio-economic changes, climate variability, and population migration. This study employed a foresight approach to explore future trends, emerging challenges, and opportunities in medical parasitology in Iran by 2035.

MATERIALS AND METHODS: A mixed-methods design was utilized, comprising: a systematic literature review (2000–2024) of national parasitology reports and WHO databases (Of the 412 retrieved articles, 68 met the inclusion criteria.); scenario building informed by STEEP (Social, Technological, Economic, Environmental, Political) analysis; and trend extrapolation of reported parasitic disease incidence.

RESULTS AND DISCUSSION: Four key scenarios emerged: 1) the increasing emergence of drug-resistant parasitic strains, particularly in regions endemic for leishmaniasis, malaria, and giardiasis; 2) an elevated zoonotic transmission risk for echinococcosis, toxoplasmosis, and fascioliasis, attributed to environmental and agricultural transformations; 3) enhanced diagnostic capabilities for intestinal protozoa and blood parasites facilitated by advancements in molecular and point-of-care technologies; and 4) the expansion of surveillance networks through digital health systems, integrating the reporting of neglected parasitic infections such as strongyloidiasis and cryptosporidiosis. This study underscores the critical importance of proactive foresight in medical parasitology to effectively anticipate and mitigate the evolving burden of parasitic diseases in Iran. Strategic investments in targeted research, capacity-building initiatives, and robust intersectoral collaboration are crucial to bolstering national preparedness and resilience over the forthcoming decade.

Keywords: Foresight, Medical Parasitology, Iran, Scenario Planning, Parasitic Diseases

Galactomannan Test in Diagnosing COVID-19–Associated Pulmonary Aspergillosis

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BACKGROUND AND OBJECTIVES: Galactomannan (GM) is a non-invasive test used to diagnose invasive aspergillosis. We collected the existing studies on the diagnostic value of GM to determine a GM level for predicting CAPA (COVID–19–associated pulmonary aspergillosis).

MATERIALS AND METHODS: All articles on the value of GM in CAPA diagnosis published until November 2023 were reviewed. The main databases were searched using the following keywords: "aspergillus", "aspergillosis", "SARS-CoV-2", "COVID", "2019 ncovnCOV", "novel coronavirus", "COVID-19", "galactomannan", and "CAPA". Studies with reported levels of serum or BAL GM were included. Patients were classified into two groups: non-confirmed and proven aspergillosis. Finally, the receiver operating characteristic (ROC) curve analysis was used to determine a GM level to predict the likelihood of CAPA.

RESULTS AND DISCUSSION: A total of 26 articles were selected, of which 239 patients were included. A count of 123 patients (50%) were in the non-confirmed group and 124 (50%) patients were proven. The median serum GM was 0.51 in the non-confirmed group and 0.47 in the proven group (p= 0.73). The level of GM in BAL fluid was 0.10 in the non-confirmed and 2.80 in the proven group, which was statistically different (p0.001). With 81.3 % sensitivity and 79.5% specificity, the BAL GM cut-off was 1.01 ODI. The results showed that BAL GM ≥1.01 can be used to predict CAPA. Serum GM did not show any predictive value in diagnosing CAPA. However, BAL GM level can be a reliable diagnostic test in patients with CAPA.

Keywords: Galactomannan, Aspergillosis, SARS-CoV-2, COVID-19, Bronchoalveolar lavage, Fungi, Viral Diseases

Geographic Mapping of Helicobacter pylori Resistance: Interactions Among Asian Host Genomes, Regional Diets, and Pathogen Evolution

bahareh Attaran [1] © Ⓟ

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BACKGROUND AND OBJECTIVES: Resistance to antibiotics in Helicobacter pylori is becoming more common in Asia and Iran, which threatens attempts made to control gastric ailments. Recent genomic studies show that H. pylori strains have a diversity of genetic types and geographical associations with resistance mutations; the phylogenetic clustering reflects host geographic ancestry and local environmental factors

MATERIALS AND METHODS: Metronidazole, clarithromycin, and amoxicillin resistance rates are worrisome in Iran, with increasing multidrug-resistant strains. Molecular tests show that point mutations in resistance genes, including frxA, rdxA, gyrA, and 23S rRNA are associated with particular virulence genotypes; thus it seems there has been co-evolution between host-pathogen relationships leading to mutualistic interaction for the development of resistance. Local dietary habits, together with antibiotic consumption patterns, modulate the selection and maintenance of resistant organisms in this community, accentuating the need for appropriate eradication strategies. High salt promotes H. pylori virulence by upregulating the expression of a critical virulence factor cagA, which causes gastric inflammation and cancerogenesis. In animal models, a high-salt diet increases cagA transcription, and strains carrying this gene increase their ability to induce cancer.

RESULTS AND DISCUSSION: Certain cagA genotypes and EPIYA motif patterns increase the risk for GIs, particularly in gastric cancer cases from Iran. Expression and presence of cagA are linked to virulence, host response and antimicrobial resistance based on a mutual mechanism. These results highlight the importance of incorporating molecular information to improve precision medicine approaches and successful interventions for multidrug-resistant H. pylori in Asia and Iran.

Keywords: Helicobacter pylori; antimicrobial resistance; genomics, antibiotic resistance, dietary factors.

Generation of a recombinant Lactococcus lactis strain expressing a multi-epitope composed of proteins S, N, nsp3, and nsp8 of SARS-Cov-2 virus and evaluation of its expression

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BACKGROUND AND OBJECTIVES: The current coronavirus COVID-19 pandemic resulted in high mortality and morbidity. Lactic acid bacteria (LABs) such as Lactococcus lactis have been considered as bacterial carriers for compounds with therapeutic or preventive effects. Therefore, we decided to construct a multi-epitope of the proteins S, N, nsp3, and nsp8, and express it in the L. lactis system to assess its efficacy in animal model.

MATERIALS AND METHODS: A novel multi-epitope-based vaccine was developed. The pUC57-multi-epitope gene was digested with NaeI and BamHI to ligate into the pT1NX plasmid. Recombinant plasmids were electroporated into competent L. lactis MG1363. The bacteria were plated in GM17 medium and the accuracy of the cloning was confirmed using PCR, enzymatic digestion and sequencing. The recombinant L. lactis.pT1NX-gene was grown and ell preparations were disrupted and proteins were evaluated by SDS-PAGE and Western blot. Immunofluorescence microscopy and whole-cell ELISA were used to confirm cell surface display of the protein on L. lactis.

RESULTS AND DISCUSSION: Cloning of gene into the pT1NX vector was confirmed using different methods. SDS-PAGE and Western blot indicated that the gene was successfully expressed (~66 kDa). There was a strong fluorescence at the cell surface of L. lactis-pT1NX-gene. According to the ELISA, L. lactis pT1NX-gene clearly showed high absorption values as compared with the L. lactis-pT1NX. The use of non-pathogenic bacteria expressing virulence antigens to prevent viral infections seems promising. According to our data, it seems that this vector can be considered as a novel mucosal vaccine candidate against SARS-Cov-2 that needs to further studies.

Keywords: SARS-Cov-2, Lactococcus lactis, multi-epitope, vaccine

Genetic Diversity and Natural Selection Pressure on the SARS-CoV-2 Spike Gene: A Review with Focus on Iranian and Global Studies

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BACKGROUND AND OBJECTIVES: The spike (S) gene of SARS-CoV-2 plays a critical role in virus entry and immune response. This review summarizes genetic diversity and natural selection patterns of the spike gene from Iranian samples during 2023 and compares them with global trends. Thirty-five haplotypes, including eleven novel types, were identified, with a higher mutation rate in the S1 than S2 subunit. Some mutations overlapped B-cell epitopes, indicating possible immune pressure. Neutrality index analysis suggested evidence of natural selection. Comparisons with international data revealed both regional similarities and differences in mutation profiles. Understanding spike gene diversity and evolution may help improve vaccine design and preparedness for future outbreaks.

MATERIALS AND METHODS: This review was conducted by analyzing scientific articles related to the genetic diversity of the SARS-CoV-2 spike gene, with a focus on Iranian and international data published up to 2023. Relevant papers were identified using databases such as PubMed and Web of Science. Key findings from original articles and relevant reviews were compared and synthesized.

RESULTS AND DISCUSSION: Analysis of Iranian SARS-CoV-2 spike gene sequences revealed 35 haplotypes, with the highest diversity observed in the S1 subunit. Compared with international studies, the Iranian haplotype diversity and mutation distribution patterns show both alignment and distinct differences with countries such as Germany, Switzerland, Colombia, and the USA. While major mutations like D614G and those within B-cell epitopes were found similarly worldwide, some unique haplotypes and amino acid substitutions appear specific to the Iranian population, likely reflecting regional viral evolution and transmission dynamics.

Keywords: "SARS-CoV-2" "spike gene" "genetic diversity"

Genomic features of pan-aminoglycoside resistant rmtB and rmtC-bearing Escherichia coli isolates of clinical origin from Iran

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BACKGROUND AND OBJECTIVES: Aminoglycosides are a class of potent, antibiotics often used in combination with beta-lactam antibiotics to treat serious bacterial infections. However, the therapeutic utility of these agents is threatened by emergence of 16S rRNA methyltransferases (16S RMTases) enzymes that can confer high-level resistance to all clinically relevant aminoglycosides. This research aimed to understand the genetic makeup of two clinical 16S RMTase-harboring E. coli isolates from Iran.

MATERIALS AND METHODS: The genomic features of isolates such as multilocus sequence types, antibiotic resistance/virulence genes and plasmid replicon types were characterized by whole-genome sequencing (WGS) using Illumina and Nanopore platforms.

RESULTS AND DISCUSSION: The two 16S RMTase -positive isolates carried rmtB or rmtC genes and belonged to sequence type ST648 and ST167. Both isolates revealed multidrug resistance phenotype showing resistance to all tested aminoglycosides (gentamicin, amikacin, tobramycin), cephalosporins, carbapenems and quinolones. While ResFinder analyses of both isolates revealed presence of rmtB/C, aadA2, qnrS1, blaNDM, sul1, dfrA12, gyrA (S83L, D87N), parC (S80I) mutations, one isolate also carried blaOXA-181, tetA and blaCTX-M-15. Both isolates possessed numerous virulence-associated genes involved in iron acquisition (irp2, fyuA, chuA, iucC, iutA,), adherence (lpfA, csgA, fdeC,yeh fimbrial genes), serum survival (iss), production of toxin (hlyE) and capsular polysaccharide (kpsE) and tellurite resistance (terC). Our study reports occurrence of pan-aminoglycoside resistant isolates harboring numerous virulence determinants, and antibiotic resistance genes form Iran. This finding has critical epidemiological importance for public health requiring urgent countermeasures to prevent dissemination of these isolates in the country.

Keywords: 16S RMTase, RmtB/C, Aminoglycosides, Antimicrobial resistance genes, whole-genome sequencing, MLST

Genotypic and Phenotypic Analysis of MRSA and MDR Staphylococcus aureus: Biofilm Formation and Antimicrobial Resistance Patterns in Isfahan Hospitals

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BACKGROUND AND OBJECTIVES: Multidrug-resistant (MDR) and Methicillin-resistant Staphylococcus aureus (MRSA) is a predominant cause of hospital-acquired infections, contributing to elevated morbidity, mortality, prolonged hospitalization, and increased healthcare costs. The primary objective of this investigation was to analyze the genotypic and phenotypic features of MRSA and MDR S. aureus clinical isolates, assessing their biofilm formation potential and antibiotic resistance trends in medical centers in Isfahan.

MATERIALS AND METHODS: A total of 51 clinical samples were collected from the Isfahan Teaching Hospital. Bacterial isolates were confirmed through biochemical testing. MRSA identification was performed using the cefoxitin disk diffusion test, with further confirmation via PCR detection of the mecA gene. Additionally, isolates were screened for the mupA gene using PCR. Antibiotic susceptibility patterns were assessed via the Kirby-Bauer disk diffusion method.

RESULTS AND DISCUSSION: Among the 51 isolates, 21.5% exhibited resistance to cefoxitin and were identified as MRSA, which was further confirmed by PCR detection of the mecA gene. None of the isolates harbored the mupA gene. Biofilm formation analysis revealed that 92% of isolates were strong biofilm producers, while 5% demonstrated moderate biofilm production. The highest resistance rates were observed against penicillin (84.31%), clindamycin (74.05%), ciprofloxacin (72.54%), and erythromycin (72.54%). Conversely, the lowest resistance was observed against linezolid (7.84%). Multidrug resistance was detected in 78.43% of isolates, and a D-zone phenotype was observed in 72.54% of cases. The majority of isolates were obtained from blood samples. This study demonstrates a significant association between strong biofilm-forming capability and MDR and MRSA isolates.

Keywords: Multidrug-resistant, Staphylococcus aureus , Methicillin-resistant S. aureus, mupA, mecA

Genotypic investigation of fluoroquinolone resistance in Pseudomonas aeruginosa clinical isolates in Bushehr, Iran

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BACKGROUND AND OBJECTIVES: Fluoroquinolones are an important class of drugs used to treat Pseudomonas aeruginosa infections, but this microorganism may develop resistance to these antimicrobial agents. This study aimed to investigate the genotypic fluoroquinolone resistance in P. aeruginosa clinical isolates in Bushehr, Iran.

MATERIALS AND METHODS: A total of 133 P. aeruginosa isolates were investigated. Fluoroquinolones (ciprofloxacin and levofloxacin) resistance pattern was determined. The presence of plasmid-mediated quinolone resistance (PMQR) genes including qnrA, qnrB, qnrC, qnrD, qnrS, qepA, oqxA, and aac(6')-Ib-cr as well as chromosomal mutations in gyrA and parC genes were investigated by PCR and sequencing.

RESULTS AND DISCUSSION: Forty-eight (36.1%) isolates were resistant to fluoroquinolone (ciprofloxacin and levofloxacin) and 85 (63.9%) were susceptible. The minimum inhibitory concentration (MIC) values of ciprofloxacin were ≥32 µg/ml for 39 resistant isolates and ranged from 4 µg/ml to 8 µg/ml for the remaining 9 resistant isolates. Of 48 resistant isolates, 1 (2.1%) isolate carried three genes qnrB, oqxA, and aac(6')-Ib-cr. In this study, qnrA, qnrC, qnrD, qnrS, and qepA were not found. Among 48 fluoroquinolone-resistant isolates, 46 (95.8%) had mutation in gyrA (Thr83→Ile) and 39 (81.2%) had mutations in parC (Ser87→Leu or Ser87→Trp). All 39 isolates for which the MIC of ciprofloxacin was ≥32 µg/ml had combined mutations in both gyrA and parC genes. The frequency of mutations in the gyrA and parC chromosomal genes was high, indicating that these mutations could play an important role in the development of fluoroquinolone resistance among P. aeruginosa clinical isolates in Bushehr.

Keywords: Pseudomonas aeruginosa, mutation, fluoroquinolone, gyrA, parC

Geographical Variations in VRSA Prevalence Across Iran: A Systematic Review and Meta-Analysis (2013–2024)

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BACKGROUND AND OBJECTIVES: Staphylococcus aureus is a major cause of severe infections in healthcare and community settings, and vancomycin resistance (VRSA) poses a significant treatment challenge. However, data on VRSA prevalence, geographic spread, and trends in Iran remain scarce, limiting effective interventions. This study addresses these gaps through a systematic review and meta-analysis of VRSA in Iran (2013–2024). Considering existing data, we aim to map VRSA epidemiology, identify high-risk areas, and track resistance patterns.

MATERIALS AND METHODS: A systematic review and meta-analysis of VRSA studies in Iran (2013–2024) was conducted using PubMed, Scopus, Embase, SID, and Web of Science. Data were analyzed in R Studio (v4.3.3).

RESULTS AND DISCUSSION: This study found VRSA prevalence of 15% in outpatients (95% CI: 0.12–0.18) and 89% in inpatients (95% CI: 0.85–0.92). The highest rates were in Eastern (13%) and Northern (12%) Iran, while the West had the lowest (1%). Central and Southern regions showed moderate rates (4% each). Over 2013–2024, VRSA prevalence remained stable (~5%), suggesting persistent resistance. The high inpatient rates highlight nosocomial transmission risks, requiring stricter hospital infection control. Regional differences may reflect variations in antibiotic use or healthcare policies. Key recommendations: • Targeted interventions in high-prevalence regions • Antimicrobial stewardship reduces vancomycin misuse. • Enhanced surveillance to track resistance trends Urgent action is necessary to curb the spread of VRSA in Iran, despite stable overall rates.

Keywords: Staphylococcus aureus, Vancomycin-Resistant Staphylococcus aureus, Drug Resistance, Bacterial, Iran

Gestational Diabetes and Microbiota: The Probiotic Connection

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BACKGROUND AND OBJECTIVES: GDM is one of the most common complications of pregnancy and is increasing in global prevalence. Despite the benefit of identifying and treating GDM, much of the current (short-term) diagnostic and management approach to GDM remains contentious. Gut microbiota dysbiosis contributes to GDM pathogenesis through inflammatory and metabolic pathways. Probiotics show promise but require more robust clinical validation before becoming standard care. New approaches are being applied in order to develop strategies that prevent GDM and its consequences on the metabolic and physiological state. The emerging connection between gut microbiota and gestational diabetes offers exciting potential for novel preventive and therapeutic approaches that could significantly improve maternal and infant health outcomes.

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RESULTS AND DISCUSSION: Gut microbiota dysbiosis contributes to GDM pathogenesis through inflammatory and metabolic pathways. Probiotics show promise but require more robust clinical validation before becoming standard care. New approaches are being applied in order to develop strategies that prevent GDM and its consequences on the metabolic and physiological state. The emerging connection between gut microbiota and gestational diabetes offers exciting potential for novel preventive and therapeutic approaches that could significantly improve maternal and infant health outcomes.

Keywords: Gestational Diabetes , Microbiota, The Probiotic

Global and Regional Patterns of Helicobacter pylori Antibiotic Resistance: A Comprehensive Review of Mechanisms, Epidemiology, and Therapeutic Challenges in Iran and Worldwide

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BACKGROUND AND OBJECTIVES: Helicobacter pylori (H. pylori) infection is one of the most common bacterial infections globally, which has become a significant challenge in treatment due to increasing antibiotic resistance. This study aimed to investigate the global and regional patterns of H. pylori antibiotic resistance, molecular mechanisms, clinical outcomes, and mitigation strategies, with a focus on Iran.

MATERIALS AND METHODS: The study methodology involved a systematic review of articles published between 1990 and 2024 from reputable databases and analysis of epidemiological data. Findings indicate high rates of resistance to clarithromycin (22.2% globally, 25.4% in Iran) and metronidazole (44.1% globally, 67.8% in Iran), which have reduced the eradication rates of standard treatment regimens, such as triple therapy, to below 55% in Iran. Resistance mechanisms include genetic mutations (e.g., A2143G in 23S rRNA for clarithromycin) and non-genetic factors (e.g., biofilm formation). In Iran, provincial differences (Tehran: 75% metronidazole resistance; Shiraz: 60.2%) emphasize the need for localized treatment regimens. Clinical outcomes include an increased risk of peptic ulcer and gastric cancer.

RESULTS AND DISCUSSION: Proposed strategies include expanding sensitivity tests (e.g., PCR), using bismuth-containing quadruple therapy, monitoring antibiotic consumption, and public and medical education. Challenges in Iran include a lack of diagnostic infrastructure and the excessive use of antibiotics. For the future, vaccine development, advanced diagnostic technologies (e.g., NGS), and extensive epidemiological studies are recommended. This study emphasizes the necessity of effective policymaking, international collaboration, and investment in research to reduce the burden of H. pylori resistance in Iran and worldwide.

Keywords: Helicobacter pylori, Antibiotic resistance, Resistance mechanism, Multidrug resistance

Global Principles of Hospital Infection Control and the Current Situation in Iran

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BACKGROUND AND OBJECTIVES: Hospital-acquired infections (HAIs) remain a significant global health challenge, adversely affecting patient outcomes, healthcare costs, and system efficiency. Effective infection control requires adherence to internationally recognized principles, including preventive measures, hygiene improvement, and ongoing staff education. This study examines the current state of hospital infection control in Iran and evaluates its alignment with global standards.

MATERIALS AND METHODS: A descriptive-analytical approach was employed, involving a systematic review of scientific literature, reports from Iran's Ministry of Health, and interviews with infection control experts. Key indicators such as HAI rates, training programs, and availability of preventive equipment were assessed in selected hospitals. Data were analyzed using descriptive statistics and compared against global benchmarks.

RESULTS AND DISCUSSION: Findings reveal that despite ongoing efforts, several Iranian hospitals face challenges such as resource limitations, insufficient specialized training, and inadequate protocol implementation. HAI rates in some centers exceeded the global average. However, hospitals with regular training programs and strict monitoring showed better compliance with international infection control standards. Improving hospital infection control in Iran requires enhancing education, increasing financial resources, and strengthening surveillance systems. Greater adherence to global infection control principles can reduce infection rates, improve healthcare quality, and reduce costs. Policymakers are encouraged to prioritize infrastructure development and cultural change in infection prevention practices.

Keywords: : Infection Control, Healthcare Associated Infection,

Green synthesis of copper oxide-silver nanoparticles using Plantago ovata seed and investigation of its antibacterial and antioxidant effects

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BACKGROUND AND OBJECTIVES: The aim of the present study was to investigate the antimicrobial and antioxidant effect of copper oxide nanoparticles doped with silver synthesized with the extract of P. ovate (CuO-Ag).

MATERIALS AND METHODS: In this exprimental study, at first, CuO-Ag were synthesized and analyzed using different analyses. After confirming the synthesis of CuO-Ag nanoparticles, the antibacterial properties of these nanoparticles were investigated by broth microdilution method against six microbial strains. Antioxidant property was also measured by DPPH method.

RESULTS AND DISCUSSION: The result of XRD analysis confirmed the synthesis of CuO-Ag nanoparticles. FTIR analysis confirmed the presence of functional groups of P. ovate plant in CuO-Ag nanoparticles. TEM and SEM images also showed spherical morphology and 100-140 nm diameter CuO-Ag nanoparticles. Examining the antibacterial properties of CuO-Ag nanoparticles showed that these nanoparticles had more antibacterial properties than the extract of P. ovate plant, copper oxide nanoparticles and copper oxide doped with silver synthesis by chemical method. CuO-Ag nanoparticles were able to inhibit the growth of Escherichia coli bacteria at a concentration of 62.5 µg/ml. Also the extract of P. ovate plant and silver nanoparticles increased the antioxidant properties of CuO-Ag nanoparticles.

Keywords: Green synthesis, Antimicrobial, Antioxidant, Plantago ovata

Green Synthesis of Silver Nanoparticles Using Oscillatoria Extract and Evaluation of Their Antibacterial and Anticancer Activities

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BACKGROUND AND OBJECTIVES: Nanotechnology offers novel strategies for combating infectious diseases through advanced antimicrobials. Silver nanoparticles (AgNPs) are known for strong antibacterial effects against multidrug-resistant pathogens. This study aimed to biosynthesize AgNPs using Oscillatoria extract via a green, eco-friendly method and assess their antibacterial potential along with cytotoxic effects on cancer cells. The antibacterial evaluation determined minimum inhibitory concentration (MIC) against Staphylococcus aureus, Escherichia coli, and Acinetobacter baumannii.

MATERIALS AND METHODS: AgNPs were synthesized by reducing silver nitrate with Oscillatoria aqueous extract. Characterization was performed using X-ray diffraction (XRD) and transmission electron microscopy (TEM). Antibacterial activity was assessed by broth microdilution method to determine MIC values. Test organisms included S. aureus, E. coli, and A. baumannii. For anticancer evaluation, the T47D breast cancer cell line was treated with different AgNP concentrations. Cell viability was determined by MTT assay, while apoptosis and necrosis were quantified via Annexin V/propidium iodide staining and flow cytometry.

RESULTS AND DISCUSSION: TEM analysis revealed predominantly spherical AgNPs with a mean size of ~30 nm. MIC values for S. aureus, E. coli, and A. baumannii were 12.5, 25, and 50 µg/mL, respectively, indicating strong antibacterial activity, particularly against Gram-positive bacteria. The potent bactericidal effect may be related to electrostatic interactions between positively charged AgNPs and negatively charged bacterial membranes, causing membrane disruption. In T47D cells, AgNPs exhibited dose- and time-dependent cytotoxicity, with 35% apoptosis at the IC_{50} concentration. The dual antibacterial and anticancer properties suggest that Oscillatoria-derived AgNPs could serve as a potential therapeutic platform.

Keywords: Silver nanoparticles; Oscillatoria; Antibacterial; Minimum inhibitory concentration; Staphylococcus aureus; Escherichia

Green synthesis of zinc oxide nanoparticles using Hymenocrater platystegius extract and their antimicrobial effect on drug-resistant Escherichia coli

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BACKGROUND AND OBJECTIVES: This study aimed to synthesize zinc oxide nanoparticles via a green method using Hymenocrater platystegius plant extract and evaluate their antimicrobial activity against drug-resistant Escherichia coli isolates. Resistant E. coli strains were collected from local hospitals, identified, and subjected to antibiogram testing to determine resistance patterns.

MATERIALS AND METHODS: The minimum inhibitory concentrations (MICs) for the most effective antibiotic and the plant extract were determined. The H. platystegius extract was obtained using the solvent extraction method. ZnO nanoparticles were synthesized using this extract, and their MIC was also measured. UV–Vis spectrophotometry confirmed successful nanoparticle synthesis.

RESULTS AND DISCUSSION: Results showed that nitrofurantoin had the highest MIC (32 µg/mL) in 22 isolates. The highest MIC for ZnO nanoparticles was observed in 16 isolates (53.33%) at a concentration of 1.95 µg/mL.

Keywords: zinc nanoparticles, alcoholic extract, Escherichia coli bacteria, Hymenocrater platystegius

Guidelines for the diagnosis, treatment, prevention, and control of infections caused by carbapenem-resistant Gram-negative bacilli

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BACKGROUND AND OBJECTIVES: The dissemination of carbapenem-resistant Gram-negative bacilli (CRGNB) is a global public health issue. CRGNB isolates are usually extensively drug-resistant or pandrug-resistant, leading to limited antimicrobial treatment options and high mortality. Some novel antimicrobial agents have been approved for clinical use in the treatment of CRGNB infections in recent years, but there is a delay for their launch in some countries, further limiting choices of antimicrobial agents in these countries, and increasing the challenge of providing effective treatment.

MATERIALS AND METHODS: In 2022, several international guidelines or guidance were published on the treatment of multidrug-resistant (MDR) GNB, including CRGNB by the Infectious Diseases Society of America, the European Society of Clinical Microbiology and Infectious Diseases, and the Infectious Diseases Society of Taiwan. The current clinical practice guideline (CPG) was developed by a multidisciplinary guideline development group based on the best available scientific evidence.

RESULTS AND DISCUSSION: While the present CPG focuses on CRGNB [carbapenem-resistant Enterobacteriales (CRE), carbapenem-resistant Acinetobacter baumannii (CRAB), and carbapenem-resistant Pseudomonas aeruginosa (CRPA)], it complements the aforementioned CPGs by including a broader scope related to the management of CRGNB infections. In addition to antimicrobial therapy, recommendations relating to diagnosis (antimicrobial susceptibility testing and synergy testing, carbapenemase detection), therapeutic drug monitoring of common antimicrobials for CRGNB and infection control are also included in the current CPG. This CPG aims to guide the management of CRGNB infections mainly for clinicians and related professionals involved in the management of infectious diseases.

Keywords: Carbapenem-resistant Gram-negative bacilli, Carbapenem-resistant Enterobacteriales, Carbapenem-resistant Pseudomonas aeruginosa, Antimicrobial susceptibility

Gut microbiota and brain axis microbes as hidden modulators

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BACKGROUND AND OBJECTIVES: The body's organs and systems require precise regulation to maintain internal stability, coordinated mainly by the endocrine and nervous systems. The communication between the brain and the gut is bidirectional, with gut microbiota—the largest microbial community in the body—emerging as a key modulator of brain functions. Studies have shown that gut microbes influence stress responses, neurotransmission, and emotional behaviors, highlighting their critical role in the gut-brain axis.

MATERIALS AND METHODS: This review analyzed published studies from PubMed, Scopus, and Web of Science. It focused on germ-free and stress-related animal models, and selected human trials on probiotics and microbiota transplants. No original data were collected; findings were synthesized to explore gut microbiota's impact on brain function

RESULTS AND DISCUSSION: Animal studies show that disruption of the gut microbiota alters the regulation of the hypothalamic-pituitary-adrenal (HPA) axis, reduces levels of brain-derived neurotrophic factor (BDNF), and increases anxiety-like behaviors. Probiotic interventions have been shown to partially reverse these changes. In germ-free mice, transplantation of microbiota from patients with irritable bowel syndrome (IBS) triggered anxiety and intestinal inflammation. Early clinical trials in humans suggest that probiotics may help reduce stress and anxiety and influence brain activity in regions responsible for emotional regulation, although current evidence is still limited. Gut microbiota act as hidden modulators of brain function, influencing neuroendocrine pathways and emotional behavior. Although preclinical studies offer valuable mechanistic insights, further well-designed clinical trials are essential to establish effective microbiota-based interventions. Continued research is needed to translate these findings into reliable treatments for brain-gut axis disorders

Keywords: Gut microbiota -Brain-gut axis-Probiotics-Stress-Neuroendocrine

Gut Dysbiosis and the Role of Mitochondria in Innate Immunity: Mechanisms and Implications

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BACKGROUND AND OBJECTIVES: The gut microbiota plays a critical role in regulating host immune responses and maintaining mitochondrial and mucosal homeostasis. Dysbiosis—an imbalance in the microbial community—has been implicated in various inflammatory and immune-mediated diseases, including inflammatory bowel disease, rheumatoid arthritis, and multiple sclerosis. Concurrently, mitochondria have emerged as central hubs in innate immunity, involved in generating reactive oxygen species (ROS), releasing mitochondrial DNA (mtDNA), and activating immune sensors such as TLR9, NLRP3, and the cGAS–STING pathway. This review aims to investigate the immunological consequences of gut dysbiosis with a particular focus on mitochondria-dependent innate immune pathways. It explores how alterations in microbial-derived metabolites—such as short-chain fatty acids and tryptophan derivatives—affect mitochondrial metabolism, redox signaling, and biogenesis, ultimately leading to mitochondrial dysfunction and immune dysregulation.

MATERIALS AND METHODS: .

RESULTS AND DISCUSSION: Gut dysbiosis has been shown to promote mitochondrial stress responses, including excessive mtROS production and mtDNA release, which in turn activate inflammasomes and type I interferon signaling cascades. These processes are linked to compromised epithelial barrier integrity and the persistence of inflammation in chronic disorders. Furthermore, mitochondria–microbiota crosstalk has been implicated in the pathogenesis of diseases such as colorectal cancer, metabolic syndrome, and neuroinflammatory conditions. Despite accumulating evidence, existing literature still lacks a cohesive understanding of how dysbiosis-derived mitochondrial stress precisely orchestrates immune responses across tissues. Addressing this gap may offer a framework for future research and guide the development of microbiome-informed strategies for inflammatory disease management.

Keywords: mtDNA, Dysbiosis, Gut microbiota, Mitochondria

Gut Microbiome Interactions Between Dogs and Humans

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BACKGROUND AND OBJECTIVES: The gut microbiome, a complex community of microorganisms residing in the gastrointestinal tract, plays a pivotal role in host health by modulating digestion, immune function, and even behavior. While much attention has been directed toward the human gut microbiome, increasing interest has emerged in understanding the microbial communities of companion animals, particularly dogs. As domestic dogs often live in close proximity to humans, share similar environments, and sometimes even diets, evidence suggests that their gut microbiota may influence—or be influenced by—that of their owners.

MATERIALS AND METHODS: This narrative review was conducted to explore the current state of knowledge regarding the interactions between the gut microbiomes of dogs and humans. A comprehensive literature search was carried out to identify relevant studies that examined microbial similarities, potential microbial exchange, and the health implications of such interactions. Literature Search Strategy : Relevant articles were identified through searches in electronic databases including PubMed, Scopus, Web of Science, and Google Scholar. The search included publications up to June 2025, without restriction on the starting date. Inclusion Criteria Peer-reviewed journal articles, systematic reviews, and original research. Studies focusing on the gut microbiome of dogs and humans.

RESULTS AND DISCUSSION: Results and Discussion (50 words) Studies reveal significant microbial overlap between dogs and their owners, particularly in cohabiting environments. Shared bacterial taxa, such as Bacteroides and Firmicutes, suggest bidirectional microbial exchange. These interactions may influence immune development and disease susceptibility in humans, highlighting the importance of pet–human microbiome dynamics in health research.

Keywords: Gut microbiome ,Canine microbiota , Human microbiome, Dog-human interaction,Microbial transmission

Gut microbiomes and treatment-resistant ulcerative colitis: a case-control study using qPCR

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BACKGROUND AND OBJECTIVES: The gut microbiome has been identified as a pivotal factor in ulcerative colitis (UC), given its role as the main reservoir of microbes in the body. However, the role of the gut microbiome in patients with refractory UC is still significant, so this study aimed to further investigate the role of these bacteria in patients with refractory UC.

MATERIALS AND METHODS: This case-control study was conducted on stool samples from four distinct groups: the first group comprised new patients diagnosed with ulcerative colitis (all of them had responded to treatment after follow-up) (N = 24); the second group consisted of patients with treatment-resistant ulcerative colitis (N = 23); the third group included first-degree relatives of group 1 patients (N = 24); and the fourth group consisted of first-degree relatives of group 2 patients (N = 23). The research tools employed in this study included a questionnaire, quantitative real-time PCR (qPCR) test, and culture on stool samples.

RESULTS AND DISCUSSION: The findings indicated a statistically significant relationship (P0.05) between Groups 2 and 4 with respect to the E. coli and Bifidobacterium ssp. microbial population. Additionally, a significant relationship was identified between the Lactobacillus ssp., Bifidobacterium ssp., and Bacteroides ssp. microbial community between groups 1 and 2 (P0.05).The findings of this study demonstrated that several intestinal microbiomes have a substantial impact on the management of ulcerative colitis.

Keywords: Ulcerative colitis, gut microbiome, qPCR

Gut Microbiota Dysbiosis and Its Impact on Headache Pathophysiology: Insights from Recent Molecular Studies

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BACKGROUND AND OBJECTIVES: The gut microbiota has recently emerged as a critical component in the regulation of the gut–brain axis, and growing evidence suggests its involvement in the development and exacerbation of primary headaches, such as migraine. This structured review aims to investigate differences in microbial composition, functional gene expression, and microbial metabolites in patients with headache compared to healthy controls.

MATERIALS AND METHODS: Studies published between 2015 and 2025 were reviewed from PubMed, Scopus, and Web of Science. Selected articles utilized 16S rRNA sequencing, shotgun metagenomics, and metabolomic profiling of fecal or serum samples.

RESULTS AND DISCUSSION: Results show that patients with headaches have reduced microbial alpha diversity and altered gut microbial composition, including increased abundance of Escherichia/Shigella and Clostridium spp., and decreased levels of beneficial taxa such as Bifidobacterium and Faecalibacterium prausnitzii. Functionally, genes involved in the biosynthesis of short-chain fatty acids (SCFAs), particularly butyrate and propionate, are downregulated in patients. Additionally, pathways related to tryptophan metabolism are disrupted, potentially affecting serotonin production and neural signaling. Elevated levels of pro-inflammatory metabolites, including lipopolysaccharides (LPS), have been reported in patients, indicating compromised intestinal barrier integrity ("leaky gut") and systemic immune activation. These microbial and metabolic changes suggest a plausible role for the gut–brain axis in headache pathophysiology. Collectively, current evidence supports the hypothesis that dysbiosis of the gut microbiota and its functional output may contribute to chronic headache. Future studies should focus on identifying specific microbial signatures and exploring microbiome-targeted therapies, such as probiotics, dietary interventions, or

Keywords: Gut microbiota, Headache, Migraine, Short-chain fatty acids, Tryptophan metabolism, Gut–brain

Harnessing the Gut-Brain Axis: Microbiome-Based Therapeutics in Neurodegeneration – From Dysbiosis to Precision Neuromicrobiotics

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BACKGROUND AND OBJECTIVES: The human gut microbiota plays a pivotal role in brain function via the microbiota–gut–brain axis, regulating immune balance, neuroinflammation, and neurotransmitter signaling. Dysbiosis is increasingly linked to the development and progression of neurodegenerative disorders including Parkinson's disease (PD), Alzheimer's disease (AD), and Multiple Sclerosis (MS). This review explores how dysbiosis disrupts blood-brain barrier (BBB) integrity and promotes neuroinflammatory cascades, while evaluating microbiota-targeted therapies such as probiotics, prebiotics, postbiotics, synbiotics, and fecal microbiota transplantation (FMT)

MATERIALS AND METHODS: A systematic review of 124 studies (2015–2024) from PubMed, Scopus, and Web of Science was conducted using terms including "gut microbiome," "neurodegeneration," "FMT," "SCFA," and related keywords. Clinical and experimental data were analyzed for therapeutic efficacy and mechanistic insights.

RESULTS AND DISCUSSION: Dysbiosis was consistently associated with increased gut permeability, elevated LPS levels, and decreased SCFA production—factors contributing to microglial activation, neuroinflammation, and protein aggregation (e.g., α-synuclein, amyloid-beta). FMT restored microbial diversity and improved cognitive function in PD and MS models. SCFA-based postbiotics enhanced BBB integrity and regulatory T cells. Prebiotics such as inulin and GOS elevated serotonin and IL-10 levels in humans. Microbiota modulation represents a promising, disease-modifying approach to neurodegenerative care. Precision microbiome therapies may complement conventional treatments and pave the way toward personalized neuromodulation strategies

Keywords: Keywords: Microbiome, Gut-Brain Axis, Neuroinflammation, FMT, SCFA, Parkinson's, Alzheimer's, Multiple

Harnessing microbial synergy: boosting antibiotic efficacy with prebiotic adjuncts

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BACKGROUND AND OBJECTIVES: Leveraging microbial synergy to enhance antibiotic efficacy through prebiotic adjuncts offers a novel approach to combat antibiotic resistance. This study investigated the combined effects of Lactobacillus acidophilus prebiotics and ciprofloxacin on multidrug-resistant Staphylococcus aureus (MRSA) strains. The aim was to assess bacterial load reduction and biofilm inhibition. MRSA strains were isolated from clinical samples of hospitalized patients in Tehran. Experiments were conducted under laboratory conditions using microbial cultures and antibiogram assays. Results demonstrated that the prebiotic-ciprofloxacin combination significantly (p0.01) reduced bacterial load by 3 logs and inhibited biofilm formation by up to 80%, whereas ciprofloxacin alone achieved only a 1-log reduction. Charts and tables derived from the data highlighted the superiority of the synergistic combination over monotherapy. These findings suggest the potential of prebiotics in enhancing antibiotic efficacy and mitigating resistance. The discussion and conclusion propose that prebiotics as adjunctive therapy could be a promising strategy for managing resistant infections,

MATERIALS AND METHODS: MRSA strains were isolated from clinical samples. Synergy experiments were performed using microtiter plate assays and antibiograms in laboratory settings. Data were analyzed using t-tests and ANOVA.

RESULTS AND DISCUSSION: The prebiotic-ciprofloxacin combination significantly reduced bacterial load by 3 logs (p0.01), compared to a 1-log reduction with ciprofloxacin alone and a 1.4-log reduction with prebiotics alone (Figure 1). Biofilm inhibition reached 80% in the combination group, markedly higher than the 20% and 35% inhibition observed with ciprofloxacin and prebiotics alone, respectively .

Keywords: antibiotic resistance,MRSA,prebiotic,

Harnessing Postbiotics derived from Pediococcus for salmonella control: Antimicrobial Efficacy and Biofilm Disruption in Food Safety and Medicine

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BACKGROUND AND OBJECTIVES: Salmonella is a major pathogen in both the food industry and medical fields, causing severe gastrointestinal infections and foodborne illnesses. It poses significant challenges in animal husbandry, where it leads to reduced livestock productivity and economic losses. Additionally, in humans, Salmonella infections can result in acute and chronic health complications, especially in immunocompromised individuals. The rise of antibiotic resistance in Salmonella strains further complicates treatment options, necessitating alternative approaches. Probiotics and their derivatives, like postbiotics, are emerging as alternatives to antibiotics. This study evaluates the effectiveness of Pediococcus-derived postbiotics against Salmonella, exploring their potential as a novel treatment.

MATERIALS AND METHODS: In this study, antimicrobial susceptibility testing was conducted on Salmonella ATCC strains using postbiotics derived from three native Pediococcus acidilactici strains: A.P 6(3), D.M II (6), and Y.L III (7), preserved as IBRC-M 11447, IBRC-M 11476, and IBRC-M 11450, respectively. Postbiotics were produced under optimized conditions, followed by cell removal through centrifugation and filtration.

RESULTS AND DISCUSSION: Inhibition zones in agar diffusion assays ranged between 18 and 23 mm, with the MIC determined to be 0.008 mg/ml and the MBC at 0.125 mg/ml. The antibiofilm assay revealed significant inhibition across all concentrations (0.016 mg/ml to 1 mg/ml), with inhibition rates ranging from 53% to 65% for A.P 6(3), 43% to 68% for D.M II (6), and 45% to 51% for Y.L III (7). These findings suggest that Pediococcus-derived postbiotics are promising agents for controlling Salmonella infections, offering effective antibacterial and anti-biofilm properties.

Keywords: Salmonella, Pediococcus acidilactici, postbiotics, antimicrobial, antibiofilm, MIC, MBC, biofilm inhibition.

Harnessing Probiotics and MACs: A Microbiota-Driven Strategy to Boost SCFA Production and Gut-Immune Homeostasis

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BACKGROUND AND OBJECTIVES: To evaluate a microbiota-based strategy combining probiotics and microbiota-accessible carbohydrates (MACs) to increase short-chain fatty acid (SCFA) production and improve gut-immune homeostasis.

MATERIALS AND METHODS: A comprehensive review of recent experimental and clinical studies was conducted to investigate how selected probiotic strains and fermentable MACs influence SCFA production. Particular focus was given to their effects on gut microbial composition, epithelial barrier integrity, and immune regulation. Mechanistic pathways involving SCFA-mediated modulation of inflammatory cytokines and T-cell responses were also examined.

RESULTS AND DISCUSSION: Combined intake of specific probiotics (e.g., Faecalibacterium prausnitzii, Lactobacillus spp.) and MACs (e.g., inulin, resistant starch) has been shown to enhance the growth of SCFA-producing microbiota. Elevated levels of butyrate, propionate, and acetate are associated with strengthened intestinal tight junctions, reduced systemic inflammation, and improved immune tolerance. These outcomes have been observed in both animal models and early-phase clinical trials involving patients with inflammatory or metabolic conditions.Targeted modulation of the gut microbiota through probiotics and MACs represents a promising nutritional approach to support SCFA production and restore gut-immune balance. This strategy may offer a safe, non-pharmacological intervention for managing chronic diseases linked to microbial dysbiosis. Further human studies are necessary to establish standardized formulations and therapeutic guidelines.

Keywords: SCFA, probiotics, microbiota-accessible carbohydrates, gut microbiota, immune regulation, inflammation

Hepatitis B Virus Infection in Iranian Hemodialysis Patients

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BACKGROUND AND OBJECTIVES: Hepatitis B virus (HBV) belongs to the Hepadnavirus family. It is an enveloped virus with a circular DNA genome and the infection with HBV can lead to chronic liver disease, acute hepatitis, liver cirrhosis and hepatocellular carcinoma (HCC). Approximately two billion people are infected with HBV worldwide, and 350 million of them are chronically infected. Hemodialysis patients are potentially susceptible to viral infections including hepatitis viruses. The aim of this study was to evaluate the prevalence of HBV infection among Iranian hemodialysis patients.

MATERIALS AND METHODS: This study was conducted on 36 patients undergoing dialysis. Viral DNA was extracted from plasma samples and the presence of HBV genome was detected using semi-nested-PCR method. The positive samples were sequences, the phylogenetic analysis was performed and HBV genotypes, sub-genotypes and subtypes were determined

RESULTS AND DISCUSSION: In a study conducted on 36 samples from Iranian hemodialysis patients, HBV DNA was detected in four samples (11%). The HBV genotype D was determined as the only genotype among the studied HBV positive patients. The incidence of hepatitis B infection in the group of people undergoing hemodialysis is relatively high and extensive monitoring on dialysis patients is necessary. To prevent hepatitis B infection, strategies such as vaccination, continuous checking of the viral hepatitis serological status of hemodialysis patients, and isolation of dialysis machines and dialysis equipment

Keywords: Hemodialysis, Hepatitis B virus, Genotype, Prevalence, chronic infection, Iran

Higher Caspase-3 Gene Expression in Symptomatic COVID-19 Patients Compared to Asymptomatic cases: A Possible Biomarker for Severity

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BACKGROUND AND OBJECTIVES: A study has shown that the ORF-3a protein of SARS-CoV-2 can induce the apoptosis pathway in vitro by increasing Caspase-3 expression[1] . On the other hand, increased expression of Caspase-3 has also been reported in lung tissue [2] and in blood samples of COVID-19 patients [3]. Another study suggested a significant association between Caspase-3 gene expression levels and the severity of COVID-19 [4]. Therefore, Caspase-3 may provide valuable information about the severity of COVID-19 and its clinical outcomes. This study aimed to compare the expression levels of Caspase-3 in symptomatic and asymptomatic COVID-19 patients and investigate its potential as a biomarker.

MATERIALS AND METHODS: Blood samples were taken from 37 COVID-19 patients, including 20 symptomatic and 17 asymptomatic cases, as well as 33 healthy individuals. Briefly, after total RNA extraction and cDNA synthesis, real-time PCR was performed to evaluate Caspase-3 expression levels. Also, ROC curve analysis was used to assess diagnostic accuracy.

RESULTS AND DISCUSSION: Our results showed that the expression level of Caspase-3 was higher in both COVID-19 patient groups compared to the controls (P values 0.0001). Caspase-3 levels were also significantly higher in symptomatic COVID-19 cases compared to asymptomatic (P value 0.0001). The area under the curve (AUC) of Caspase-3 for asymptomatic and symptomatic COVID-19 cases was 0.90 (p value0001/0) and the optimal cut-off value was calculated to be 0.50 (Sensitivity 90.00%; Specificity 94.12%). According to our results, blood Caspase-3 expression levels can serve as a potential biomarker for discriminating symptomatic from asymptomatic COVID-19 cases.

Keywords: COVID-19, SARS-CoV-2, Asymptomatic Infections, Caspase 3, Biomarkers

High Prevalence of Metronidazole and Clarithromycin Resistance in Helicobacter pylori from Gastric Cancer Patients

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BACKGROUND AND OBJECTIVES: This study investigated the prevalence of resistance to metronidazole, clarithromycin, and ciprofloxacin among Helicobacter pylori strains isolated from gastric cancer patients.

MATERIALS AND METHODS: A total of 65 distinct H. pylori strains were isolated from biopsy corpus samples obtained from patients diagnosed with gastric cancer. Antimicrobial susceptibility testing for metronidazole, clarithromycin, and ciprofloxacin was performed using the agar dilution method, following the guidelines and breakpoints established by the Clinical and Laboratory Standards Institute (CLSI). 10 out of 65 samples were applied to confirm the results. SPSS was used to analyze the results after reviewing by the 1 blind person.

RESULTS AND DISCUSSION: The results revealed a high frequency of resistance to these key antibiotics: Metronidazole resistance: Extremely prevalent, observed in 49 out of the 65 tested strains (75.4%). Clarithromycin resistance: Significant resistance was detected in 17 strains (26.2%). Ciprofloxacin resistance: Present, but at a lower level, found in 3 strains (4.6%). This study highlights alarmingly high rates of antimicrobial resistance in H. pylori strains isolated from gastric cancer patients, particularly concerning for metronidazole and clarithromycin. Metronidazole resistance was the most widespread. The substantial clarithromycin resistance is especially critical as this antibiotic is a cornerstone of first-line eradication therapies. While ciprofloxacin resistance was less common in this cohort, its presence is noteworthy given its use in salvage regimens. The high resistance rates to first-line antibiotics like clarithromycin and metronidazole significantly compromise the effectiveness of standard treatment protocols.

Keywords: Helicobacter pylori, antibiotic resistance, clarithromycin, metronidazole

Hybrid AI for Predicting Zoonotic Risk from Incomplete Microbiological Data

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BACKGROUND AND OBJECTIVES: In order to extract significant signals from incomplete microbiological data originating from human, animal, and environmental sources, this study suggests a hybrid AI framework that combines weakly supervised learning and natural language processing. Without completely identifying the pathogen, the model predicts zoonotic hotspots by identifying geographic trends, co-infection patterns, and resistance markers. It creates probabilistic risk maps to facilitate early intervention and is intended for low-resource environments. With this strategy, microbiology is reframed as a cross-sector, predictive tool for zoonotic outbreak prediction and prevention.

MATERIALS AND METHODS: This framework collects microbiological information from clinical, veterinary, and environmental sources, such as partial culture results, free-text notes, and antibiotic profiles. Structured features will be extracted using NLP techniques, and resistance markers, co-infections, and regional trends will be found using weakly supervised learning. The model is intended to function without centralized databases and learn from small, fragmented data in real-world scenarios. It will be tested on anonymized or simulated datasets.

RESULTS AND DISCUSSION: An AI system that can identify zoonotic hotspots from incomplete and unstructured microbiological data is one of the anticipated results. The model seeks to produce probabilistic risk maps to assist early interventions by integrating weak signals across sectors. It provides a scalable tool for One Health surveillance and cross-species outbreak prevention, and because it doesn't require centralized databases, it can be used in low-resource environments.

Keywords: Artificial Intelligence, Zoonoses, Microbiology, Natural Language Processing (NLP)

Identification and antimicrobial susceptibility testing of Streptococcus agalactiae associated urinary tract infections using VITEK 2 system

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BACKGROUND AND OBJECTIVES: As a Gram-positive bacterium, Streptococcus agalactiae or Group B Streptococcus (GBS) is normally found as a transient flora of the gastrointestinal and genitourinary tracts of women. The high prevalence of GBS in the urethra warrants investigation of UTIs and antibiotic resistance frequency associated with GBS. Given the paucity of research on antibiotic resistance of GBS in Iran, the present study investigated the UTIs associated with GBS and the antibiotic susceptibility patterns associated with GBS.

MATERIALS AND METHODS: This study included 65 GBS strains collected from urine samples obtained from the Bouali Laboratory Complex, one of the largest laboratories in western Iran. VITEK 2 GP ID cards were used to identify all GBS isolates. VITEK 2 susceptibility testing for Gram-positive bacteria was performed according to the manufacturer's instructions using the AST-ST card. MIC method was performed after the detection of GBS strains.

RESULTS AND DISCUSSION: We found that 53 (81.5%) of the GBS isolates showed resistance to tetracycline; 47 (72.3%), 40 (61.5%), and 30 (46.15%) of these had a resistance to erythromycin, clindamycin and ampicillin respectively. In the present study, the VITEK 2 system was validated as a user-friendly system that can serve as a rapid and accurate tool for identification and antimicrobial susceptibility testing of GBS.

Keywords: Identification, Streptococcus agalactiae, Urinary tract infections, VITEK 2 System

Identification and assessment of Antagonistic Yeasts against Penicillium digitatum for Bio-preservation of oranges

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BACKGROUND AND OBJECTIVES: Fungal pathogens are the primary biotic barrier to the productivity of economically important fruits and vegetables. Moreover, misuse of chemical fungicides leads to serious environmental and human health issues. Regarding the increasing demand for pesticide-free foods, the purpose of this study was to find potential yeast strains for biological control of green mold on oranges.

MATERIALS AND METHODS: Yeasts were isolated from the peel of oranges and evaluated for their antagonistic activity against Penicillium digitatum and strains with growth inhibition above 25% were identified by molecular technique based on sequencing of the D1/D2 region of the large subunit (LSU) rRNA gene. For determination of antagonistic mechanisms, the ability of the strains to produce volatile compounds and their enzymatic profiles were evaluated.

RESULTS AND DISCUSSION: Twenty out of 50 strains showed antagonistic effects ranging from 15.7-33.3%, based on the dual assay method. Five strains with the highest antagonistic activity demonstrated two or more potential mechanisms of action. Three of these strains (Cryptococcus sp., Barnettozyma californica, Meyerozyma guilliermondii) were capable of producing volatile compounds which suppressed the pathogen growth from 62.2-87.5%. Moreover, Cryptococcus sp. showed the greatest antagonistic effect (27%) and a versatile enzymatic activity including protease, amylase, cellulase, Beta-glucosidase, and esterase activity. The results show that antagonistic yeasts can be considered as possible biocontrol agents against the green mold of oranges, though issues such as large-scale production, formulation, shelf life, and application methods should be evaluated precisely prior to the development of an effective biocontrol agent.

Keywords: biological control, postharvest decay, orange, Penicillium digitatum

Identification and Characterization of Antifungal Resistance and Exoenzyme Production in Candida albicans Isolated from Nail Infections

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BACKGROUND AND OBJECTIVES: Candidiasis is the most common yeast infection globally, with Candida albicans as the main cause. Despite its importance, data on its pathogenic mechanisms and resistance are limited. Understanding its drug resistance, enzyme activity, and biofilm formation is vital for diagnosing and treating rising C. albicans infections, especially nail candidiasis.

MATERIALS AND METHODS: Thirty suspected candida isolates were obtained from infected nails. Following phenotypic identification using CHROMagar and the antifungal susceptibility, phospholipase activity, and biofilm formation ability of the strains were evaluated

RESULTS AND DISCUSSION: All Candida albicans isolates exhibited high susceptibility to the four tested antifungal agents following incubation. Phospholipase activity was observed in six isolates. Additionally, all strains demonstrated the ability to form biofilms, indicating a significant potential for persistent infection and resistance to treatment.

Keywords: C. albicans, drug, biofilm, pathogenic, analysis, Candidiasis

Identification of gyrB mutations in ciprofloxacin resistant Klebsiella pneumoniae isolated from urinary tract infection

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BACKGROUND AND OBJECTIVES: Fluoroquinolone resistance in gram negative bacteria has been mainly associated with mutation in gyr and par genes and specific amino acids alteration. Urinary tract infection isolates of Klebsiella pneumoniae were investigated for fluoroquinolone resistance and the gyrB gene mutation patterns of ciprofloxacin resistant isolates.

MATERIALS AND METHODS: Susceptibility to fluoroquinolones in ٤٠ isolates of Klebsiella pneumoniae was tested by the agar dilution method and broth macrodilution method was used to investigate ciprofloxacin minimum inhibitory concentration. Mutations in the quinolone resistance-determining regions (QRDR) in chromosomal gyrB gene was investigated in quinolone-resistant Klebsiella pnemoniae isolates by PCR amplification of gyrB gene and sequencing.

RESULTS AND DISCUSSION: Results. In total, ١٤ (٣٥٪) isolates recognized as fluoroquinolones resistant. Minimum inhibitory concentration of ciprofluxacine for resistant isolates were more than ٣٢ µg/ml. Based on sequencing results, it was found that eight isolates lacked any type of mutation. In four isolates missence mutations of Ala٥٥٨Ser, Asn٥٧١Ser, Pro٥٧٩Ala, Ala٥٨٥Ser, Phe٥٨٧Tyr, Gly٥٩٥Asn and Phe٦٠١Tyr were identified in gyrB gene. Conclusion. In this study, the occurrence of new mutations in gyrB gene in resistant isolates was investigated. Also, we had ٨ ciprofloxacin resistant isolate which lacked any amino acid substitutions in gyrB genes. So it suggested the importance of other possible involvement of fluoroquinolone resistance mechanism in test bacteria.

Keywords: Klebsiella pnemoniae, Enterobacteriaceae, ciprofluxacine resistance, gyrB

Identification of Polymorphism of Acinetobacter baumannii Isolated from Clinical Samples by MLVA Method

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BACKGROUND AND OBJECTIVES: Acinetobacter baumannii is some gram-negative coccobacilli that is considered a pathogen of a wide range of nosocomial infections.Molecular typing can distinguish suspicious and rapidly growing bacterial strains from serious outbreaks.MLVA is a molecular typing method for sub classifying microbial isolates based on variable copy number and number of consecutive repeats. investigate the genomic polymorphism of Acinetobacter baumannii isolated from clinical samples byMLVA.

MATERIALS AND METHODS: In this study,60 isolates of Acinetobacter baumannii were used from clinical sources collected in the Pasargard Microbiology Laboratory.Gram staining and biochemical tests were performed to confirm the microbial bank.Genomic DNA of the isolates was extracted using a commercial kit.PCR was performed to identify the regions of repetitive sequences with seven pairs of primers.After data collection and electrophoresis,a phylogenetic tree was drawn using PHYLOViZ software.A significance level of P0.05 was considered using SPSS22 software.

RESULTS AND DISCUSSION: Among the 60 isolates studied, 9 clusters were obtained, of which clusters A and C had the most members(each with 9 members) and were the most diverse clades. In this study, 6 clonal complexes(CC)were obtained, of which CCVI had the most diversity of strains. Based on the Simpson index and the Shanus index, the closer the diversity index is to one, the better the marker is for separating isolates. The genetic diversity of each of the four markers indicates that the Ms-07 and Ms-23 markers with Simpson index of 0.9 and Shanus entropy of 3.4 were the best markers for separating 60 Acinetobacter baumannii isolates.

Keywords: Acinetobacter baumannii, nosocomial infection, repetitive sequences, MLVA, polymorphism.

Identification of Pseudomonas aeruginosa biofilms in cystic fibrosis patients using molecular methods in Urmia, Iran, 2025

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BACKGROUND AND OBJECTIVES: The persistence of chronic Pseudomonas aeruginosa lung infections in cystic fibrosis (CF) patients is due to biofilm-growing mucoid (alginate-producing). The purpose of this study is to investigate the effect of antibiotic treatment in preventing the formation of biofilm caused by Pseudomonas aeruginosa.

MATERIALS AND METHODS: The susceptibility of the isolates to different antibiotics was determined using the disk diffusion method on cation-adjusted Müller-Hinton agar. Antibiotic discs tested with ceftazidime, piperacillin/tazobactam, ciprofloxacin, and levofloxacin, Were treated with gentamicin, amikacin, tobramycin, imipenem and meropenem. The adhesive biofilms were fixed with 100% methanol for 15 minutes, the solutions were removed and the plate dried. The biofilms were stained with 200 µl of 0.1% crystalline violet for 10 minutes at room temperature and then washed with water and dried. Biofilm was obtained in each well by treatment with 200 µl of 96% ethanol for 30 minutes. All Pseudomonas aeruginosa isolates for the three genes encoding biofilm, algD, and pslD using the polymerase chain reaction (PCR) method, using specific primers.

RESULTS AND DISCUSSION: 18.36% produce strong biofilms. 30.15% produced average biofilm. 31.75% produced poor biofilm, while 19.74% of isolates did not produce as film-free. Pseudomonas aeruginosa development of resistance to many antimicrobial agents is a major challenge in controlling its infections.

Keywords: Pseudomonas aeruginosa, biofilms, cystic fibrosis

Identification of Staphylococcus aureus isolates from patients hospitalized in intensive care units and assessment of effective risk factors contributing to increased patients' mortality

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BACKGROUND AND OBJECTIVES: Staphylococcus aureus is a common cause of infections in both community and healthcare settings. Methicillin-resistant S. aureus (MRSA) strains are associated with longer hospital stays and higher mortality rates. This study aimed to assess the prevalence of S. aureus isolates, their antibiotic resistance patterns, and the risk factors linked to mortality.

MATERIALS AND METHODS: A total of 160 respiratory samples were collected from ICU wards in two hospitals in Tehran. S. aureus isolates were identified using biochemical and molecular methods, and antibiotic resistance was tested through disk diffusion and minimum inhibitory concentration (MIC) methods. Demographic data were recorded for analysis

RESULTS AND DISCUSSION: Out of the 30 positive isolates (18.75%), 14 (46.7%) isolates were identified as MRSA. The infected patients had a median age of 60.5 years, with 60% being male and 53.3% having underlying diseases. The total mortality rate was 50%. A significant association was found between the duration of ICU stay and mortality (P = 0.002), and vancomycin use was higher in MRSA cases (P = 0.007). Resistance rates for the isolates were 100% to penicillin, 70% to azithromycin, 63.3% to ofloxacin, and 56.7% to ciprofloxacin. Conclusion: The association between the duration of ICU stays and mortality highlights the need for improved management of S. aureus infections. This includes ongoing surveillance, antibiotic stewardship, and the implementation of effective infection control policies.

Keywords: Staphylococcus aureus, MRSA, hospitalization duration, intensive care unit, risk factors,

Identification of Streptococcus mutans bacteria by polymerase chain reaction in dental plaque samples through detection of the gene encoding glucosyltransferase enzymes

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BACKGROUND AND OBJECTIVES: Dental caries is among the most common infectious diseases worldwide and remains a significant public health concern. Streptococcus mutans is widely recognized as a primary causative agent in the initiation and progression of dental caries. This study aimed to assess the prevalence of S. mutans in dental plaque and saliva samples from adults with varying caries activity and to explore the relationship between bacterial presence and caries severity.

MATERIALS AND METHODS: A total of 128 adult participants from diverse age groups underwent dental examinations following World Health Organization (WHO) criteria. Caries status was quantified using the DMFT index (decayed, missing, and filled teeth). Dental plaque and saliva samples were collected and analyzed for S. mutans using polymerase chain reaction (PCR) targeting the glucosyltransferase B (GTFB) gene. Data analysis was performed using SPSS software.

RESULTS AND DISCUSSION: The mean DMFT score among participants was 5.6, indicating moderate caries experience. S. mutans was detected in 16.17% of plaque and saliva samples. The presence of S. mutans correlated with higher caries activity, confirming its significant role in caries pathogenesis. Additionally, findings suggest that other mutans streptococci species may also contribute to dental caries development.

Keywords: Streptococcus mutans-dental plaque-saliva-DMFT-GTFB gene

Immunoinformatic evaluation for the development of a potent multi-epitope vaccine against bacterial vaginosis caused by Gardnerella vaginalis

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BACKGROUND AND OBJECTIVES: Gardnerella vaginalis (G. vaginalis) is a facultative anaerobic bacillus known as the main pathogen responsible for Bacterial vaginosis (BV). In this study, using bioinformatics and immunoinformatics methods, a multi-epitope vaccine with optimal population coverage against BV caused by G. vaginalis was designed.

MATERIALS AND METHODS: Amino acid sequences of two important virulence factors (Vaginolysin and Sialidase) of G. vaginalis were retrieved from NCBI and UniProt databases. At first, three online servers ABCpred, BCPREDS and LBtope were used to predict linear B-cell epitopes (BCEs) and IEDB server was used for T cells. After modeling the three-dimensional (3D) structure of the vaccine by Robetta Server, molecular docking and molecular dynamics were performed. Finally, immune simulation and in silico cloning were considered effective for the design of vaccine production strategy.

RESULTS AND DISCUSSION: In total, six epitopes of BCEs, eight epitopes from CD4+ and seven epitopes from CD8+ were selected. After the 3D structure was predicted, it was refined and validated, which resulted in an optimized model with a Z-score of -7.4. Molecular docking and molecular dynamics simulation of the designed vaccine revealed stable and strong binding interactions. Finally, the results of vaccine immunity simulation showed a significant increase in immunoglobulins, higher levels of IFN-γ and IL-2. According to the findings, the candidate multi-epitope vaccine has stable structural features. It also has the potential to stimulate long-term immunity in the host, but wet-lab validation is needed to justify it.

Keywords: Multi-epitope vaccine, Vaccine design, Gardnerella vaginalis

Immunoinformatics Analysis of (LytA) to Predict Novel Multi-Epitope Vaccine Candidates against Streptococcus pneumoniae Infections

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BACKGROUND AND OBJECTIVES: To overcome the serotype-dependent limitation of polysaccharide-based vaccines, the development of conserved protein-based vaccines is crucial. This study aimed at investigate epitope mapping and immunogenicity profile of LytA protein, major pneumococcal autolysin, to design the multi-epitope based vaccines candidates by focusing on induction of both humoral and cellular immunities.

MATERIALS AND METHODS: The linear B-cell and MHCII binding epitopes, IL-4, and IFN-γ inducer epitopes of LytA (UniprotID:P06653) were predicted using IEDB, IL-4Pred, and IFNepitope databases, respectively. The immunogenicity, allergenicity, toxicity, and conservation score of the predicted epitopes among pneumococcal serotypes were evaluated using VaxiJen, AllerTop, ToxinPred, and IEDB databases, respectively. Physicochemical properties of LytA were assessed by Protparam server. Finally, the immune simulation of LytA administration in mammals and potential regions involved in LytA-TLRs interactions were analyzed by C-ImmSim site and molecular docking via ClusPro server, respectively.

RESULTS AND DISCUSSION: This protein had 8 and 13 predicted linear B-cell and helper T-cell epitopes, respectively, with a vaxijen score of 0.8-2.2 and conservation score of 70-99% among pneumococcal serotypes without any toxicity and allergenicity properties. Furthermore, LytA was considered an IL-4 and IFN-γ inducer protein. The immune simulation demonstrated induction of both humoral and cellular immunity against LytA. LytA had good interaction with TLR2 and TLR4(binding energy of-916 and-903kcal/mol).Protparam analysis showed this protein with molecular weight of 36544.38Da was considered as a stable vaccine candidate.Although our results revealed that LytA could be considered as a conserved promising candidate vaccine with good immunogenicity profiles,further in vitro and in vivo validations are necessary.

Keywords: Streptococcus pneumoniae, LytA, Multi-Epitope Vaccine, Immunoinformatics

Immunoinformatics Analysis of Choline-binding protein G to Predict Novel Multi-Epitope Vaccine Candidates against Streptococcus pneumoniae Infections

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BACKGROUND AND OBJECTIVES: Choline-binding protein G (CbpG) of Streptococcus pneumoniae is a key virulence factor involved in adhesion, colonization, and immune evasion. This study focuses on epitope mapping and immunogenicity profile of CbpG to design multi-epitope based vaccines inducing robust humoral and cellular immunity.

MATERIALS AND METHODS: The linear B-cell and MHCII binding epitopes, IL-4, and IFN-γ inducer epitopes of CbpG were predicted using the IEDB, IL-4Pred, and IFNepitope databases, respectively. The immunogenicity, allergenicity, toxicity, and conservation score of the predicted epitopes among pneumococcal serotypes were evaluated using the VaxiJen, AllerTop, ToxinPred, and IEDB databases, respectively. Physicochemical properties were assessed by Protparam server. Finally, immune simulation of CbpG administration in mammals and potential regions involved in CbpG-TLRs interactions were analyzed by C-ImmSim site and molecular docking via ClusPro server, respectively.

RESULTS AND DISCUSSION: This protein had three and nine predicted linear B-cell and helper T-cell epitopes, respectively, with a vaxijen score of 1-2.2 and conservation score of 74-97% among pneumococcal serotypes without any toxicity and allergenicity properties. Furthermore, CbpG was considered an IL-4 and IFN-γ inducer protein. The immune simulation demonstrated induction of both humoral and cellular immunity against CbpG. In addition, CbpG had good interaction with TLR2 and TLR4 (binding energy of -840.7Da). Protparam analysis showed this protein with molecular weight of 17649.15 g/mol was considered as a stable vaccine candidate. Although, our results revealed that CbpG could be considered as a conserved promising candidate vaccine with good immunogenicity profiles, further in vitro and in vivo validations are necessary.

Keywords: Streptococcus pneumoniae, CbpG, Multi-epitope vaccine, Immunoinformatics.

Immunoinformatics Analysis of Glycosyltransferase E (GlyE) to Predict Novel Serotype-Independent Vaccine Candidate against Streptococcus pneumoniae

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BACKGROUND AND OBJECTIVES: To prevent pneumococcal infections, the development of conserved protein-based vaccines is critical. This study aimed at investigate epitope mapping and immunogenicity profile of GlyE, as enzyme that participates in O-glycosylation of PsrP, contributing critically to adherence and virulence during lung infection.

MATERIALS AND METHODS: The linear B-cell and MHCII binding epitopes, IL-4, and IFN-γ inducer epitopes of GlyE protein (Accession number:A0A0H2URJ6) were predicted using the IEDB, IL-4Pred, and IFNepitope databases, respectively. The immunogenicity, allergenicity, toxicity, and conservation score of predicted epitopes among pneumococcal serotypes were evaluated using VaxiJen, AllerTop, ToxinPred, and IEDB databases, respectively. Physicochemical properties of GlyE were assessed by Protparam server. Finally, the immune simulation of GlyE administration in mammals and potential regions involved in GlyE-TLRs interactions were analyzed by C-ImmSim site and molecular docking via ClusPro server, respectively.

RESULTS AND DISCUSSION: This protein had 4 and 15 predicted linear B-cell and helper T-cell epitopes, with a vaxijen score of 1 and conservation score of 89-99% among pneumococcal serotypes without any toxicity and allergenicity properties. Furthermore, GlyE was considered an IL-4 and IFN-γ inducer protein. The immune simulation demonstrated induction of both humoral and cellular immunity against GlyE. In addition, GlyE had good interaction with TLR2 and TLR4 (binding energy of -869kcal/mol and -950 kcal/mol). Protparam analysis showed GlyE with molecular weight of 47412.31Da was considered as a stable candidate. Although our results revealed that GlyE could be considered as a conserved promising candidate vaccine with good immunogenicity profiles, further in vitro and in vivo validations are necessary.

Keywords: Streptococcus pneumoniae, GlyE, Multi-epitope vaccine, Immunoinformatics.

Immunoinformatics design of a multi-epitope mucosal vaccine candidate against helicobacter pylori

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BACKGROUND AND OBJECTIVES: Helicobacter pylori is a globally prevalent pathogen linked to gastrointestinal disorders such as chronic gastritis, peptic ulcers, and gastric cancer. Due to rising antibiotic resistance and lack of a licensed vaccine, novel immunotherapeutic strategies are urgently needed. This study aimed to design a peptide-based multi-epitope vaccine capable of eliciting robust immune responses. Conserved immunodominant regions from several virulence factors were selected and assembled into a single construct with appropriate linkers.

MATERIALS AND METHODS: Antigenic outer membrane and extracellular proteins of H. pylori were identified using various online servers, and a final vaccine construct was designed and analyzed for immunogenicity and immune cell stimulation. Immunoinformatics tools were used to predict CTL, HTL, and B-cell epitopes from antigenic proteins of H. pylori. Fully conserved epitopes were selected, followed by analysis of population coverage, autoimmune potential, and epitope accessibility. A multi-epitope vaccine construct was designed and evaluated for antigenicity, allergenicity, and stability. The 3D structure was modeled, validated, and subjected to docking, dynamics simulation, codon optimization, and immune simulation via C-ImmSim.

RESULTS AND DISCUSSION: Key results include 3D modeling and validation of the vaccine structure, molecular docking with immune receptors (TLR4, MHC-I/II), and molecular dynamics confirming structural stability. Codon optimization and in-silico cloning ensured expression feasibility, while immune simulation predicted strong, long-lasting cellular and humoral responses. This construct demonstrated favorable immunological properties and may serve as a potential vaccine against Helicobacter pylori infection. However, these computational findings require experimental validation to confirm their effectiveness.

Keywords: Multi-epitope vaccine, Immunoinformatics, Helicobacter pylori, mucosal immunity

Immunoinformatics Evaluation of Enolase to Predict Novel Multi-Epitope Vaccine Candidates against Streptococcus pneumoniae

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BACKGROUND AND OBJECTIVES: Enolase of Streptococcus pneumoniae is a plasminogen-binding protein and key virulence factor involved in adhesion, neutrophil extracellular trap formation, and complement evasion. This study focuses on epitope mapping and immunogenicity profile of enolase to design multi-epitope based vaccines inducing robust humoral and cellular immunity.

MATERIALS AND METHODS: The linear B-cell and MHCII binding epitopes, IL-4, and IFN-γ inducer epitopes of enolase were predicted using the IEDB, IL-4Pred, and IFNepitope databases, respectively. The immunogenicity, allergenicity, toxicity, and conservation score of the predicted epitopes among pneumococcal serotypes were evaluated using the VaxiJen, AllerTop, ToxinPred, and IEDB databases, respectively. Physicochemical properties were assessed by Protparam server. Finally, immune simulation of enolase administration in mammals and potential regions involved in enolase-TLRs interactions were analyzed by C-ImmSim site and molecular docking via ClusPro server, respectively.

RESULTS AND DISCUSSION: This protein had four and seven predicted linear B-cell and helper T-cell epitopes, respectively, with a vaxijen score of 1.5-2.1 and conservation score of 70-99% among pneumococcal serotypes without any toxicity and allergenicity properties. Furthermore, enolase was considered an IL-4 and IFN-γ inducer protein. The immune simulation demonstrated induction of both humoral and cellular immunity against enolase. In addition, enolase had good interaction with TLR2 and TLR4 (binding energy of -705.1and 863.3kcal/mol). Protparam analysis showed this protein with molecular weight of 47102.94 Da was considered as a stable vaccine candidate. Although, our results revealed that enolase could be considered as a conserved promising candidate vaccine with good immunogenicity profiles, further in vitro and in vivo validations are necessary.

Keywords: Streptococcus pneumoniae, CbpG,Multi-epitope vaccine Immunoinformatics

Impact of Bacteremia Duration on Clinical Outcomes in Staphylococcus aureus Infections: A Study from a Tertiary Hospital

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BACKGROUND AND OBJECTIVES: Staphylococcus aureus represents a significant infectious burden within hospital settings. Its clinical manifestations are diverse and include septicemia, and bacteremia. Staphylococcus aureus is one of the leading causes of bacteremia and mortality. Approximately one third of cases progress into persistent type which increases mortality even more. This study aimed to evaluate clinical outcomes associated with the duration of Staphylococcus aureus bacteremia.

MATERIALS AND METHODS: The study was conducted following ethical approval from the Ministry of Health and Medical Education. All patients older than 18 years old with a definitive diagnosis of staphylococcus aureus and complete consent to study were recruited to the study. Patients were followed until discharge or until the occurrence of study-defined outcomes.

RESULTS AND DISCUSSION: Overall, 45 patients entered the study, 71.1% had bacteremia for 1-2 days, 20% for 3-6 days, and 8.9% for 7 days and more. MRSA infection was seen in 26 patients with no significant association with duration of bacteremia (P-value: 0.76). Source of infection was identified in a third of cases and nosocomial source of infection was the most prevalent cause of in bacteremia for 1-2 days. No significant associations were observed between comorbid conditions and the duration of bacteremia. Longer durations of bacteremia were associated with extended hospital stays (P-value: 0.12). Metastatic complications were most frequently observed in the group with 3–6 days of bacteremia (55.6%, P-value: 0.47). Additionally, this group exhibited the highest mortality rate (44.4%, p=0.79).

Keywords: Bacteremia, Duration, Staphylococcus aureus, Prolonged bacteremia, Outcome

In silico analysis of biosynthetic genes involved in the synthesis of antibiotic compounds in cyanobacteria strains located in Almagol wetland

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BACKGROUND AND OBJECTIVES: Cyanobacteria represent a promising source of novel pharmaceutical lead compounds, yielding a diverse array of bioactive metabolites. This study aimed to amplify NRPS and PKS genes to predict a novel peptide compound and an amino acid activated by a specific unknown NRPS A-module in three cyanobacterial strains isolated from Almagol wetland.

MATERIALS AND METHODS: Following 16S rRNA sequencing, the strains were designated as Aliinostoc sp. Me1355, Aliinostoc sp. Ay1375, and Desmonostoc sp. 1387. PCR amplification of NRPS and PKS genes was performed using molecular techniques to analyze phylogeny and secondary metabolite production. Bioinformatics tools predicted peptide composition, activated amino acids, and NRPS adenylation module signature sequences.

RESULTS AND DISCUSSION: Results confirmed NRPS genes in Aliinostoc sp. Me1355 and Ay1375, and PKS genes in Desmonostoc sp. 1387. Furthermore, the results of the Bioinformatics analyses revealed the type of natural compound, the signature sequences, and the predication of the activated amino acid. Clustering of NRPS/PKS protein sequences showed no phylogenetic correlation between adenylation domains and activated amino acid types, indicating substantial domain diversity. These findings suggest that analyzing PKS and NRPS genes can identify natural product-producing species and elucidate their role in biosynthesizing pharmaceutical bioactive compounds.

Keywords: Peptide synthetase gene, Polyketide synthase gene, Cyanobacteria, Secondary metabolites.

In Silico Design and Immunoinformatic Evaluation of a Chimeric Vaccine Candidate Against Salmonella Typhi

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BACKGROUND AND OBJECTIVES: Salmonella Typhi is the causative agent of typhoid fever, a potentially fatal illness transmitted through contaminated food and water, especially in areas with poor sanitation. The emergence of multidrug-resistant strains has made treatment more challenging and highlighted the urgent need for novel vaccine approaches. Since S. Typhi is an intracellular pathogen, a vaccine that can elicit robust cell-mediated immunity is essential. This study aimed to design and evaluate a chimeric protein combining the FliC and T2942 antigens as a potential vaccine candidate.

MATERIALS AND METHODS: A rigid peptide linker was used to join the antigens FliC (flagellar protein) and T2942 (outer membrane protein). Structural modeling was conducted using Phyre2, and stability was evaluated using the Ramachandran plot and IUPred2A. B-cell and T-cell epitopes were predicted using immunoinformatic tools such as Bcepred, CBTOPE, and MHC-binding predictors. Allergenicity and antigenicity analyses were also performed to ensure the safety and immunogenic potential of the construct.

RESULTS AND DISCUSSION: According to the Ramachandran plot, 91.1% of the residues were located in favored regions, indicating good structural quality. Multiple B-cell and T-cell epitopes were predicted with strong binding affinity to MHC molecules. The chimeric protein was predicted to be non-allergenic, structurally stable, and immunogenic, supporting its potential as a safe and effective vaccine against S. Typhi. Further experimental validation is recommended.

Keywords: Salmonella Typhi, Multi-epitope vaccine, Reverse vaccinology, Chimeric protein, Immunoinformatics

In Silico Exploration of Aotaphenazine from Streptomyces spp. for Inhibitory Activity Against OXA-48 Carbapenemase

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BACKGROUND AND OBJECTIVES: Antibiotic resistance, particularly carbapenem resistance, is a major global health challenge, and the OXA-48 carbapenemase plays a significant role in conferring this resistance. This study employed molecular docking approaches to identify novel compounds capable of inhibiting the OXA-48 carbapenemase.

MATERIALS AND METHODS: This was a descriptive-analytical study. To investigate the binding mode of Aotaphenazine, the crystal structure of the OXA-48 carbapenemase was retrieved from the Protein Data Bank and prepared using AutoDock Tools 4.2. The chemical structure of the compound was obtained from the PubChem database and optimized using ChemDraw (3D). Molecular docking was performed using AutoDock Vina.

RESULTS AND DISCUSSION: The results of the docking studies indicated that hydrophobic interactions were the most important interactions involved in the binding of Aotaphenazine compound to the OXA-48 carbapenemase. The compound showed a high affinity for binding to the key amino acids of the enzyme's active site, with binding energies of -9.9 kcal/mol. Based on the molecular docking results, Aotaphenazine can be considered as potential inhibitors of the OXA-48 carbapenemase. However, the therapeutic efficacy of this compound needs to be confirmed through in vitro and in vivo studies.

Keywords: Bioinformatics, Molecular docking, Phenazine, Carbapenemase OXA-48

In Silico Molecular Docking Analysis of Quercetin with Biofilm-Associated Proteins of Staphylococcus aureus

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BACKGROUND AND OBJECTIVES: The urgent challenge of combatting drug-resistant Staphylococcus aureus has intensified the search for novel therapeutic agents. Quercetin, a natural flavonoid, exhibits antimicrobial properties, but its molecular interactions with S. aureus proteins remain underexplored. This study employed in silico molecular docking to investigate the interaction between quercetin and selected S. aureus proteins involved in biofilm formation using the SwissDock webserver (www.swissdock.ch), selecting the Attracting Cavities 2.0 algorithm

MATERIALS AND METHODS: Three-dimensional (3D) Protein structures of 14 biofilm-associated proteins of S. aureus, including FnBPA, ClfB, SasG, Bap, Psmα3, Can, SarA, AgrA, AgrC, WalK, WalR, VraS, VraR, and Atl were retrieved from the Protein Data Bank. Ligand preparation involved conversion of quercetin's 3D structure (CID: 5280343) from SDF to SMILES format (using Online SMILES Translator). Protein and ligand files were uploaded to SwissDock, automatically processed for optimization, and docked.

RESULTS AND DISCUSSION: Docking results revealed that quercetin exhibits the most favorable binding to WalK, with AC scores as low as 4.30 and binding energies below -7.5 kcal/mol, indicating strong interaction potential. Other notable targets included ClfB, FnBPA, and SasG, all of which are involved in adhesion and biofilm formation, with docking scores in the range of -7.4 to -7.1 kcal/mol. Proteins such as AgrA, Atl, and AgrC showed moderate binding, while quercetin exhibited weak or negligible interaction with SarA, VraR, and Cna based on high energy values or absence of favorable clusters. Conclusion:These findings suggest that quercetin may exert its anti-S. aureus effects partly through inhibition of biofilm-associated proteins, especially WalK.

Keywords: Staphylococcus aureus, Quercetin, Molecular docking, Antibacterial agents, Biofilm

In silico Screening of ethyl 3-(4-methoxyanilino)-6-(trifluoromethyl)quinoxaline-2-carboxylate as a Novel DprE1 inhibitor against Mycobacterium tuberculosis

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BACKGROUND AND OBJECTIVES: Mycobacterium tuberculosis, the causative agent of tuberculosis (TB), is a major global health concern due to its ability to evade immune responses and persist in host macrophages. One of its key virulence factors, Decaprenylphosphoryl-β-D-ribose 2′-epimerase (DprE1), plays a crucial role in cell wall biosynthesis. Targeting DprE is a crucial strategy in tuberculosis therapy. Therefore, the objective of this study was to identify the most potent ligand capable of inhibiting DprE1 through molecular docking analysis.

MATERIALS AND METHODS: The 3D structure of DprE1 (PDB ID: 6HEZ) was extracted from the RCSB PDB. TY38c and 20 structural analogs, as inhibitory ligands, were retrieved from PubChem database in SDF format. After preparation, molecular docking was performed using Molegro Virtual Docker v.6. The best pose of each ligand was analyzed, and the top inhibitor was selected based on binding energy and interactions. Finally, the pharmacokinetic properties of ligand were predicted using the SwissADME server.

RESULTS AND DISCUSSION: Among the evaluated analogs, the most effective inhibitor was identified as ethyl 3-(4-methoxyanilino)-6-(trifluoromethyl)quinoxaline-2-carboxylate (PubChemCID: 387139), with a molecular weight of 391.3 g/mol and binding free energy of –142.794 kcal/mol. Interaction analysis revealed two hydrogen bonds with Phe231 and Tyr297 residues, and 3 steric interactions with Trp230, Phe231, and Ile234. ADME analysis showed acceptable solubility (LogS: –5.4), lipophilicity (XLOGP3: 5.04), polarity (TPSA: 73.34), 8 hydrogen acceptors, and 1 hydrogen donor. These findings suggest PubChemCID 387139 as a promising DprE1 inhibitor, warranting further in vitro and in vivo validation.

Keywords: Mycobacterium tuberculosis, DprE1, Molecular Docking

In Silico Screening of Natural Compounds Targeting the Rv0933 Efflux Transporter in Mycobacterium tuberculosis

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BACKGROUND AND OBJECTIVES: : Acquired and intrinsic resistance, is the critical obstacle to effective treatment and control of TB. Efflux pump activity, particularly through ATP-binding cassette (ABC) transporters like Rv0933, contributes significantly to drug resistance. Despite its potential role in isoniazid and rifampin resistance, Rv0933 has not been widely studied as a drug target . The principal goal of our study is to design a docking model that could be useful in Rv0933 inhibitors, in order to restore drug sensitivity in Mycobacterium tuberculosis

MATERIALS AND METHODS: The 3D structure of Rv0933 was prepared from the AlphaFold database. A library of natural compounds, including ellagic acid and salicylic acid, was retrieved from PubChem. Molecular docking was performed using AutoDock to predict ligand–protein binding affinities and interaction sites.

RESULTS AND DISCUSSION: Following molecular docking, ellagic acid showed the strongest affinity to Rv0933 with a binding energy of –7.13 kcal/mol, and salicylic acid –6.45 kcal/mol. The hydrogen bonds between key residues (residues 54–61) and the ligand suggesting a potential mechanism for efflux pump inhibition. The results suggest that ellagic acid may function effectively as a natural efflux pump inhibitor against Rv0933, potentially enhancing the efficacy of standard anti-TB drugs. In vitro experiments are proposed to substantiate our findings and evaluate the therapeutic potential of the compound

Keywords: Mycobacterium tuberculosis, Drug resistance, Molecular Docking Simulation, ATP-binding cassette transporters

In Vitro Activity of Meropenem and Ciprofloxacin Combined with Diclofenac against Extensively Drug-Resistant Acinetobacter baumannii Isolates from Intensive Care Units Patients

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BACKGROUND AND OBJECTIVES: Acinetobacter baumannii is a predominant etiological agent of healthcare-associated infections, posing a significant clinical challenge due to its remarkable capacity for antimicrobial resistance and biofilm formation, particularly in extensively drug-resistant (XDR) strains. Diclofenac, a non-steroidal anti-inflammatory drug (NSAID), has demonstrated intrinsic antimicrobial activity against bacterial pathogens. Therefore, this study aimed to evaluate the synergistic efficacy of meropenem and ciprofloxacin in combination with diclofenac against both planktonic and biofilm phenotypes of A. baumannii clinical isolates.

MATERIALS AND METHODS: The study utilized the broth microdilution method to determine the minimum inhibitory concentrations (MICs) and minimum biofilm eradication concentrations (MBECs). The potential synergistic interactions between meropenem-diclofenac and ciprofloxacin-diclofenac combinations were assessed using a checkerboard assay, evaluating their efficacy against both planktonic and biofilm-embedded A. baumannii isolates

RESULTS AND DISCUSSION: Results: In the planktonic state, the combination of meropenem and diclofenac exhibited synergistic activity against 46.1% of the isolates, whereas ciprofloxacin and diclofenac demonstrated synergy against 61.5%. Under biofilm conditions, the minimum biofilm eradication concentration (MBEC) reduction fold ranged from 2 to 16 for meropenem combined with diclofenac, while the MBEC reduction fold for ciprofloxacin and diclofenac ranged from 4 to 32. Conclusion: The present study demonstrates significant synergistic activity between diclofenac and both meropenem and ciprofloxacin against XDR A. baumannii isolates. The observed enhancement of antibacterial efficacy suggests that this antibiotic-NSAID combination strategy could represent a valuable therapeutic approach for combating resistant A. baumannii infections. Further investigation is warranted to fully characterize the clinical potential of these combinations.

Keywords: Acinetobacter baumannii, Combination therapy, Meropenem, Ciprofloxacin, Diclofenac, Biofilm, Checkerboard assay

In Vitro Antifungal and Cytotoxic Assessment of Magnesium Oxide Nanoparticles on Candida albicans and Candida glabrata

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BACKGROUND AND OBJECTIVES: Introduction: Candida infections are a major health concern, and current antifungal treatments face issues like toxicity and resistance. Magnesium oxide nanoparticles have shown promise as alternative antifungal agents. This study investigates the antifungal and cytotoxic effects against Candida albicans and Candida glabrata compared to nystatin.

MATERIALS AND METHODS: Methods: Antifungal activity was evaluated using the broth microdilution technique, while cytotoxic effects were measured in J774 mouse macrophage cells using the MTT assay.

RESULTS AND DISCUSSION: Results: The minimum inhibitory concentration (MIC) and minimum fungicidal concentration (MFC) for MgO nanoparticles were found to be 1–4 mg/mL and 4 mg/mL, respectively, whereas for nystatin they ranged from 8–32 µg/mL and 32–64 µg/mL. Both agents demonstrated dose-dependent antifungal activity. However, MgO nanoparticles exhibited significantly lower cytotoxicity (CC_{50} = 5887 µg/mL) than nystatin (CC_{50} = 8.61 µg/mL) (P 0.001). These findings highlight the promising antifungal potential of MgO NPs, with the added advantage of minimal cytotoxicity. Magnesium oxide nanoparticles showed strong antifungal activity and significantly lower cytotoxicity than nystatin. Conclusion: These results suggest that MgO nanoparticles may serve as a safe and effective alternative for treating Candida infections.

Keywords: Keywords: Magnesium oxide nanoparticles; Candida; Antifungal activity; Cytotoxicity

In Vitro Assessment of the Antibacterial Activity of Lavandula Angustifolia Essential Oil: Implications for Natural Antimicrobial Agent

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BACKGROUND AND OBJECTIVES: The rise in antibiotic resistance, especially in pathogens like Pseudomonas aeruginosa (PA), highlights the need for alternatives. Lavandula angustifolia has shown promising antimicrobial activity, offering potential for infection control strategies.

MATERIALS AND METHODS: The essential oil extracted from L. angustifolia (Zardband Pharmaceutical Co., Iran) was evaluated for its antibacterial activity using well diffusion agar (WDA) and microdilution-based minimum inhibitory concentration (MIC) assays, with concentrations ranging from 16 to 0.031 mg/mL. Antibacterial activity was assessed against Escherichia coli ATCC 25922 and 11 clinical isolates of PA (Gram-negative bacteria), as well as Bacillus cereus ATCC 11778 and Staphylococcus aureus ATCC 23235 (Gram-positive bacteria). The bacterial strains were tested using both the WDM and MIC. After incubation, bacterial growth was quantified by measuring the optical density (OD) using an ELISA reader.

RESULTS AND DISCUSSION: In Gram-negative bacteria, no inhibition zones were observed in the WDA assay, except for one clinical isolate of PA, which exhibited a 10 mm inhibition zone at 100% essential oil concentration. In contrast, Gram-positive bacteria showed clear inhibitory zones in the WDA assay. The MIC for six clinical isolates of PA was 16 mg/mL, while three isolates exhibited MICs of 32 mg/mL, and one isolate had an MIC of 64 mg/mL. One clinical isolate showed a significantly lower MIC of 2 mg/mL. The MIC for E. coli and the tested Gram-positive strains was uniformly 16 mg/mL. L. angustifolia essential oil showed limited Gram-negative activity, stronger Gram-positive effects, and concentration-dependent inhibition, especially against pathogenic strains like PA.

Keywords: Pseudomonas aeruginosa, Essential oil, Lavandula angustifolia, Antimicrobial activity

In Vitro Assessment of Antimicrobial Properties of Native Postbiotics against Common Human Pathogens

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BACKGROUND AND OBJECTIVES: A postbiotic refers to the byproduct produced by probiotics during the fermentation process in environments. The objective of this study was to assess the antimicrobial activity of postbiotics derived from native probiotic strains, with a focus on their effectiveness against common human pathogens.

MATERIALS AND METHODS: The cell-free supernatant (CFS) from 33 probiotic strains were collected by centrifuging of liquid probiotic cultures and subsequently filtering through a 0.45 µm filter. The filtered CFS was freeze-dried and used as a source of postbiotics for further investigation. The antimicrobial activity of these postbiotics was assessed against human pathogens, including Escherichia coli (IBRC-M 10698), Pseudomonas aeruginosa (IBRC-M 10832), and Staphylococcus aureus (IBRC-M 10917), utilizing the well diffusion method on Mueller-Hinton agar.

RESULTS AND DISCUSSION: Nine postbiotics derived from strains by the name of DM II (6), YL III (7), MP II (4), Chq 1(7), Mq 4(11), AP 12(4), FS II (5), YL IV (4) and AP 6(3) demonstrated significant efficacy against pathogens which characterized as Pediococcus acidilactici (IBRC- M 11476), Pediococcus acidilactici (IBRC- M 11450), Levilactobacillus brevis (IBRC- M 11496), Enterococcus faecium (IBRC- M 11443), Enterococcus faecium (IBRC- M 11449), Levilactobacillus brevis (IBRC- M 11448), Levilactobacillus brevis (IBRC- M 11478), Levilactobacillus brevis (IBRC- M 11489) and Pediococcus acidilactici (IBRC- M 11447), respectively.It seems that strains from Pediococcus sp. showed the best results however, Levilactobacillus sp. and Enteroccocus sp. also have promising results. Yeasts has no antimicrobial activity against human pathogens. Studies are underway to examine the nature and structure of these postbiotics.

Keywords: Postbiotics, Antimicrobial activity, human pathogen

In vitro evaluation of the antimicrobial effects of hydroalcohlic exctracts of purtalaca oleracea leaves and seeds on selected pathogens

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BACKGROUND AND OBJECTIVES: Introduction and Objective: The oral cavity, as a site for colonizing various microorganisms, is prone to multiple infections, including dental caries and periodontal diseases. The emergence of microbial resistance to existing chemical drugs has highlighted the need to explore alternative antimicrobial compounds. This study aimed to investigate the antimicrobial effects of hydroalcoholic extracts of purslane (Portulaca oleracea L.) leaves and seeds against certain oral pathogens under laboratory conditions

MATERIALS AND METHODS: : In this experimental study, hydroalcoholic extracts of purslane leaves and seeds were prepared using the maceration method. Their antimicrobial effects were tested against five oral pathogenic microorganisms (Streptococcus mutans, Streptococcus sanguinis, Streptococcus sobrinus, Lactobacillus acidophilus, and Candida albicans). The agar diffusion method and microdilution broth technique were employed to determine the minimum inhibitory concentration (MIC) and minimum bactericidal/fungicidal concentration (MBC/MFC). The antimicrobial effects of the extracts were compared with chlorhexidine (0.12%) and nystatin (100,000 units) as positive controls and DMSO as a negative control. The primary active component of the extracts was identified using high-performance liquid chromatography (HPLC).

RESULTS AND DISCUSSION: HPLC analysis identified caffeic acid as the primary active compound in the extracts. Both leaf and seed extracts demonstrated inhibitory and bactericidal effects against all tested pathogens, although these effects were weaker compared to 0.12% chlorhexidine and 100,000-unit nystatin. The leaf extract exhibited stronger antimicrobial activity than the seed extract. Among the pathogens, the extracts were most effective against Streptococcus species, particularly Streptococcus mutans, while the lowest efficacy was observed against Lactobacillus acidophilus.

Keywords: purslane leaves, purslane seeds, oral pathogens

In Vivo Effects of Lacticaseibacillus rhamnosus and Lacticaseibacillus reuteri Lysates on Oral Wound Healing in Rats

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BACKGROUND AND OBJECTIVES: Oral wounds face distinct healing challenges due to constant microbial presence and mechanical stress. Bacterial lysates, as non-viable probiotic derivatives, have shown promise in supporting tissue regeneration. This study aimed to assess the effect of lysates from Lacticaseibacillus rhamnosus and L. reuteri, applied topically, on the healing of full-thickness oral wounds in a rat model, both separately and in combination.

MATERIALS AND METHODS: Forty-eight healthy female Wistar rats were assigned to four groups (n=12): PBS control, L. rhamnosus lysate, L. reuteri lysate, and a combined lysate group. A standardized 1×1 mm wound was created on the buccal mucosa of each rat. Treatments (50 µg/mL) were applied every other day. Healing progression was monitored macroscopically and histologically on days 3, 7, 14, and 21. Microbial depletion was confirmed via 16S rRNA PCR. Histopathological changes were assessed using hematoxylin and eosin staining.

RESULTS AND DISCUSSION: By day 7, complete wound closure was observed in the combined lysate group (0.00 ± 0.00 mm), significantly outperforming other groups (P 0.0001). Groups treated with individual lysates also showed improved healing compared to the control. Histological results confirmed enhanced epithelial regeneration and reduced inflammation in all lysate-treated groups, especially the combination group, which showed no signs of scarring. These findings suggest synergistic effects of lysate co-treatment in promoting oral wound healing.

Keywords: Probiotics, Wound healing, Oral mucosa, L. rhamnosus, L. reuteri.

In-silico design and computational analysis of a novel chimeric antigen as a vaccine candidate against Salmonella Typhi

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BACKGROUND AND OBJECTIVES: Typhoid fever, caused by Salmonella enteritidis serovar Typhi (S. Typhi), remains a significant global health challenge, especially in regions with poor sanitation. Despite available vaccines, limitations such as short-term efficacy and variable immune responses necessitate novel strategies.

MATERIALS AND METHODS: A chimeric vaccine candidate was designed by integrating three key S. Typhi antigens: full-length SteD, the D1 domain of flagellin, and full-length STIV, linked via rigid EAAAK sequences to enhance structural stability. The construct was evaluated using in silico tools for antigenicity (VaxiJen), physicochemical properties (ProtParam), allergenicity (AlgPred), and toxicity (ToxinPred). Structural modeling was conducted using I-TASSER, Phyre2, and RaptorX, and validated via Ramachandran plot, ProSA z-score, and ERRAT. Epitope prediction (IEDB, ABCPred, Discotope 2.0), molecular docking with TLR-4 and TLR-5, 100-ns molecular dynamics (MD) simulations (NAMD/VMD), and immune response simulations (C-ImmSim) were performed.

RESULTS AND DISCUSSION: The vaccine construct demonstrated high antigenicity (VaxiJen score: 0.9228), stability, and non-allergenic, non-toxic properties. Structural validation confirmed a stable 3D conformation (90% residues in favored Ramachandran regions, ProSA z-score: –5.54). Epitope predictions indicated strong HLA binding. Docking studies revealed stable interactions with TLR-4 and TLR-5, and MD simulations showed low RMSD and RMSF values. Immune simulations predicted robust IgG/IgM responses and elevated Th1/Th2 cytokines. This in silico study presents a structurally stable, immunogenic chimeric vaccine candidate against S. Typhi, supporting its potential for further experimental validation.

Keywords: Salmonella Typhi, multi-protein vaccine, immunoinformatics, molecular docking, immune simulation

Individual and Combined effects of the dietary Lactobacillus sakei and Lactobacillus delbrueckii on antioxidant capacity, innate immunity, and relative gene expression of Zebrafish Embryos, with Implications for Human Applications

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BACKGROUND AND OBJECTIVES: Abstract Introduction: Due to the importance of Zebrafish in the aquaculture sector, the present study aimed to evaluate the adverse impacts of the individual and combined dietary Lactobacillus sakei (LS) and Lactobacillus delbrueckii (LD) on inflammation, immune, and antioxidant response.

MATERIALS AND METHODS: A total of 240 fish were randomly distributed in 12 tanks and fed with diets containing 0% LS and LD, 108 CFU/g LS, 15 g/kg LD and combination of 106 CFU/g LS and 15 g/kg LD for 45 days.

RESULTS AND DISCUSSION: At the end of the feeding trial, the results showed that growth parameters were enhanced in LS + LD groups compared to the control group (p0.05). LS + LD supplemented dietary was significantly increased the final weight, specific growth rate(SGR) and weight gain (P0.05) compared to the control. A noticeable increase in protease and lysozyme activity was observed in treatment groups fed with both LS and LD, compared to the control fish (P0.05). The mixture of LS and LD improved Superoxide dismutase(SOD), glutathione peroxidase (GPX), and malondialdehyde (MDA). The expression of catalase (CAT) and lysozyme genes were upregulated in T4 treatment. The mRNA levels of lysozyme, IL6, IL-1β, IL-8, TGF, and TNF-α transcription were higher in fish fed with both LS and LD (P0.05). Conclusion: The mixture of LS and LD is more effective than using each individually for improving the inflammation, immune, and antioxidant responses in Zebrafish (Danio rerio).

Keywords: Lactobacillus sakei, Lactobacillus delbrueckii, antioxidant capacity, inflammation, Gene expression

Influence of Medium Composition on Antibiotic Susceptibility Testing: A Case Study on Staphylococcus aureus

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BACKGROUND AND OBJECTIVES: Background: With the growing resistance of bacteria to antibiotics, antimicrobial susceptibility testing (AST) has become a vital part of clinical microbiology. The disk diffusion method remains widely used due to its standardization and cost-effectiveness. Mueller-Hinton agar (MH agar), recommended by CLSI and EUCAST, plays a key role in AST accuracy, particularly due to its starch and ionic content. Objective: This study aimed to evaluate the impact of five different commercial MH agar brands on the results of AST for Staphylococcus aureus.

MATERIALS AND METHODS: Methods: Antibiotic susceptibility of 20 clinical isolates and one standard strain (S. aureus ATCC 25923) was tested against vancomycin, gentamicin, and methicillin. Tests were performed using three culture methods: double-layer, pour plate, and swabbing. The resulting inhibition zones were analyzed in relation to the cation content of each medium.

RESULTS AND DISCUSSION: Results: The double-layer method produced smaller inhibition zones, while pour plate and swabbing methods yielded more consistent results. Cation analysis revealed differences among the five MH agar brands. Quelab medium contained the highest essential cation levels, while Merck and Sigma brands provided the most reliable, CLSI-compliant AST results. Conclusion: The ionic composition of MH agar—especially calcium and magnesium—has a significant effect on AST outcomes. Ensuring media standardization is essential for achieving accurate and reproducible results in clinical settings.

Keywords: Keywords: Staphylococcus aureus, antimicrobial susceptibility testing, Mueller-Hinton agar, disk diffusion,

Inhibition of ermB Gene Expression in Enterococcus faecalis by Postbiotics from Lactobacillus plantarum

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BACKGROUND AND OBJECTIVES: Enterococcus faecalis is a major hospital-acquired pathogen with high resistance to antibiotics, especially macrolides. The ermB gene encodes a methylase that reduces macrolide binding to ribosomes, compromising treatment. Due to rising antibiotic resistance, alternative agents like postbiotics non-viable metabolic products from probiotics have gained interest. This study investigates the effect of Lactobacillus plantarum postbiotics on ermB gene expression in E. faecalis using Real-Time PCR.

MATERIALS AND METHODS: Clinical antibiotic-resistant E. faecalis strains harboring ermB were isolated. L. plantarum ATCC 8014 was cultured in De Man, Rogosa and Sharpe (MRS) medium, and cell-free supernatants (CFS) were obtained by centrifugation and filtration. Chemical composition of CFS was identified by gas chromatography–mass spectrometry (GC-MS). Total RNA was extracted from treated and control bacteria; cDNA was synthesized. ermB expression was quantified by RT-qPCR with SYBR Green, normalized to gdh gene. Statistical analysis used Student's t-test; relative expression was calculated by the Pfaffl method.

RESULTS AND DISCUSSION: GC-MS revealed butyric acid (14.31%), lactic acid (5.94%), and hydroxyacetone as the main postbiotic compounds. RT-qPCR showed significant downregulation of ermB in treated bacteria versus controls ($P = 0.007$), suggesting postbiotics inhibit antibiotic resistance gene expression. L. plantarum postbiotics significantly reduce ermB expression in E. faecalis, likely via butyric and lactic acids. These findings support postbiotics as promising agents against antibiotic resistance, though further in vivo studies are needed.

Keywords: E. faecalis, ermB, Postbiotics, L. plantarum

Inhibition of Staphylococcus aureus biofilm formation using bacterially synthesized silver nanoparticles

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BACKGROUND AND OBJECTIVES: The emergence of antibiotic-resistant pathogens and the ability of Staphylococcus aureus to form strong biofilms have made effective antimicrobial strategies an essential need. Silver nanoparticles, especially those synthesized through bacterial processes, have attracted significant attention due to their remarkable antimicrobial properties and environmentally friendly production.

MATERIALS AND METHODS: Titanium samples coated with silver nanoparticles were incubated in bacterial suspension of S.aureus (ATCC 29737) for 24 hours, then washed in sterile saline and sonicated to dislodge adherent bacteria. The resulting suspensions were cultured on nutrient agar to determine the number of colony-forming units, assessing bacterial viability and adhesion.

RESULTS AND DISCUSSION: Bacteria-synthesized silver nanoparticles inhibited S. aureus biofilm formation by up to 90%. Biosynthesized silver nanoparticles exhibit potent antibiofilm activity, with inhibition rates of up to 90% at relatively low concentrations, effectively preventing bacterial adhesion and biofilm maturation.

Keywords: Biofilm, Bacteria, Silver nanoparticle, Antimicrobial activity

Inhibitory effect of Lactobacillus plantarum on resistant Candida albicans and combination therapy with fluconazole

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BACKGROUND AND OBJECTIVES: As antibiotic resistance accelerates beyond drug development, fungal infections, especially Candida albicans, pose mounting risks. Traditional antifungals frequently fail against resilient biofilms, prompting interest in postbiotics: non-living microbial by-products from organisms like Lactiplantibacillus plantarum. These compounds offer targeted antifungal action without probiotic-related risks, potentially disrupting Candida growth and biofilms through safer, synergistic strategies.

MATERIALS AND METHODS: Postbiotic compounds were extracted from the cell-free supernatant of Lactiplantibacillus plantarum. Clinical and standard strains of Candida albicans were cultured, and standardized suspensions were prepared. Antifungal activity was assessed using the microbroth dilution method to determine MIC and MFC values. The synergistic interaction between postbiotics and fluconazole was evaluated using the checkerboard assay. Biofilm formation and eradication were quantified spectrophotometrically. Data analysis was performed using GraphPad Prism

RESULTS AND DISCUSSION: The postbiotic compound showed a minimum inhibitory concentration (MIC) of 250 µg/mL and a minimum fungicidal concentration (MFC) of 500 µg/mL against Candida albicans, with an MFC/MIC ratio of 2, indicating a fungicidal effect. Ergosterol levels decreased by 18.37% at 500 µg/mL, showing significant disruption of fungal cell membranes. Biofilm formation was reduced at all tested concentrations, with the greatest inhibition at the MIC (250 µg/mL), suggesting a concentration-dependent but saturable effect. Additionally, a checkerboard assay revealed synergy between the postbiotic and fluconazole, lowering fluconazole's MIC from 64 to 16 µg/mL when combined with 125 µg/mL postbiotic (FICI = 0.5). These results highlight the postbiotic's strong antifungal and anti-biofilm potential, especially in combination therapy.

Keywords: Candida albicans, Drug Resistance, Probiotics

Innovation in vaccine design for neglected diseases with a focus on leishmaniasis: challenges, opportunities, and the future path for targeted vaccines against neglected pathogens

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BACKGROUND AND OBJECTIVES: Neglected tropical diseases (NTDs) represent a critical public health challenge, caused by a variety of infectious agents, including viruses, bacteria, parasites, fungi, and non-infectious agents like toxins. The devastating health, social, and economic impacts of these diseases cannot be overstated. A significant barrier to progress is the lack of information and insufficient public and professional awareness regarding the epidemic situation, its causes, and effective treatment or prevention methods. Modern research is vital for advancing the discovery of new treatments, vaccines, and improved diagnostic and control methods. Leishmaniasis presents major challenges due to long treatment durations, drug side effects, and rising drug resistance. Utilizing robust scientific data empowers researchers to design vaccines that effectively stimulate the immune system.

MATERIALS AND METHODS: L. tarentolae, a non-pathogenic species for humans, offers a promising avenue as a live vector for developing vaccines against both cutaneous and visceral leishmaniasis. Various cell types have demonstrated the ability to utilize extracellular vesicles to transport regulatory proteins, lipids, and nucleic acids to distant and nearby cells. The discovery of extracellular vesicles from L. tarentolae is a groundbreaking development that opens new avenues for therapeutic applications. These include vaccine development, drug delivery, and the production of therapeutic proteins. L. tarentolae extracellular vesicles can serve as powerful diagnostic tools and therapeutic agents.

RESULTS AND DISCUSSION: In conclusion, the key message of this presentation is the importance of continuing and enhancing efforts to utilize these vesicles in the production of vaccines and drugs.

Keywords: Neglected tropical diseases, leishmaniasis, Leishmania tarentolae, extracellular vesicles, vaccine, drug

Innovations in bacteriophage applications

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BACKGROUND AND OBJECTIVES: Bacteriophages, highly specific-targeting viruses, has been re- emerged as significant promising antimicrobials for post-antibiotic era. Increasing rate of antibiotic resistance, cause some concerns in different sectors especially in therapeutics. Although, one of the most important field of using bacteriophages is medicine, antibacterial activity of phages attracted the attention of researchers to solve the problem of antibacterial resistance in other fields.

MATERIALS AND METHODS: Recently published peer-reviewed articles with the aid of demonstrating new approaches to use antibacterial potential of bacteriophages in various sectors like biotechnology, remediation and environmental sciences were gained. Then, different possibilities of using antibacterial potential of bacteriophages were surveyed and reviewed.

RESULTS AND DISCUSSION: Due to recent advances in genetic engineering technologies, expanding application of bacteriophages in wide range of biotechnology has been explained. This review as a comprehensive guide, showed the relatedness between fundamental information of phages with their application and could bridge some gaps to help better understanding of optimization methods and functional protocols in using bacteriophages. Finding new prospective of bacteriophage applications can open new approaches of using re-emerged bacterial viruses efficiently.

Keywords: bacteriophage, antibiotic resistance, innovation,

Innovative Alginate-Based Hydrogels for Targeted Antimicrobial Delivery in Chronic Wound Infections

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BACKGROUND AND OBJECTIVES: Chronic skin wound infections, especially those complicated by multidrug-resistant bacteria and persistent biofilms, pose a significant health burden in Iran. Traditional antimicrobial therapies frequently fail due to poor penetration and rapid resistance emergence, highlighting the need for innovative drug delivery systems.

MATERIALS AND METHODS: This review synthesizes advances in alginate-based hydrogel technologies engineered for controlled, localized delivery of both natural and synthetic antimicrobial agents. Structural optimization, hybridization with functional biopolymers, and incorporation of stimuli-responsive elements were critically evaluated. Emphasis was placed on preclinical and clinical evidence relevant to Iranian healthcare settings.

RESULTS AND DISCUSSION: Alginate hydrogels demonstrate high biocompatibility, moisture retention, and tunable gel properties, making them ideal carriers for antimicrobials. Integration of plant-derived agents (such as quercetin, honey, and antimicrobial peptides) and synthetic compounds (ZnO/Ag nanoparticles, ciprofloxacin, nitric oxide donors) has significantly improved efficacy against key pathogens, including Staphylococcus aureus and Pseudomonas aeruginosa. Innovations in hydrogel design—such as nanocomposite formation and pH/ROS-responsive systems—enable on-demand release and enhanced biofilm disruption. Notably, Iranian-developed alginate hydrogels have shown positive results in burn and chronic wound management. Nonetheless, scalability, regulatory pathways, and long-term safety remain principal challenges in translation to routine clinical use. Advanced alginate hydrogels offer promising solutions for targeted antimicrobial therapy in chronic wound infections, with demonstrated advantages over conventional treatments. To accelerate clinical translation in Iran, multidisciplinary collaboration, pilot clinical trials, and regulatory harmonization are essential.

Keywords: Hydrogels, Alginate, Wound Infection, Antimicrobial Agents, Drug Delivery Systems, Iran

Innovative Antibacterial Approaches in Periodontitis and Peri-Implantitis: The Role of Photodynamic Therapy"

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BACKGROUND AND OBJECTIVES: Periodontitis and peri-implantitis are biofilm-associated inflammatory diseases that often persist despite conventional debridement and antimicrobial measures. The rise of antibiotic resistance and the complex architecture of subgingival biofilms have prompted exploration of alternative antibacterial therapies. Photodynamic therapy (PDT) has gained attention as a minimally invasive, adjunctive method for microbial control in periodontal and peri-implant sites.

MATERIALS AND METHODS: This review evaluates current and emerging antibacterial strategies for managing periodontal and peri-implant infections, with a specific focus on the application and clinical potential of PDT. The mechanism of action, commonly used photosensitizers and light sources, and treatment protocols are discussed. Clinical outcomes from recent trials and comparative studies are analyzed to assess the efficacy of PDT in combination with mechanical debridement.

RESULTS AND DISCUSSION: Data from multiple clinical studies indicate that adjunctive PDT can significantly reduce pathogenic bacterial counts and improve clinical parameters, such as probing depth and clinical attachment level. Unlike systemic antimicrobials, PDT offers localized, targeted action without inducing bacterial resistance or systemic side effects. Additionally, biostimulatory effects on surrounding tissues have been reported, potentially enhancing wound healing and reducing inflammation. Conclusion: Photodynamic therapy represents a promising addition to the contemporary periodontal and peri-implant treatment arsenal. Its ability to disrupt biofilms, target a broad spectrum of pathogens, and avoid the drawbacks of antibiotics makes it particularly valuable in cases with recurrent or refractory infection. Future research should aim to standardize treatment parameters and explore long-term outcomes to fully integrate PDT into routine clinical protocols.

Keywords: Periodontitis/therapy, photosensitizing Agents, light therapy

Integrated Diagnostic Approaches for Human Brucellosis: Comprehensive Analysis of Classical, Serological, Molecular, and Emerging Methods

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BACKGROUND AND OBJECTIVES: Human brucellosis continues to challenge clinicians and laboratories in endemic regions due to non-specific symptoms and overlapping clinical features, emphasizing the need for robust, multi-tiered diagnostic protocols.

MATERIALS AND METHODS: This abstract evaluates all currently applied diagnostic modalities, including classical blood and bone marrow culture, serological techniques (Rose Bengal, Wright, 2-Mercaptoethanol, Coombs Wright, Brucellacapt, IgG/IgM ELISA, rapid immunochromatographic tests, nano/paper-based ELISA), contemporary molecular assays (conventional PCR, quantitative/real-time PCR, LAMP, digital PCR, isothermal amplification, CRISPR/Cas-based detection), as well as innovative platforms like MALDI-TOF MS and biosensor-based diagnostics. Sensitivity, specificity, diagnostic window, feasibility, and limitations were extracted from studies published between 2015–2025.

RESULTS AND DISCUSSION: Culture, though highly specific (99%), is limited by slow growth and low sensitivity (40%). Serological tests, like RBT and Wright, are quick and cost-effective for screening, while 2ME, Coombs, and Brucellacapt enhance precision in active/chronic differentiation. ELISA platforms (including nano-labeled and rapid tests) offer high analytical accuracy (up to 100% sensitivity/specificity). Molecular assays, particularly qPCR, LAMP, and CRISPR provide rapid, highly sensitive detection, critical for acute, atypical, or seronegative cases, but are limited by equipment availability in low-resource settings. Novel diagnostics, such as MALDI-TOF MS and biosensors, promise rapid pathogen identification and resistance profiling, pending large-scale validation. Integration of advanced serological and molecular assays into existing classical protocols substantially improves diagnostic accuracy, reduces misdiagnosis, and facilitates timely management of brucellosis, especially in endemic, resource-constrained areas. Field-deployable platforms and algorithm optimization remain priorities for future implementation.

Keywords: Brucellosis, Diagnosis, Serologic tests, ELISA, qPCR

Integration of genome editing and intelligent expression systems in Corynebacterium glutamicum for optimizing recombinant protein production

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BACKGROUND AND OBJECTIVES: With remarkable advances in biotechnology and the advent of technologies such as CRISPR-Cas9 and precise point-mutation methods, an ideal platform has emerged to enhance the performance of Corynebacterium glutamicum in diverse biological applications. These genome modifications targeting secretion systems,promoters, and regulatory elements have significantly improved host functionality. As C.glutamicum is a powerful industrial and pharmaceutical chassis for recombinant protein production, its rational engineering is particularly critical.This study examines genetic engineering strategies to expand host capacity and boost its efficiency in modern bioprocessing.

MATERIALS AND METHODS: In this structured review, studies published from 1995 to 2024 were rigorously examined. The analysis focused on the genome editing systems of Corynebacterium glutamicum, strong native and inducible promoters, synthetic promoter libraries, and shuttle vectors such as pPBEx2.

RESULTS AND DISCUSSION: Efficient promoters were identified and engineered through combined experimental and bioinformatic approaches, optimizing native (PporB), inducible (PlacUV5), and synthetic (Ptrc) promoters to achieve precise expression control. Secretion pathways Sec and Tat were enhanced by overexpressing tatA and tatC and employing engineered signal peptides such as TorA and PorB, resulting in markedly increased protein export. Deletion of the CGP3 prophage and other mobile genetic elements bolstered genomic stability. Concurrent modulation of metabolic pathways and upregulation of stress-response genes (e.g.,DnaK), together with the use of optimized shuttle vectors (pEKEx2 and pVWEx1), not only raised production yields but also enabled tighter regulation of recombinant gene expression. Finally, cell-wall engineering improved permeability, facilitating more efficient release of complex proteins and transforming C.glutamicum into a robust host for biomanufacturing.

Keywords: Corynebacterium glutamicum, Genome-editing, Recombinant protein

Interplay among vitamin D deficiency and dysbiosis and their roles in diseases

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BACKGROUND AND OBJECTIVES: Vitamin D (VitD) deficiency and downregulation of the vitamin D receptor (VDR) and their immunomodulatory properties are also associated with the pathogenesis of diseases such as inflammatory bowel disease, cancers, obesity, diabetes, asthma, diabetes and neurological diseases. the microbiome has a major impact on human physiology and plays a critical role in enhancing or impairing various physiological functions such as regulation of the immune system, metabolic activities, and biosynthesis of vitamins and hormones. gut microbial imbalance (dysbiosis) play a critical role in several diseases.

MATERIALS AND METHODS: We searched PubMed, Scopus, Google Scholar, and Medline databases using the keywords: "gut microbiota AND vitamin D deficiency", "dysbiosis AND vitamin D deficiency", "vitamin D deficiency AND disease.

RESULTS AND DISCUSSION: VDR significantly impacts microbial profile, requiring restoration to prevent and treat diseases by promoting healthy interactions between microbes and hosts. VitD deficiency altered the composition and functionality of the fecal microbiota as exemplified by a decreased abundance of Lactobacillus and significantly different α- and β-diversity and increase in the relative abundance of Enterococcus and correlated with VitD deficiency and, as consequence, with several disease such as memory impairments and Alzheimer. The study highlights the intricate link between gut microbiota, host metabolism, and VitD deficiency-related diseases, suggesting the need for targeted dysbiosis in future preventive and therapeutic strategies.Gut microbiota and VitD play crucial roles in disease development and improvement, controlling VitD levels and changes in microbiota, these two important factors can play a role in the improvement of many diseases.

Keywords: vitamin D deficiency, gut microbiota, dysbiosis

Investigating of combined native Nocardia bioremediation and sunflower (Helianthus annuus) phytoremediation: A breakthrough enzymatic synergy for sustainable PAH and heavy metal soil remediation

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BACKGROUND AND OBJECTIVES: Heavy metals and PAHs are persistent soil contaminants threatening human health, environmental stability, and agricultural productivity through oxidative stress, neurotoxicity, carcinogenicity, and reduced crop yields. Due to this issue in this study we evaluated the bioremediation potential of native Iranian Nocardia species and sunflower phytoremediation for remediate the PAHs and heavy metal contaminated soils.

MATERIALS AND METHODS: 36 soil samples from Fars Province, Iran, were analyzed to isolate bioremediating Nocardia species using turbidometric, chromatographic, biochemical, molecular, and enzymatic assays. Greenhouse experiments used soil spiked with PAHs (100–200 mg/kg) and heavy metals (As, Hg, Cd, Pb, Cr; 3–400 mg/kg) at low, medium, and high levels. Five treatments—control, phytoremediation (P), bioremediation (B), combined phytoremediation and bioremediation (MB), and sterile control, were assessed over 90 days, analyzing soil properties, contaminant levels, plant growth, TF, and BAF.

RESULTS AND DISCUSSION: 13 Nocardia isolates (36.11%) from eight species were identified. N. farcinica (85%), N. otitidiscaviarum (82%), and N. cyriacigeorgica (80%) led in PAH degradation; N. wallacei (75%), N. kruczakiae (70%), and N. cyriacigeorgica (65%) excelled in heavy metal removal. A consortium of these five species in the MB treatment achieved 84.5–92.3% PAH degradation and 69.7–78.9% heavy metal removal, significantly outperforming B (76.8–85.6%, 63.4–72.5%), P (55.2–65.4%, 48.6–58.7%), and controls (p 0.001). MB enhanced soil fertility (OC: 1.8%, TN: 42 mg/kg), microbial activity, and reduced metal translocation (TF/BAF: 0.20–0.60). Integrated phytoremediation and Nocardia bioremediation offers a sustainable strategy for remediating multi-contaminated soils in industrial and agricultural settings.

Keywords: Bioremediation, Nocardia, sunflower, PAHs, heavy metals, soil remediation,

Investigating the Action Mechanisms of Cationic Antimicrobial Peptides

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BACKGROUND AND OBJECTIVES: Multidrug-resistant bacteria are emerging as a serious global challenge. Researchers are exploring alternative solutions, including the use of natural antibiotics derived from living organisms. Antimicrobial peptides (AMPs) denote a promising agent in this effort. Hence, to recognize the mechanism of the peptides, it is critical to study the dynamics and structural changes of the cell membrane in the presence of the peptide. Herein, the dynamics and structural properties of model membranes (including DOPC-DOPE (7:3) and POPE-POPG (1:2) have been studied in the presence of antimicrobial and anticancer peptides.

MATERIALS AND METHODS: The interaction of the peptides with the different membranes was studied by performing an all-atom molecular dynamics (MD) simulation. The initial lipid bilayer structures and their topologies were created using the CHARMM-GUI web tool. All analyses were performed by the GROMACS package and FATSLiM, and GridMAT.

RESULTS AND DISCUSSION: In the DOPC-DOPE (7:3) bilayer, the peptide revealed an increased helical structure, suggesting enhanced stabilization. Conversely, minimal changes were observed in the helical percentage within the POPE-POPG (1:2) membrane. Moreover, the slope of the peptide at the end of the simulation was lower in the DOPC-DOPE (7:3) bilayer compared to POPE-POPG (1:2), likely due to interactions between the peptide's cationic residues and the negatively charged surface of the POPE-POPG (1:2) membrane. • Conclusion These results provide valuable insights into peptide-membrane interactions and offer a foundation for developing non-toxic antimicrobial peptides tailored to mammalian physiology. Such developments could pave the way for innovative treatments to combat multidrug-resistant bacteria effectively.

Keywords: Multidrug-resistant, Antimicrobial peptides, Molecular dynamics simulation

Investigating the effect of aqueous and alcoholic extracts of Otostegia persica on the growth and expression of enterotoxin genes (SEA) of Staphylococcus aureus

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BACKGROUND AND OBJECTIVES: Staphylococcus aureus is a significant pathogen that can cause severe infections and complications in humans. The bacterium is responsible for serious health issues due to the production of enterotoxins such as SEA. Hence, the aim of this study was to investigate the effects of aqueous and alcoholic extracts of the Otostegia persica on the growth and expression of the gene.

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

RESULTS AND DISCUSSION: Among the 100 samples examined, 19 isolates of Staphylococcus aureus were identified. Staphylococcus aureus exhibited the highest antibiotic resistance to penicillin (100%) and the lowest resistance to gentamicin (36.84%). The investigation of the effects of Otostegia persica extracts indicated that these extracts have the capability to reduce the expression of SEA gene. Due to drug resistance, it is essential to discover new antimicrobial compounds, with minimal side effects. The findings suggest that the aqueous extract of this plant can be utilized as a therapeutic option to reduce the expression of evaluated gene.

Keywords: Staphylococcus aureus, Enterotoxin SEA, Otostegia persica.

Investigating the Effect of Cold Atmospheric Plasma on the Growth Candida albicans Strain ATCC10231.

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BACKGROUND AND OBJECTIVES: Candida albicans, a prevalent opportunistic fungal pathogen, causes a spectrum of infections in humans, complicated by its biofilm-forming capability and increasing resistance to azole antifungals. Atmospheric cold plasma (CAP), a non-thermal, non-pharmacological technology, exhibits promising antifungal properties. Combining CAP with conventional antifungals like fluconazole may enhance therapeutic efficacy.

MATERIALS AND METHODS: The reference strain Candida albicans ATCC10231, sourced from the Pasteur Institute's microbial bank, was cultured for 48 hours. Fungal cells were exposed to CAP for durations of 90, 120, 180, and 210 seconds, with an untreated group as the control. Parallel treatments included fluconazole alone and in combination with CAP. the minimum inhibitory time was determined based on growth reduction. Ergosterol content and biofilm formation was evaluated across all groups.

RESULTS AND DISCUSSION: CAP treatment significantly reduced fungal growth and fungal biomass in a time-dependent manner, with 90 seconds identified as the minimum inhibitory time. The combination of CAP and fluconazole exhibited a synergistic effect, resulting in greater inhibition of fungal growth and biofilm formation compared to individual treatments. Ergosterol content was also significantly reduced in the combined treatment group. The synergistic interaction between atmospheric cold plasma and fluconazole offers a promising approach to inhibit Candida albicans growth and biofilm formation, potentially addressing challenges posed by antifungal resistance. Further clinical studies are warranted to validate these findings.

Keywords: Keywords: Candida albicans, atmospheric cold plasma, fluconazole, antifungal resistance, synergistic

Investigating the Effect of Probiotics on Oral Microbiome and Antibiotic Resistance Reduction in Dogs and Cats

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BACKGROUND AND OBJECTIVES: The oral microbiome in dogs and cats plays a crucial role in maintaining oral health, and imbalance in this microbiome can lead to gum diseases, tooth decay, and bacterial infections. With the increased use of antibiotics, bacterial resistance to these drugs is spreading, making the treatment of many oral infections challenging. In this context, probiotics have been introduced as a novel approach to improving the balance of the oral microbiome and combating antibiotic-resistant bacteria. The aim of this study is to investigate the impact of probiotics on oral microbiome changes and antibiotic resistance reduction in dogs and cats

MATERIALS AND METHODS: 30dogs and 30 cats were divided into an experimental group (receiving Lactobacillus rhamnosus GG probiotics) and a control group. The experimental group received daily probiotics for 4 weeks. Saliva samples were collected before and after treatment to identify oral bacteria. Antibiotic resistance was measured using the disk diffusion method, and microbiome changes were analyzed through 16S rRNA sequencing. Data were analyzed using statistical tests, and ethical guidelines were followed.

RESULTS AND DISCUSSION: After four weeks of probiotic treatment, the experimental group showed a significant reduction in antibiotic-resistant bacteria and an increase in beneficial bacteria like Lactobacillus and Bifidobacterium. The control group showed no notable changes. Antibiotic susceptibility tests revealed improved bacterial sensitivity in the experimental group. These results suggest that probiotics can improve the oral microbiome balance in dogs and cats, reduce antibiotic resistance, and support oral health, aligning with previous studies on probiotics' benefits in controlling oral infections.

Keywords: Probiotics,Antibiotic resistance, Oral microbiome, Bacterial diversity

Investigating the Effects of Various pH Levels on Human Prion Protein Using Molecular Dynamic Simulation

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BACKGROUND AND OBJECTIVES: Prion diseases are a group of neurodegenerative disorders caused by the misfolding of prion proteins, leading to severe neurological dysfunction. Human prion protein (HuPrP) plays a crucial role in these diseases, and its stability and conformation are influenced by various environmental factors, including pH. Understanding how pH affects HuPrP is vital for developing effective therapeutic strategies.

MATERIALS AND METHODS: In the present work, using the coordinate file of PrPC (available on the PDB) as a starting structure, separate molecular dynamic simulations were carried out at various pH levels in an explicit water box at 37°C and 1 atmosphere pressure for 100ns second period.

RESULTS AND DISCUSSION: Molecular dynamics simulations were conducted across a range of pH levels to assess the conformational changes in HuPrP. The results show that at low pH, the protein exhibits significant denaturation, characterized by increased root mean square deviation (RMSD) and decreased hydrogen bonding. Conversely, at high pH levels, the protein experiences alterations in its secondary structure, affecting its overall stability. The analysis of interaction networks among amino acids indicates that pH-induced changes disrupt critical interactions, which could lead to functional impairment. These findings suggest that maintaining an optimal pH range is essential for the structural integrity and functionality of HuPrP. The implications of these results extend to understanding the pathogenesis of prion diseases, as pH fluctuations in the cellular environment may contribute to pathological misfolding. Further research is needed to explore the implications of these findings in vivo and their potential role in prion disease progression.

Keywords: Prion protein, pH, MD Simulation

Investigating the Link Between Agr Type and Beta-Lactamase Gene in S. pseudintermedius from Broiler Chickens

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BACKGROUND AND OBJECTIVES: We tried to find S. pseudintermedius in broilers, check how often the beta-lactamase gene (blaZ) was found and make a link between different agr types and how blaZ is made. We took 50 samples from the noses of broilers. We confirmed S. pseudintermedius using PCR for the nuc gene. The antibiotics test showed that 63% of the blaZ positive bacteria were resistant to penicillin. We wanted to know what group the blaZ positive bacteria fit into and did this with a Multiplex PCR. The results showed most of the bacteria fit into groups I (70%), II (21%) and IV (9%). No bacteria fit into group III. We found the blaZ gene was much more active in bacteria from group I than the other groups ($p \leq 0.05$). This means that the agr factor has a strong effect on the beta-lactamase make in S. pseudintermedius.

MATERIALS AND METHODS: Nasal swabs from 50 broilers were taken.S.pseudintermedius was found with PCR that looked for the nuc gene. Antibiotic suscep was tested with the Kirby Bauer method. The gene blaZ was found with PCR. Agr typing of blaZ positive isolates was done using Multiplex PCR. They were put in groups I, II and IV. The fold change was found between agr groups. The difference was found with stats at $p \leq 0.05$.

RESULTS AND DISCUSSION: Our work links agr I to make the S. pseudintermedius in chicken S. pseudintermedius make more blaZ. This is the first time the S. pseudintermedius was found in the nose of a chicken.

Keywords: agr,blaZ,broiler,Staphylococcus pseudintermedius,pcr

Investigating the Prevalence of Extended-spectrum beta-lactamase Escherichia coli and Klebsiella pneumoniae isolated from Urinary Tract Infections In Karaj, Iran

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BACKGROUND AND OBJECTIVES: Urinary tract infections (UTIs) are recognized as one of the most common infectious diseases in the world and are a severe public health problem. Among the uropathogens, Escherichia coli and Klebsiella pneumoniae are the most common bacteria in both the community and hospital infections. The prevalence of extended-spectrum beta-lactamase (ESBL)-producing E.coli and K.pneumoniae UTIs is increasing worldwide. The purpose of this study was to determine the prevalence of UTIs caused by extended-spectrum beta-lactamase E.coli and K.pneumoniae

MATERIALS AND METHODS: In this study, 15153 consecutive patients with symptomatic and asymptomatic UTI were investigated for urinary tract infections attending Behnoud Molecular and Pathobiology Laboratory, Karaj from March 2022 to March 2025. Clean-catch midstream urine samples were collected and processed in the microbiology laboratory, using standard microbiological methods. Identification of ESBLs Antimicrobial susceptibility testing was performed by the double-disc synergy test, according to CLSI guidelines.

RESULTS AND DISCUSSION: A total of 607 E.coli and 85 K. pneumoniae isolates were collected from patients with UTIs. ESBL-harboring E.coli and K.pneumoniae were 337 (55.5%) and 28 (32.9%) isolates, respectively. ESBL-producing E.coli and K.pneumoniae isolates were mostly collected from female patients. ESBL-producing E.coli and K.pneumoniae isolates increased from 2022 to 2025. In this study, the rate of antibiotic resistance was high, and the prevalence of UTI caused by ESBL-producing bacteria has increased in Karaj. ESBL-producing E.coli was most commonly isolated from urine. Identification of these isolates are essential to find effective antibiotics and eliminate the infection.

Keywords: Urinary tract infection, ESBL-Escherichia coli, ESBL-Klebsiella pneumoniae, Antimicrobial resistance

Investigating the prevalence of Prevotella and Veillonella bacteria in the saliva of healthy people and heart patients by molecular method

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BACKGROUND AND OBJECTIVES: The oral microbiome plays an important role in overall health, and disturbances in its composition (dysbiosis) can be linked to systemic diseases, including cardiovascular diseases. Prevotella and Veillonella species are two major bacterial groups in the oral microbiome. These bacteria show higher relative abundance in both health and disease. This study aimed to determine the prevalence of Prevotella and Veillonella in the saliva of healthy individuals and cardiovascular patients using a molecular method. The main objective was to identify differences in abundance between the two groups and examine their possible role in cardiovascular diseases. These findings may help better understand the link between oral microbiome and heart health.

MATERIALS AND METHODS: In this study, 103 saliva samples were collected from patients suspected of having cardiovascular disease. Then, DNA extraction was performed using an extraction kit, and the abundance of Prevotella and Veillonella species was evaluated using Real-Time PCR.

RESULTS AND DISCUSSION: Out of 103 saliva samples from patients, 53 individuals were categorized as healthy. Among healthy individuals, Prevotella species were found in 51 cases, and Veillonella species in 44 cases. The remaining 50 individuals were classified as cardiovascular patients, in whom Prevotella species were found in 48 cases and Veillonella species in 38 cases. Given the high prevalence of Prevotella and Veillonella species in the saliva of both healthy and cardiovascular patients, these findings suggest a strong association between changes in the oral microbiome and cardiovascular diseases. Moreover, further investigation of these bacteria may assist in early diagnosis and prevention of cardiovascular diseases.

Keywords: Oralmicrobiome,cardiovascular diseases,dysbiosis,Prevotella, Veillonella

Investigating the relationship between clinical symptoms of patients suspected of pulmonary tuberculosis and the final laboratory diagnosis

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BACKGROUND AND OBJECTIVES: Pulmonary tuberculosis is one of the most important infectious diseases. Although diagnostic technology has advanced, the accurate and differential diagnosis of pulmonary tuberculosis remains challenging. This study aimed to determine the relationship between clinical symptoms and laboratory diagnosis of pulmonary tuberculosis.

MATERIALS AND METHODS: This study was conducted on patients suspected of having pulmonary tuberculosis who were referred to Shahid Beheshti and Sina Farshchian hospitals in Hamedan and the Hamedan Province TB Reference Laboratory from April to March 2024. Data analysis was performed using SPSS-26 software and using t-test, Chi-square, and Fisher tests.

RESULTS AND DISCUSSION: A total of 1481 participants with a mean and standard deviation of 52.64±15.54 years of age were included. The present study showed that weight loss, bloody sputum, chronic obstructive pulmonary disease, and fatigue were significantly more common, a history of tuberculosis and bronchiectasis was significantly more common in patients with pulmonary tuberculosis than in those without. Chest pain was more common in those without tuberculosis than in those with pulmonary tuberculosis. In contrast, chronic cough, shortness of breath, and fever, despite their high prevalence, did not show a statistically significant difference between the affected and non-infected groups. These findings emphasize the need to emphasize laboratory methods (culture and PCR) along with clinical evaluation for a more accurate diagnosis of tuberculosis. Identification of more specific symptoms (such as bloody sputum and weight loss) can help in more targeted screening.

Keywords: Pulmonary tuberculosis, clinical findings, laboratory findings

Investigating the specific inhibitory level and pharmacological properties of Shirazi thyme (Zataria multiflora) essential oil compounds on carbapenemase KPC-2 of Klebsiella pneumoniae by molecular docking tools

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BACKGROUND AND OBJECTIVES: The emergence and spread of drug resistance in bacteria has become one of the major challenges in the treatment and control of infectious diseases. According to studies, thyme (Zataria multiflora) essential oil has antimicrobial properties against both Gram-positive and Gram-negative bacteria. Klebsiella pneumoniae is a multidrug-resistant Gram-negative bacterium that causes various infections. Here, we intend to investigate the inhibitory potential of compounds present in natural thyme essential oils on the KPC-2 enzyme present in the MDR K. pneumoniae.

MATERIALS AND METHODS: We performed molecular docking of vaborbactam and 40 Zataria multiflora essential-oil constituents against the KPC-2 crystal structure (PDB: 7TI2), calculating binding free energies (ΔG) and ligand efficiencies. Top candidates underwent in silico ADMET profiling to assess absorption, distribution, metabolism, excretion, and toxicity parameters.

RESULTS AND DISCUSSION: Results: Vaborbactam displayed a ΔG of –5.9 kcal/mol. Isospathulenol and Ent-spathulenol exhibited stronger binding (–6.9 and –6.8 kcal/mol) with ligand efficiencies of 0.4313 and 0.4250, respectively, while (+)-aromadendrene showed moderate affinity (–6.5 kcal/mol). ADMET analysis revealed high intestinal absorption (93%), favorable volume of distribution (log VDss ~0.58), non-substrate status for P-glycoprotein, minimal cytochrome P450 inhibition except for CYP2C9 and CYP2C19, and absence of hERG liability or hepatotoxicity for indicated compounds. Also, acute and chronic toxicity endpoints were within acceptable ranges. Conclusion: Isospathulenol and Ent-spathulenol emerge as promising scaffolds for KPC-2 inhibition, warranting further in vitro validation and structural optimization to combat carbapenem-resistant K. pneumoniae.

Keywords: Essential oil of Zataria multiflora, blaKPC gene, KPC-2, Vaborbactam, Klebsiella

Investigation of a number of pathogenic bacteria isolated from hospitalized patients, environmental sources, medical equipment and devices in Imam Khomeini Educational and Medical Center, Khomein, using PCR, determining their antibiotic pattern using the

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BACKGROUND AND OBJECTIVES: Hospital-acquired infections (HAIs) are significant challenges in healthcare systems, often caused by antibiotic-resistant microorganisms. These infections have a major impact on patient health, treatment costs, and hospital resource utilization. The aim of this study was to examine the prevalence, identification, and antibiotic resistance patterns of pathogenic bacteria isolated from clinical and environmental samples in hospitals.

MATERIALS AND METHODS: A total of 180 clinical samples and 100 environmental samples were collected. The isolates were identified using biochemical and molecular methods, and their antibiotic resistance patterns were assessed using standard testing procedures.

RESULTS AND DISCUSSION: The results revealed that 41% of the samples contained pathogenic bacteria, with Escherichia coli and Klebsiella pneumoniae being the most prevalent pathogens. In environmental samples, Acinetobacter baumannii was the most frequently isolated pathogen. The isolates showed high resistance to cephalosporins and other antibiotics, indicating a significant challenge for treatment. Genetic similarity between clinical and environmental isolates was observed, suggesting cross-transmission of bacteria from the environment to patients. The study underscores the importance of continuous monitoring of the hospital environment and the application of advanced molecular methods for rapid identification of infectious agents. Additionally, targeted antibiotic use and improved hygiene protocols are essential for reducing the prevalence of hospital-acquired infections. This study emphasizes the need for strict infection control measures, including regular disinfection of hospital environments, training healthcare workers, and monitoring antibiotic resistance patterns to minimize the risk of infections and ensure better patient outcomes.

Keywords: Nosocomial Infection, Antibiotic, 16S rRNA, Hospital environment

Investigation of antibacterial and antioxidant properties of bromelain encapsulated in liposome tagged with silver nanoparticles

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BACKGROUND AND OBJECTIVES: Breast cancer and antibiotic-resistant infections by Escherichia coli and Staphylococcus aureus are major health concerns. Silver nanoparticles show strong antimicrobial and anticancer effects, especially when synthesized via eco-friendly methods. Bromelain, with antioxidant and anti-inflammatory properties, enhances these effects. This study evaluated the antibacterial, antioxidant, and anticancer activities of bromelain encapsulated in liposomes with silver nanoparticles against Escherichia coli, Staphylococcus aureus, and MCF-7 breast cancer cells.

MATERIALS AND METHODS: In this study, silver nanoparticles were green-synthesized with apple extract and co-encapsulated with bromelain in liposomes. Their structure was analyzed using FESEM, FTIR, and XRD. Antibacterial effects were tested against Escherichia coli and Staphylococcus aureus, and anticancer activity was assessed on MCF-7 cells. TAC and MDA levels were measured to evaluate antioxidant capacity and oxidative stress.

RESULTS AND DISCUSSION: XRD analysis confirmed the crystalline structure of silver nanoparticles, while FTIR identified functional groups related to bromelain, silver nanoparticles, and liposomes. FESEM images showed suitable morphology, confirming successful encapsulation. The liposomal formulation demonstrated pH-dependent drug release, with faster release under acidic conditions. Antibacterial tests against Escherichia coli and Staphylococcus aureus revealed notable inhibition zones, especially with the silver nanoparticle–bromelain–liposome complex. MIC and MBC assays indicated bromelain had the strongest antibacterial activity. In anticancer studies, the encapsulated complex showed the highest total antioxidant capacity (TAC) in MCF-7 cells, while silver nanoparticles alone increased malondialdehyde (MDA) levels, indicating oxidative stress. MTT assays demonstrated that bromelain, silver nanoparticles, and their encapsulated forms significantly inhibited cancer cell proliferation at higher concentrations.

Keywords: Silver nanoparticles, Bromelain, Liposome, Escherichia coli, Staphylococcus aureus, MCF-7 Cells

Investigation of antibacterial and antioxidant properties of royal gelly encapsulated in liposome tagged with silver ferrite nanoparticles in gram-negative bacteria Escherichia coli and gram-positive bacteria Staphylococcus aureus.

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BACKGROUND AND OBJECTIVES: Background and Introduction: Rising resistance to antibiotics and cancer therapies necessitates innovative treatment strategies. This study investigates the green synthesis of silver ferrite nanoparticles using green apple extract, their encapsulation with royal jelly in nanoliposomes, and their biomedical evaluation. Materials and Methods: Nanoparticles were synthesized and encapsulated using thin-film hydration. Characterization involved FESEM, FTIR, and XRD. Antibacterial activity was tested against Escherichia coli and Staphylococcus aureus. Cytotoxicity on MCF-7 cells was evaluated by MTT assay; antioxidant activity was assessed via MDA and TAC levels. Results: Physicochemical analyses confirmed successful synthesis and encapsulation. The nanoformulation showed enhanced antibacterial efficacy and dose-dependent cytotoxicity on MCF-7 cells. Elevated MDA and TAC levels indicated oxidative stress induction and activation of antioxidant responses. Conclusion: The combination of silver ferrite nanoparticles and royal jelly, particularly through liposomal encapsulation, demonstrated strong antimicrobial and anticancer potential, suggesting their suitability for nanomedical applications. Keywords: Silver ferrite, Royal jelly, Liposome

MATERIALS AND METHODS: Nanoparticles were synthesized and encapsulated using thin-film hydration. Characterization involved FESEM, FTIR, and XRD. Antibacterial activity was tested against Escherichia coli and Staphylococcus aureus. Cytotoxicity on MCF-7 cells was evaluated by MTT assay; antioxidant activity was assessed via MDA and TAC levels

RESULTS AND DISCUSSION: Physicochemical analyses confirmed successful synthesis and encapsulation. The nanoformulation showed enhanced antibacterial efficacy and dose-dependent cytotoxicity on MCF-7 cells. Elevated MDA and TAC levels indicated oxidative stress induction and activation of antioxidant responses.

Keywords: Silver ferrite, Royal jelly, Liposome, Antibacterial, Cytotoxicity

Investigation of antibiotic resistance, biofilm formation ability, virulence factors, and molecular typing of Klebsiella oxytoca strains isolated from patients hospitalized in Hamadan hospitals

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BACKGROUND AND OBJECTIVES: Klebsiella oxytoca, a gram-negative bacterium, causes infections in hospitalized patients, especially newborns, affecting blood, urinary tract, lungs, and skin. It forms biofilms, reducing antibiotic effectiveness, and shows multi-drug resistance. This study examines its antibiotic resistance, biofilm formation, virulence factors, and molecular typing in Hamedan hospital isolates.

MATERIALS AND METHODS: In a cross-sectional study, 35 Klebsiella oxytoca samples from Hamedan hospitals were analyzed. Isolates were identified using standard microbial and biochemical tests. Antibiotic resistance was assessed via disk diffusion per CLSI 2022 guidelines. Biofilm formation was evaluated using the crystal violet method in microplates. Virulence genes were detected by PCR, and molecular typing was performed using ERIC PCR. Statistical analysis was conducted with SPSS (version 22) and the Chi-square test. 1.5s

RESULTS AND DISCUSSION: Out of a total of 35 Klebsiella Oxytoca clinical samples, the highest antibiotic resistance is related to ciprofloxacin antibiotic (91.4%) and the lowest resistance is related to amikacin (31.4%). In this study, 14 (40%) clinical samples did not form biofilm. Biofilm formation was observed in 10 (28.5%) samples with weak strength, 5 (14.2%) with medium strength and in 6 (17.1%) samples with high strength. Also, according to the PCR results of 35 Klebsiella oxytoca clinical isolates, the amount of bacterial virulence genes, respectively fimA, matB, mrkA, npsB and pilQ genes (77.1%), (42.8%), (65.7%), (22.8%)) and (57.1%) are there. And the results of ERIC-PCR analysis of Klebsiella oxytoca isolates showed the existence of genetic diversity among these isolates.

Keywords: biofilm, antibiotic resistance, virulence genes, molecular typing, Klebsiella oxytoca

Investigation of Antifungal Resistance and Virulence Factors of Candida albicans Isolated from Non-Hematologic Cancer Patients

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BACKGROUND AND OBJECTIVES: Candidiasis has increased due to immunosuppression and medical interventions. Candida causes most hospital fungal infections with high mortality in immunocompromised patients. Rising antifungal resistance, especially to azoles, is a major challenge. This study assesses drug resistance and virulence of Candida albicans in solid organ cancer patients.

MATERIALS AND METHODS: The study examined drug susceptibility to fluconazole, voriconazole, amphotericin B, and caspofungin, along with phospholipase activity and biofilm formation in 40 Candida albicans isolates from cancer patients' non-blood samples. Identification used CHROMagar, and virulence factors including phospholipase, proteinase, and biofilm were assessed.

RESULTS AND DISCUSSION: Among the isolates, 40 Candida albicans strains demonstrated high sensitivity to all four antifungal agents following incubation. Nine isolates exhibited phospholipase activity, and all isolates showed the ability to form biofilms.

Keywords: C.albicans,drug,biofilm,pathogenic, analysis, Candidiasis

Investigation of antimicrobial resistance patterns and related genes in methicillin-resistant Staphylococcus aureus clinical isolates in Bushehr, Iran

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BACKGROUND AND OBJECTIVES: Methicillin-resistant Staphylococcus aureus (MRSA) remains a global health threat due to its resistance to multiple antibiotic classes and its association with severe clinical outcomes. This study aimed to characterize the antimicrobial resistance patterns and the distribution of resistance-associated genes in MRSA clinical isolates from Bushehr, Iran.

MATERIALS AND METHODS: A total of 160 S. aureus isolates were collected from three hospitals between November 2023 and September 2024. Initial identification was performed using biochemical tests and confirmed by PCR targeting the nucA gene. MRSA isolates were screened via cefoxitin disk diffusion and confirmed by detection of mecA gene and SCCmec typing. Antimicrobial susceptibility testing was assessed using disk diffusion and vancomycin agar screen methods. PCR and sequencing were used to detect blaZ, ermC, aac(6′)-Ie-aph(2″), ant(4′)-Ia, aph(3′)-IIIa, tetK, tetM, tetL, and vanA resistance genes.

RESULTS AND DISCUSSION: Of the total isolates, 44 (27.5%) were confirmed as MRSA. SCCmec typing revealed that 70.45% of MRSA isolates belonged to type IV, followed by types IVc (20.45%) and V (13.63%). All MRSA isolates were susceptible to rifampin, linezolid, ceftaroline, and vancomycin. High resistance was observed to penicillin (90.91%), cefoxitin (90.09%), and erythromycin (70.45%). The prevalence of resistance genes among MRSA isolates was: blaZ (47.72%), ermC (29.5%), tetL (15.9%), aph(3′)-IIIa (13.63%), tetK (9.09%), and ant(4′)-Ia (2.27%). The predominance of SCCmec type IV and its high rate of multidrug resistance (87.09%) underscore the growing public health risk posed by community-acquired MRSA in Bushehr. These findings emphasize the need for regional antimicrobial resistance monitoring and infection control strategies.

Keywords: Staphylococcus aureus, MRSA, SCCmec typing, MDR

Investigation of bacterial and fungal infectious causes of otitis in dogs and cats of specific breeds and determination of antibiotic sensitivity in vitro

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BACKGROUND AND OBJECTIVES: Otitis externa is the swelling and inflammation of the external ear canal. Following swelling and inflammation of the external ear, the natural environment of the canal undergoes changes. Clinical signs are more indicative of middle ear infection. These signs of disease in the middle ear area, especially in cats, are often subclinical or mild, but in dogs, the symptoms are more indicative of concurrent otitis externa.

MATERIALS AND METHODS: A study was conducted on 30 dogs and 30 cats of different ages, sexes, and breeds. Samples isolated from ear secretions of dogs and cats referred to Avina Veterinary Hospital in Tehran were sent to the laboratory to identify the pathogens present. Bacterial examination Swabs taken from animals were cultured in blood agar and Mueller-Hinton agar. Antibiotic discs of ampicillin, cefazolin, gentamicin, piperacillin, imipenem, ciprofloxacin, amikacin, and erythromycin were used. Surface culture in sabrodextrose agar was used to identify fungi. Antifungal discs of fluconazole, itraconazole, clotrimazole, and econazole were used.

RESULTS AND DISCUSSION: The fungi isolated from dogs are sensitive to: Penicillium (sensitive to itraconazole), Rhodotrola (sensitive to econazole), Geotrichum (sensitive to clotrimazole), Alternaria(sensitive to fluconazole), Elocladium (sensitive to itraconazole), Aspergillus(sensitive to itraconazole), Cladosporium(sensitive to itraconazole), and in the ear secretions of cats, the fungi are Aspergillus(sensitive to itraconazole), Penicillium (sensitive to itraconazole), Rhodotrola(sensitive to econazole), and Geotrichum(sensitive to clotrimazole).

Keywords: Keywords: dog ear, cat ear, otitis, fungal flora, otitis media

Investigation of drug resistance status of Helicobacter pylori to clarithromycin and of rfaF and 23S rRNA genes mutations

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BACKGROUND AND OBJECTIVES: Introduction: Helicobacter pylori is a Gram-negative, spiral-shaped bacteria that lives in the human stomach. It is the main cause of chronic gastritis, peptic ulcers, and stomach cancer. A major problem in treating H. pylori is the growing resistance to antibiotics, especially clarithromycin, which is a key drug in first-line treatment regimens. Point mutations in the 23S rRNA and rfaF genes cause antibiotic resistance to clarithromycin.

MATERIALS AND METHODS: Methods: Stomach biopsy samples were collected from adult patients. The homogenized samples were grown under microaerophilic conditions for H. pylori isolation. The bacterial isolates were characterized using biochemical tests and confirmed by PCR . Clarithromycin resistance was measured using the Epsilometer test (E-test). To study the genetic causes of resistance, the 23S rRNA and rfaF genes were amplified by PCR and sequenced to find mutations linked to resistance.

RESULTS AND DISCUSSION: Results: From 765 biopsies, 165 isolates of H. pylori were detected (21.5%). Among these, 68% showed resistance to clarithromycin. Genetic analysis found known mutations, such as A2142G in the 23S rRNA gene, as well as new mutations, including A2056G, A2055G, T2095C, and A2213G. All these mutations were strongly linked to resistance. Analysis of the rfaF gene showed different patterns of mutations between resistant and sensitive strains. Conclusion: The rise of clarithromycin-resistant H. pylori strains makes treatment more difficult. Misuse of antibiotics has made this problem worse. Developing new drugs and managing antibiotic use carefully are also important to control resistance and reduce diseases caused by H. pylori.

Keywords: Keywords: Helicobacter pylori, clarithromycin-resistance, 23S rRNA, rfaF, Antibiotic susceptibility

Investigation of human T-lymphotropic virus type 1 (HTLV-1) and Helicobacter pylori cagA gene presence in colorectal cancer compared to the control group using ELISA and PCR methods in Northwest Iran

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BACKGROUND AND OBJECTIVES: Colorectal cancer (CRC) is the second leading cause of cancer-related deaths worldwide. This study was conducted to investigate the association between HTLV-CagA gene of the bacterium Helicobacter pylori (H. pylori) in patients with CRC.

MATERIALS AND METHODS: In this descriptive cross-sectional study, 50 cancerous samples, including blood and paraffin-embedded tissue specimens, along with 50 control samples, were collected over a seven-month period from September to March 2025. The samples were analyzed using polymerase chain reaction (PCR) and enzyme-linked immunosorbent assay (ELISA) methods.

RESULTS AND DISCUSSION: In the demographic results, the gender distribution among patients was balanced (54% male and 46% female), with a mean age of 59.98 ± 8.31 years at the time of colorectal cancer diagnosis, while the control group had a mean age of 52.38 ± 12.27 years. HTLV-1 antibodies were detected in 3% of cancer patients, and 20% were positive for H. pylori infection. However, no cases of co-infection with both HTLV1 and CagA were identified. Ultimately, statistical analysis showed no significant association between these infectious agents and the incidence of CRC ($p = 0.372$). This study found no statistically significant association between HTLV-1 infection and the cagA gene of H. pylori with the incidence of colorectal cancer. However, certain clinical findings such as advanced tumor stages in HTLV-1 positive patients and the correlation between H. pylori infection and family history highlight the need for further investigation.

Keywords: Human T-lymphotropic virus 1, Helicobacter pylori, colorectal neoplasm, coinfection

Investigation of Inducible Clindamycin Resistance and Macrolide Resistance Genes in Clinical Isolates of Staphylococcus aureus from Bushehr, Iran

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BACKGROUND AND OBJECTIVES: Staphylococcus aureus is a major cause of nosocomial and community-acquired infections worldwide. Resistance to macrolide-lincosamide-streptogramin B (MLSB) antibiotics, especially inducible clindamycin resistance, poses a significant therapeutic challenge. The aim of this study was to determine the prevalence of inducible resistance and detect the presence of macrolide resistance genes among clinical S. aureus isolates in Bushehr, Iran.

MATERIALS AND METHODS: A total of 160 clinical S. aureus isolates were collected from three hospitals between November 2023 and September 2024. Initial identification was performed using biochemical tests and confirmed by PCR targeting the nucA gene. Antimicrobial susceptibility testing for erythromycin and clindamycin was carried out using the disk diffusion method according to CLSI guidelines. The D-zone test was used to detect inducible clindamycin resistance. PCR assays were performed to detect ermA, ermB, ermC, ereA, ereB, lunA, mphC, msrA, and vgaA genes.

RESULTS AND DISCUSSION: Of the 160 isolates, 67.5% were resistant to erythromycin. Among these resistant isolates, 23.1% exhibited the inducible MLSB (iMLSB) phenotype, 64.8% showed the constitutive MLSB (cMLSB) phenotype, and 12% demonstrated the MSB phenotype. The ermB gene was the most prevalent (38.9%), followed by ermC (21.3%), msrA (9.2%), ermA (2.8%), and mphC (2.8%). No isolates carried ereA, ereB, lnuA, or vgaA. Our findings indicate that ermB is the primary gene associated with macrolide resistance in S. aureus isolates from this region. The high rate of inducible clindamycin resistance underlines the necessity of routine D-zone testing and molecular monitoring to guide effective antimicrobial therapy.

Keywords: Staphylococcus aureus, D-zone test, Macrolide Resistance

Investigation of mixed probiotic in IBD model as a novel helped treatment

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BACKGROUND AND OBJECTIVES: Probiotics are live microorganisms that, when administered in sufficient quantities in an individual's diet, can bring health benefits to them. Given the importance of using probiotics in the treatment of various diseases and the many reported effects and advantages associated with their use, it seems that investigating the effect of a mixture of Lactobacillus plantarum and Bacteroides fragilis in evaluating immune system pathways and gaining insight in this field will be helpful in the treatment and reduction of inflammation in many diseases such as IBD. This study aims to identify potential changes in the expression levels of the secreted cytokines IL-6 and IL-4 as inflammatory and anti-inflammatory cytokine. Initially, the HT-29 colon cancer cell line was obtained from the Pasteur Institute of Iran, and subsequently, induced through TNF-alpha for inducing inflammatory similar as IBD patients. Then mixed probiotic treated in cell line to investigate the expression of related cytokines.

MATERIALS AND METHODS: Standard bacterial strains were obtained from the microbial bank of the Pasteur Institute of Iran and will be cultured on MRS and BBE specialized media.

RESULTS AND DISCUSSION: The decrease in IL-4 expression compared to the control group was significant, and probiotics play a role in modulating immune responses, and in relation to IL-6 , Bacteroides fragilis, unlike Lactobacillus plantarum, had an increase in expression compared to the control group. This indicates a high inflammatory or immunogenic potential of this strain in this model.

Keywords: Probiotic, Bacteroides fragilis, Lactobacillus plantarum, IBD

Investigation of Peppermint (Mentha piperita) Extract on the Inhibition of Biofilm Formation by Acinetobacter baumannii Strains Isolated from Clinical Samples

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BACKGROUND AND OBJECTIVES: Acinetobacter baumannii is a hospital-acquired opportunistic pathogen, with biofilm formation playing a crucial role in its multidrug resistance. Given the rise in antibiotic resistance, herbal medicines, including peppermint (Mentha piperita), have gained attention for their potential antibacterial properties.

MATERIALS AND METHODS: A total of 25 A. baumanniistrains were isolated from clinical samples at the Faculty of Allied Medical Sciences, Tehran. Their biofilm-forming ability and antibiotic susceptibility against nine antibiotics were assessed using the disk diffusion method. The antibacterial activity of peppermint extract was evaluated by well diffusion, with its minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) compared to ciprofloxacin. Synergistic effects between the extract and ciprofloxacin were analyzed, followed by a time-kill assay. Polymerase chain reaction (PCR) was used to detect the presence of PgaA and AbaI genes linked to biofilm formation.

RESULTS AND DISCUSSION: The study found that 88% of A. baumannii strains exhibited strong biofilm formation. Peppermint extract effectively inhibited biofilm formation, with MIC values ranging from 1.5 to 6 mg/mL (mean MIC: 3.75 ± 1.38 mg/mL) and MBC values equivalent to their respective MIC concentrations. For ciprofloxacin, the MIC for all samples was greater than 2048 mg/mL. No significant synergistic effect was observed between peppermint extract and ciprofloxacin. Both PgaA (involved in biofilm matrix synthesis) and AbaI (quorum sensing-related autoinducer synthase) genes were present in all tested strains.Peppermint extract demonstrates biofilm-inhibitory properties against A. baumannii, suggesting its potential as an alternative therapeutic approach for combating biofilm-associated infections.

Keywords: Acinetobacter baumannii,Biofilm,Mentha piperita,Peppermint,PCR

Investigation of phenotypic and genotypic characteristics of Escherichia coli strains isolated from recurrent urinary tract infections

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BACKGROUND AND OBJECTIVES: Uropathogenic Escherichia coli (UPEC) is the primary pathogen responsible for urinary tract infections (UTIs), and the recurrence of these infections presents a substantial challenge to effective treatment. This study aimed to investigate and compare the phenotypic and genotypic features of E. coli isolates from recurrent and non-recurrent UTIs

MATERIALS AND METHODS: E. coli isolates were collected from urine cultures in various hospitals and labs in Hamadan. Confirmed through biochemical tests, these isolates' antibiotic resistance was tested using disk diffusion, biofilm formation was assessed. PCR analyzed virulence genes and phylogroups, with real-time PCR comparing the expression of the adhesion genes

RESULTS AND DISCUSSION: The study found that 27% of E. coli strains isolated from recurrent UTI with higher rates in females and children under 10. Significant differences in underlying diseases and pap gene expression were observed between recurrent and non-recurrent cases. Most strains (77%) were multi-drug resistant. ESBL production was higher in recurrent cases (53%) compared to non-recurrent (42.5%). There were no significant differences in antibiotic resistance, biofilm formation, virulence factors, or phylogroups between groups. Phylogenetic analysis showed a predominance of groups B2 and D and high genetic diversity among the isolates. In conclusion, factors such as high antibiotic resistance, ESBL and MDR strains, female gender, underlying diseases, and elevated pap gene expression may influence UTI recurrence. A broader study is needed for more definitive insights. Understanding these pathogenic mechanisms is crucial for developing targeted prevention and treatment, especially for recurrent UTIs, to reduce disease duration and complications.

Keywords: Recurrent urinary tract infection, Uropathogenic Escherichia coli

Investigation of Potential Inhibitors Targeting Outer Membrane Protein A of Acinetobacter baumannii Using Molecular Docking Analysis

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BACKGROUND AND OBJECTIVES: Acinetobacter baumannii is a gram-negative bacterium that primarily causes hospital-acquired infections in individuals with compromised immune systems. The outer membrane protein A (OmpA) plays a key role in the pathogenicity of this bacterium and contributes to antibiotic resistance. Due to the rising prevalence of multidrug-resistant strains, targeting OmpA represents a promising therapeutic strategy. In this study, molecular docking was utilized to identify potential inhibitors of OmpA.

MATERIALS AND METHODS: The 3D structure of OmpA protein (PDB ID: 6gie) was obtained from the RCSB PDB database. Dipropan-2-yl pyridine-3,5-dicarboxylate ligand (PubChem CID: 62520), along with 50 of its analogs, was retrieved from the PubChem database in SDF format. Molecular docking was performed using Molegro Virtual Docker v.6. The ligand with the lowest binding energy was selected and analyzed using Molegro Molecular Viewer software. Subsequently, the pharmacokinetic properties of the best ligand were evaluated using SwissADME.

RESULTS AND DISCUSSION: The best ligand for OmpA was identified as Pyridine-3-carboxylic acid, 5-(3-hydroxy-3-methyl-1-butynyl)-ethyl ester (PubChem CID: 612616) with a molecular weight of 233.26 g/mol and a binding energy of -105.81 kcal/mol. This ligand formed -2.064 hydrogen bonds. Additionally, the ADME results indicated that this ligand had a LogS score of -2, a lipophilicity of 2.44, a polarity of 59.42, and hydrogen bond donors and acceptors of 1 and 4, respectively. Based on these findings, after further in vitro and in vivo validation, PubChem CID 612616 could be considered a potential candidate for designing inhibitory drugs against the pathogenesis of A. baumannii.

Keywords: Acinetobacter baumannii, Drug Resistance, Molecular Docking.

Investigation of resistance to aminoglycosides and the prevalence of certain aminoglycoside-modifying enzyme genes among clinical isolates of Staphylococcus aureus

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BACKGROUND AND OBJECTIVES: Staphylococcus aureus is known to be a hospital-acquired pathogenic bacteria that can produce a wide range of infections. Aminoglycosides are among the selective drugs used to treat septicemia caused by this bacterium. The aim of this study was to evaluate the resistance to aminoglycosides, the frequency of aminoglycosides modifing enzy genes and the synergistic effect of some antibiotics on aminoglycoside resistant Staphylococcus aureus isolates.

MATERIALS AND METHODS: In this study, the resistance of 50 isolates of multi drug resistant Staphylococcus aureus to aminoglycosides were investigated by disc diffusion method and MIC determination. The frequency of aac(6')-Ie-aph(2") and aph(3')-IIIa genes in resistant isolates were determined by PCR. The synergistic effect of gentamicin, ciprofloxacin and ceftazidime on resistant isolates of Staphylococcus aureus was investigated by disc diffusion method and MIC determination.

RESULTS AND DISCUSSION: Out of 50 isolates, 74.5% were resistant to gentamycin and 87.2% were resistant to kanamycin. In the genotypic study, the frequency of aac(6')-Ie-aph(2") and aph(3')-IIIa genes were 70% and 93%, respectively. MIC of gentamicin in resistant isolates ranged from 250-2000 µg / ml. The use of gentamicin in combination with ciprofloxacin and ceftazidime reduced the effective concentration of both antibiotics. The results showed high resistance to aminoglycosides in multi drug resistant Staphylococcus aureus strains and high frequency of aac(6')-Ie-aph(2") and aph(3')-IIIa aminoglycoside modifying genes. Also, according to the results of this study, the concomitant use of gentamicin with ciprofloxacin and ceftazidime antibiotics can be effective in the treatment of Staphylococcal infections.

Keywords: S. aureus, aminoglycosides, synergism, aac(6')-Ie-aph(2") and aph(3')-IIIa genes

Investigation of Staphylococcus aureus in synovial fluid from patients with Septic arthritis in educational hospitals of Mazandaran University of Medical Sciences

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BACKGROUND AND OBJECTIVES: This study aimed to investigate the prevalence of Staphylococcus aureus in the synovial fluid of patients with septic arthritis hospitalized in the teaching hospitals of Mazandaran University of Medical Sciences. Septic arthritis is a significant infectious joint disease that can lead to joint destruction and severe complications if not promptly treated. The most common causative agent is Staphylococcus aureus.

MATERIALS AND METHODS: This descriptive-cross-sectional study was2023-2024 conducted on 230 synovial fluid samples from patients with septic arthritis. Samples were analyzed using specific culture media, and final identification was performed through culture and laboratory tests to detect the nuc gene. Data were analyzed using SPSS software.

RESULTS AND DISCUSSION: Among the 230 patients, 66.5% were male, and 33.5% were female. The most commonly affected joint was the knee (53.5%), followed by the shoulder and elbow. Out of 20 positive cultures, 12 cases (60%) were identified as Staphylococcus aureus. A significant correlation was observed between patients' age and positive culture results (P=0.043). Staphylococcus aureus was identified as the most common infectious agent in septic arthritis. These findings underscore the importance of rapid and accurate diagnosis of joint infections to prevent long-term complications. Future studies are recommended to focus on identifying antibiotic resistance patterns.

Keywords: Staphylococcus aureus, septic arthritis, synovial fluid, Mazandran

Investigation of the anticancer properties of hydatid cyst fluid in induced with breast cancer

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BACKGROUND AND OBJECTIVES: Hydatid cyst is the larval stage of Echinococcus granulosus, which leads to humoral and cellular immune responses in the host. We aim to investigate the effect of HCF and Antigen B (AgB) on 4T1 breast cancer cells in BALB/c mice.

MATERIALS AND METHODS: AgB was obtained using a boiling water bath for 15 min and centrifuged at Polyacrylamide gel electrophoresis for 60 minutes with 12.5% sodium dodecyl sulfate (SDS PAGE) and Coomassie brilliant blue staining It was used to evaluate presence and quality. Mouse breast adenocarcinoma cell line (4T1) was cultured in rpmi medium and fetal bovine serum was added to it along with L-glutamine. 36 mice were divided into 4 groups, the first group was given PBS and the second, third, and fourth groups were injected intraperitoneally with concentrations of 100, 200, and 300 µg/ml of HCF and AgB in 100 µl of PBS along with naltrexone adjuvant.

RESULTS AND DISCUSSION: The results indicated that the mice that received different concentrations of the desired antigen along with the adjuvant had a significantly smaller tumor size compared to the control group, and the higher the injection dose, the smaller the tumor size. Was more Also, the level of Th1 cytokines was increased compared to the control group. On the other hand, the level of Th2 cytokines showed a significant decrease.

Keywords: anticancer, hydatid cyst, breast cancer

Investigation of the antimicrobial effects of extracts of Moringa, Garlic, and Shirazi Avyush plants on Staphylococcus aureus bacteria

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BACKGROUND AND OBJECTIVES: The antimicrobial effects of Moringa, Garlic, and Shirazi Ovation plants on Staphylococcus aureus bacteria were investigated. Each of the extracts was administered at concentrations of 200, 400, and 800 mg/mL. Microbial cultivation of Staphylococcus aureus in Petri dishes was performed in 3 replicates. All extracts at a concentration of 800 mg/mL significantly reduced bacterial growth, and at higher concentrations, they killed the bacteria.Shirazi ayush extract, garlic, and moringa can be a suitable alternative to selective antibiotics of plant origin.

MATERIALS AND METHODS: First, plant extracts were prepared and then microbial culture was performed. Microbial culture in Petri dishes was performed in 3 replicates, including 36 treatments. Antimicrobial activity was evaluated using the well method. The diameter of the growth inhibition zone was measured. Antibiogram was performed. The minimum bacterial growth concentration was determined.

RESULTS AND DISCUSSION: Staphylococcus aureus bacteria were tested and studied in the prepared and used dilutions according to the laboratory protocol. Also, in all assay tests, ethanol and dimethyl sulfoxide solution in exactly equal proportions were considered as negative controls and tetracycline and erythromycin antibiotic discs were considered as positive controls. The antimicrobial activity of ethanol extracts was investigated and showed that in all dilutions, 800 mg/mlThey caused a significant reduction in bacterial growth and, at higher concentrations, caused the destruction of these bacteria, which can be concluded that garlic, moringa, and Shirazi olive extracts can be suitable alternatives to selective antibiotics of plant origin.

Keywords: Antimicrobial, Moringa, Garlic, Shirazi Avyush, Staphylococcus aureus bacteria

Investigation of the effect of thymol Liposomal nanocarriers on ERG11 gene expression in fluconazole-resistant Candida albicans clinical isolates

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BACKGROUND AND OBJECTIVES: Today, drug resistance and the antimicrobial effects of natural compounds are of particular importance, and methods for encapsulating such compounds have received attention. Candidiasis is a significant invasive infection. The ERG11 gene plays a role in the development of drug resistance in Candida albicans to fluconazole. Thymol is one of the natural antifungal compounds. This study aims to investigate the effect of thymol on the expression of the ERG11 gene.

MATERIALS AND METHODS: Isolates were investigated for resistance to fluconazole and the ERG11 gene. Thymol was purchased, and nanoliposomes were prepared using the thin film and water method. The release rate, appearance, chemical structure, size, dispersion index, and zeta potential of the nanoliposomes were examined. An antibiogram and the expression of the ERG11 gene were evaluated.

RESULTS AND DISCUSSION: Three resistant Candida albicans isolates were selected. Nanoliposomes were reported to have a size of 185 nm, a diameter of 0.63-0.92 µm, an entrapment percentage of 67.22-86.5%, a dispersion index of 0.195, a surface charge of -41.7 mV, and were characterized as spherical vesicles with smooth and even surfaces. The minimum inhibitory concentration for the three selected isolates 9, 1, and 10 was reported to be 2.156, 2.156, and 39, respectively, and the reduction of ERG11 gene expression was reported to be 1.27, 1.04, and 1.17 times, respectively. The effects of thymol nanoliposomes were shown to reduce ERG11 gene expression and fluconazole resistance; however, more extensive research is needed under in vitro and in vivo conditions for future application.

Keywords: ERG11 gene, Candida albicans, Fluconazole, Nanoliposome, Liposomal nanocarrier

Investigation of the frequency of different viruses in children with upper respiratory tract infection during 2023-2024

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BACKGROUND AND OBJECTIVES: This cross-sectional study aimed to determine the prevalence and epidemiological features of common viral upper respiratory tract infection in children with respiratory symptoms in Mofid Children's Hospital from February 2023 to February 2024.

MATERIALS AND METHODS: A total of 123 nasopharyngeal swab samples from 1 to 19 years old children with upper respiratory tract infection were enrolled. Clinical and demographic data were recorded and viral nucleic acids were extracted using commercial kits. Multiplex real-time PCR using FTD respiratory pathogens 21 assay was used for detection of the viral agents. Statistical analysis was performed using SPSS version 27 with Chi-square and Fisher's exact tests.

RESULTS AND DISCUSSION: The most frequent viruses were adenovirus (48.8%), enterovirus (15.4%), rhinovirus (12.2%), human metapneumovirus (8.9%), and RSV (3.3%). Less common viruses included influenza B (2.4%), parainfluenza virus-2, and influenza H1N1 (0.8%). Co-infection was observed in 22.7% of the cases. The highest infection rate occurred in winter (43/82, 52.4%) (p-value= 0.01). No significant differences were found based on age or gender. No differentiating signs or symptoms were detected for most of the viruses; however, pharyngitis, hoarseness of voice, and exudate were significantly detected in cases with enterovirus infection. Conclusion: The study highlights the value of molecular diagnostics for accurate viral detection, which can reduce unnecessary antibiotic use, guide targeted treatment, and improve pediatric care. The findings also underline the importance of seasonal surveillance, and healthcare preparedness to manage respiratory viral infections effectively.

Keywords: Epidemiology, Adenovirus, Enterovirus, Rhinovirus, Upper Respiratory Tract Infection, Metapneumovirus.

Investigation of the frequency of Lactobacillus rhamnosus and Bifidium bacterium bifidum in the saliva of patients with arteriosclerosis compared to healthy people by Real-Time PCR method

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BACKGROUND AND OBJECTIVES: The oral microbiome consists of a set of microorganisms that play a role in the balance between oral health and disease.Disturbance in this balance can lead to tooth decay,gingivitis,and even systemic diseases. Environmental factors such as diet, oral hygiene, and antibiotic use affect the composition of the microbiome.Recent research has focused on the use of probiotics and methods of microbiome modulation to improve oral health. The present study aimed to investigate the frequency of Bifidiumbacteriumbifidum and Lactobacillusrhamnosus in the saliva of patients with atherosclerosis compared to healthy individuals.

MATERIALS AND METHODS: 103 saliva samples were collected from patients suspected of having atherosclerosis. Then genome extraction steps were performed using an extraction kit, and the frequency of two bacteria was examined using the Real-time PCR method.

RESULTS AND DISCUSSION: Of the 103 saliva samples, 53 people were in the healthy group and the frequency of B.bifidum was not seen in these people and the frequency of L.rhamnosus in the healthy group was seen in 27 people.Of the 50 people in the patient group the frequency of B. bifidum was seen in 4 people,and the frequency of L.rhamnosus was seen in 21 people. Considering the two frequency bacteria present in the saliva of healthy and sick individuals The results of this study showed that the composition of the oral microbiota differs significantly between healthy individuals and patients.The bacterium L.rhamnosus was found in both groups but with different frequency. Additionally,B.bifidum was observed only in patients.These findings may indicate a potential association between these bacteria and the disease.

Keywords: Oral microbiome,Bifidiumbacteriumbifidum,Lactobacillusrhamnosus

Investigation of the frequency of resistance to beta-lactam antibiotics and the presence of the AmpC enzyme-producing gene in Escherichia coli isolates collected from Tabriz hospitals

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BACKGROUND AND OBJECTIVES: Escherichia coli is a gram-negative bacterium, commonly found as normal flora in the human and animal intestines and is a significant causative agent of opportunistic infections. Beta-lactam antibiotics are among the primary drugs utilized for treating E.coli infections. However, resistance to these antibiotics presents a considerable challenge in the effective management of such infections. The production of extended-spectrum beta-lactamase enzymes is a major mechanism contributing to the development of resistance in Escherichia coli isolates. The AmpC enzyme is recognized as one of these extended-spectrum beta-lactamases. The present study aimed to determine the prevalence of resistance to beta-lactam antibiotics and the frequency of the extended-spectrum beta-lactamase-producing gene, AmpC, in E.coli isolates collected from hospitals in Tabriz.

MATERIALS AND METHODS: The antibiotic resistance profiles of 80 E.coli isolates, obtained from urinary tract infection cases referred to Tabriz hospitals and identified through microbial tests, were determined using the disk diffusion (Kirby-Bauer) method. Phenotypic identification of beta-lactamase-producing isolates was performed using the combined disk method. The presence of the AmpC enzyme-producing gene was investigated by polymerase chain reaction (PCR).

RESULTS AND DISCUSSION: The highest resistance among the isolates was observed against ampicillin (100%), while the lowest resistance was noted for gentamicin (20%). Phenotypic testing identified 17% of the isolates as beta-lactamase producers. Furthermore, 10% of all isolates harbored the AmpC gene.Given the crucial role of extended-spectrum beta-lactamase enzymes in the emergence of antibiotic resistance, their early identification, coupled with the correct and rational prescription and usage of antibiotics, is imperative for controlling microbial resistance.

Keywords: Escherichia coli, beta-lactam antibiotics, AmpC gene

Investigation of the Frequency of Resistance to Fluoroquinolones and the Presence of Plasmid Resistance genes aac (6)-lb-cr and qepA in klebsiella pneumoniae Isolates Collected from Tabriz Hospitals

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BACKGROUND AND OBJECTIVES: klebsiella pneumoniae is one of the most important bacteria that cause opportunistic infections. Fluoroquinolones are widely used for the treatment of various infections due to their high potential and broad antibacterial spectrum, as well as low side effects. Antibiotic resistance against fluoroquinolones, like other antibiotics, is increasing in the world. The present study was conducted with the aim of investigating the frequency of resistance to fluoroquinolones and determining the presence of plasmid genes aac(6)-lb-cr and qepA in klebsiella pneumoniae isolates collected from Al-Zahra and Sina hospitals in Tabriz in 2024.

MATERIALS AND METHODS: In this study, 65 klebsiella pneumoniae isolates collected from hospitalized patients were identified by biochemical and microbial methods. Resistance to commonly used antibiotics was measured by disk diffusion method. Amplification and identification of aac(6)-lb-cr and qepA genes was done by PCR, using specific primers.

RESULTS AND DISCUSSION: The most effective antibiotic on the studied isolates was gentamicin with 81% sensitivity and the most resistant antibiotic was ampicillin with 100% resistance. Resistance to nalidixic acid and ciprofloxacin was 82% and 54%, respectively. The aac(6)-lb-cr gene was detected in 12 isolates and the qepA gene was detected in 4 isolates, all of which showed resistance to nalidixic acid and ciprofloxacin by phenotypic method.

Keywords: klebsiella pneumoniae, Fluoroquinolones, Antibiotic resistance, aac(6)-lb-cr and qepA genes

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 OBJECTIVES: Shigella is recognized as one of the primary causes of diarrhea worldwide. This study aimed to investigate the prevalence of resistance genes and assess the biofilm-forming ability of Shigella isolates.

MATERIALS AND METHODS: Seventy samples of various Shigella species were collected from patients admitted to Kamkar Arabnia Hospital, Qom, 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. The presence of mcr-1, mcr-2, fosA3, and mphA resistance genes was tested after extracting bacterial DNA.

RESULTS AND DISCUSSION: Out of the 70 isolated samples, 30 (43%) were female and 40 (57%) were male. The antibiogram test results showed the highest resistance to trimethoprim-sulfamethoxazole, with a resistance rate of 65%. Resistance to colistin was observed in 15 (21%) of the isolates, while 10 (14%) showed resistance to Fosfomycin and 12 (17%) to Azithromycin. The presence of resistance genes mcr-1, mcr-2, fosA3, and mphA was confirmed in 25 (36%) of the isolates. Understanding antibiotic resistance profiles and associated genes enhances our knowledge of local epidemics, optimizing infection treatment. Characterizing this diarrhea-causing bacterium and its resistance patterns can reduce infection prevalence and treatment costs.

Keywords: Diarrhea; Shigella; Antibiotic resistance; Carbapenemase; ESBLs; Biofilm

Investigation of the prevalence of common HPV genotypes in cervical samples from Urmia County during 2024

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BACKGROUND AND OBJECTIVES: There are numerous high-risk HPV types that can lead to squamous cell carcinoma in epithelial areas such as the cervix, vagina, vulva, penis, anus, oropharynx, and skin. This study aims to investigate the prevalence of different HPV genotypes in cervical samples from women in Urmia County

MATERIALS AND METHODS: In this study, 120 cervical samples were analyzed, and the presence of various HPV types was detected using the polymerase chain reaction method. DNA was extracted from each sample using a DNA extraction kit purchased from Intron, South Korea. Specific primers were used for PCR to amplify genes corresponding to different HPV genotypes

RESULTS AND DISCUSSION: Out of 120 samples analyzed, 22 samples (15%) tested positive for HPV. Among these, 14 genotypes were identified in the positive samples. Genotype 16 was present in 8 cases (44.4%), and genotypes 18 and 45 were each found in 5 cases (27.7%). Genotypes such as 31, 33, 35, 52, 58, 56, 66, and 68 were identified in 4 cases (22.2%), genotype 58 was present in 3 cases (16.6%), and genotypes 51 and 59 were each found in 2 cases (11.1%). The study showed that the youngest age group (18 years) had the lowest prevalence of HPV, while the oldest age group (54 years) had the highest prevalence. The findings suggest that high-risk behaviors outside a framework and inadequate personal hygiene practices could contribute to the spread of this virus. Additionally, the failure to receive the HPV vaccine may play a role in its persistence.evalence

Keywords: Cervical samples, Various HPV genotypes, Women, Urmia

Investigation of the role of efflux pump activity in the development of imipenem resistance among clinical isolates of Pseudomonas aeruginosa in Gilan

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BACKGROUND AND OBJECTIVES: Increasing antimicrobial resistance in gram-negative bacteria including Pseudomonas aeruginosa has become a global problem. Secretory pumps are considered as one of the mechanisms of antibiotic resistance in this bacterium. The aim of this study was to investigate the role of efflux pump in the development of imipenem resistance in clinical isolates of P. aeruginosa in Guilan.

MATERIALS AND METHODS: In this study, 67 isolates of P. aeruginosa were identified by culture and biochemical tests. Imipenem resistance and identification of carbapenemase-producing strains in these isolates were performed by disk diffusion and combined disk methods. Phenotypic study of the presence and activity of efflux pumps was performed by cartwheel method and the use of CCCP efflux inhibitor respectively and the frequency of mexA efflux gene was investigated by PCR.

RESULTS AND DISCUSSION: 21isolates (34.31%) were resistant to imipenem in the antibiogram test. In phenotypic test, 13 isolates (9.61% of resistant isolates) were identified as carbapenemase producing and 16 isolates (76.19%) were positive for presence of efflux pump. In all efflux positive isolates, the secretion process was active and the MIC level of imipenem in the presence of CCCP was reduced by 2 to 10 times and in 10 isolates (62.5%) the intense activity of the secretion pump was detected. The presence of mexA gene was also positive in 87.5% of efflux positive isolates. The results of this study indicate a high contribution of efflux pumps to imipenem resistance in P. aeruginosa isolates that can spread rapidly among strains of this bacterium.

Keywords: Pseudomonas aeruginosa, Influx pump, Carbapenem, Antibiotic resistance

Investigation of Virulence Gene Profiles, Biofilm Formation, and Resistance to Disinfectant Agents in Avian Pathogenic Escherichia coli (APEC) Isolated from Broiler Farms

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BACKGROUND AND OBJECTIVES: Avian pathogenic Escherichia coli (APEC) is a major causative agent of colibacillosis in poultry, resulting in systemic infections and considerable economic impact on the poultry sector. This research investigates the virulence gene patterns, biofilm-producing abilities, and resistance to antibiotics and disinfectants among E. coli isolates obtained from broiler chickens diagnosed with colibacillosis in Qazvin, Iran.

MATERIALS AND METHODS: Liver samples were obtained from 50 broiler chickens diagnosed with colibacillosis. E. coli strains were isolated from these samples and confirmed through biochemical testing. Antibiotic susceptibility was evaluated using the disk diffusion method, while virulence genes were detected via PCR. Biofilm formation was assessed using the crystal violet staining technique. The broth microdilution assay determined the MIC and MBC for three disinfectants: formaldehyde, glutaraldehyde, and hydrogen peroxide.

RESULTS AND DISCUSSION: A total of 50 confirmed E. coli isolates were identified, with 82% exhibiting multidrug resistance (MDR) and 30% classified as ESBL producers. The iss gene was the most frequently detected virulence factor, while the papC gene was the least common. All isolates were biofilm producers, with 72% forming strong biofilm. Formaldehyde and hydrogen peroxide emerged as the most effective disinfectants against these strains. The study emphasizes the concerning high prevalence of antibiotic resistance and virulence determinants among APEC strains in broiler chickens in Qazvin, Iran. Their notable ability to form biofilms further complicates control efforts. These findings highlight the critical need for enhanced hygiene and disinfection protocols in poultry farming to effectively combat APEC infections.

Keywords: Escherichia coli; antimicrobial resistance; pathogenic genes; Biofilm, broilers

Investigation the effect of live Lactobacillus helveticus on Murine Colon Carcinoma Cell Line (CT26)

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BACKGROUND AND OBJECTIVES: Probiotics are gaining interest in cancer research due to their immunomodulatory effects and potential to inhibit tumor cell growth. This study aimed to investigate the effect of live Lactobacillus helveticus cells on the viability of CT26 colorectal cancer cells.

MATERIALS AND METHODS: Live L. helveticus cells were co-cultured with CT26 cells at three multiplicities of infection (MOI = 1:1, 1:10, and 1:100) for 24, 48, and 72 hours. Cell viability was assessed using the MTT assay. Data were analyzed using GraphPad Prism software, and statistical comparisons were performed using Tukey's test ($P \leq 0.05$).

RESULTS AND DISCUSSION: Live L. helveticus significantly reduced CT26 cell viability at all MOIs and time points. The strongest effect was observed at MOI = 1:1 after 48 hours ($P \leq 0.0001$). A similar trend was observed at MOI = 1:10, with significant reductions at all time points and maximal inhibition at 48 hours ($P \leq 0.0001$). At MOI = 1:100, viability was still significantly decreased at 48 and 72 hours but to a lesser extent. The antitumor effect of L. helveticus was both time- and dose-dependent. Live L. helveticus cells effectively suppressed CT26 cell viability in vitro, with the strongest effect after 48 hours. These results demonstrate the potential antitumor activity of this probiotic strain. Future studies should include experiments on normal (non-cancerous) cell lines to assess possible cytotoxic effects on healthy tissues and to better evaluate the safety profile before therapeutic applications.

Keywords: Probiotic, Lactobacillus helveticus, Antitumor effect, CT26, In Vitro Techniques

investigationof the antifungal properties of carvacrol and nano carvacrol against Aspergillus parasiticus

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BACKGROUND AND OBJECTIVES: Aspergillus parasiticus isolates often infect agricultural products in fields and warehouses in tropical regions. In recent years, the study of plant compounds to reduce the growth of toxin-producing microorganisms has increased. Loading the effective substances of medicinal plants such as marjoram in lipid nanocarriers reduces the reaction of the active substance of the plant with the surrounding environment such as water and oxygen and reduces the intensity of transfer or evaporation of the external environment.

MATERIALS AND METHODS: In this experimental-laboratory study, based on the microdilution method in accordance with the latest version of the CLSI standard methods, modified M38-A2 protocol, the minimum growth inhibitory concentration (MIC) and the minimum fungicidal concentration (MFC) in different concentrations of carvacrol and Nanocarvacrol was tested against the standard strain of Aspergillus parasiticus in the laboratory.

RESULTS AND DISCUSSION: In this study, it was observed that nanocarvacrol has more antifungal effect against Aspergillus parasiticus than pure carvacrol. Based on this, the minimum growth inhibitory concentration (MIC) of nanocarvacrol was 0.97 ml/ µg and pure carvacrol was 97 ml/ µg. Such minimum fungicidal concentration (MFC) of nano-carvacrol was 3.9 ml/ µg and 390 ml/ µg of carvacrol extract, which showed the higher antifungal effect of nano-carvacrol compared to pure carvacrol extract. In general, the effect of nanoparticles containing carvacrol showed the lack of growth of Aspergillus parasiticus fungus, which can be a promising antifungal agent with high antifungal effects and low side effects.

Keywords: Aspergillus parasiticus, carvacrol, electron microscope, microdilution, nanocarvacrol.

Investigating the anti-inflammatory effect of Lactobacillus helveticus on Caco2 cell line inflamed by Bacteroides fragilis

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BACKGROUND AND OBJECTIVES: Intestinal microbiota as an important factor for controlling colorectal cancer(CRC) and inhibiting its progressive growth in human body is known. because of the high mortality rate of CRC, as the third cancer in the world, we decided to investigate the anti-inflammatory effect of Lactobacillus helveticus on Caco2 cell line inflamed by Bacteroides fragilis

MATERIALS AND METHODS: Cells were treated with ETBF (1 ng/mL) to induce inflammation, followed by heat-killed L. helveticus (0.5 mg/mL) or CFS (0.5 mg/mL) for 48 hours. Gene expression of cytokines (IL-1β, IL-8, IL-10) and NF-κB was analyzed via qRT-PCR.

RESULTS AND DISCUSSION: . ETBF significantly upregulated NF-κB and induced morphological disruption. Treatment with heat-killed L. helveticus and CFS upregulated IL-10 (2- and 5-fold, respectively) and reduced IL-8 expression ($p = 0.005$)Treated cells exhibited reduced inflammation and cytotoxicity. These findings highlight the efficacy of non-viable L. helveticus in modulating inflammatory responses, potentially via NF-κB inhibition and postbiotic metabolites. While the monoculture model limits ecological complexity, the results underscore the therapeutic potential of heat-killed probiotics and CFS in CRC prevention by targeting dysbiosis and inflammation. Future studies should explore strain-specific mechanisms, in vivo validation, and broader cytokine profiling to optimize probiotic-based strategies for CRC therapy..

Keywords: Bacteroides fragilis, Inflammation, Lactobacillus helveticus

Investigating the effect of cold plasma as an antimicrobial agent against Staphylococcus aureus

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BACKGROUND AND OBJECTIVES: Staphylococcus aureus is recognized as a major pathogen responsible for a wide range of infections and diseases. Treatment of these infections has become increasingly challenging due to the growing resistance to antibiotics. Cold plasma has emerged as a promising non-thermal disinfection technology that produces reactive oxygen and nitrogen species, charged particles that can inactivate bacteria without the need for high temperatures

MATERIALS AND METHODS: S.aureus (ATCC 29737) was cultured on four nutrient agar plates, each inoculated with a bacterial suspension at a concentration of 1.5 × 10^8 CFU/mL. One plate served as a control group, and three other plates were treated with cold plasma for different periods of time. After 24 h of incubation at 37°C, bacterial colonies were counted on all plates to assess the effect of cold plasma treatment on bacterial survival.

RESULTS AND DISCUSSION: Cold plasma treatment effectively reduced the viability of S. aureus in vitro in a time-dependent manner. The bactericidal effect of cold plasma against S. aureus can be attributed to the production of reactive oxygen and nitrogen species. The time-dependent decrease in colony number indicates that longer exposure to plasma enhances the antimicrobial effect.

Keywords: Cold plasma, Bacteria, Reactive oxygen, Antimicrobial agent

Investigation of common bacterial agents and determination of antibiotic susceptibility in urine sample cultures of patients referred to diagnostic and therapeutic centers in Mashhad city in 2023-2024

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BACKGROUND AND OBJECTIVES: Urinary tract infection (UTI) is a common infectious disease which may cause chronic renal failure and hypertention. Empiric therapy to treat UTI should be tailored to the surveillance data on the epidemiology and resistance patterns of common uropathogens to reduce treatment failures and emergence of bacterial resistance within the community, the aim of this study is evaluation of common bacterial microorganism and their antibiograms in urine cultures.

MATERIALS AND METHODS: This discriptive study was done on 1200 patients suspicious to UTI who refered to clinical laboratories in Mashhad, with 2022-2023Urine sample was taken, cultured and antibiotic sensitivity pattern was assessed by Kirby – Bauer method. Demographic information of patients was also registered. Data was statistically analysed by SPSS V.18.

RESULTS AND DISCUSSION: There were 74% women, and mean age of patients was 34.9±22.7 (±SD). Bacteriuria, Pyuria and hematuria was seen in 86.2%, 84.3% and 20.3% of patients respectively. Ecoli (51.4%), Klebsiella pneumonia (9.2%) and Coagolase negative staphylococcus (8.7%) were the most commonly grown pathogens. The difference between men and women considering the isolated micro organisms was statistically meaningful (p=0.001). Also the difference between age groups was significant considering pathogens (p=0.0001). Imipenem (86.7%), ceftizoxim (79%) and ciprofloxacin (75.5%) had the highest rate of sensitivity and penicillin (65.9%) , tetracyclin (65.3%), Erythromycin (61.8%) had the highest rates of resistance. Conclusion: E.coli remains the most common uropathogen. Antimicrobial therapy should be based on the results of urine culture and antimicrobial susceptibility test.

Keywords: UTI(Urine Tract Infection), resistance, sensitivity.

Investigation of microbial contamination and antibiotic sensitivity patterns in operating rooms of Islamic Azad University of Mashhad hospitals in 1401-1402

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BACKGROUND AND OBJECTIVES: Due the role of the most important sources and reservoirs of microbial contamination surgical ,wounds in the operating room,namely ,personal , the environment and equipment of the operating room, the study of the type and amount of microbial contamination will help to determine the success rate in controlling them ,Due to the time spent and the limted cost save a lot of medical expenses.

MATERIALS AND METHODS: this is a descriptive-analytic cross –sectional study conducted to evaluate the operating room of Aria and 22bahaman hospital of Mashhad Islamic Azad University in terms of yype and amount of microbial contamination and their susceptibility to antibiotics.the specimens were cultured using standard microbial methods.Data were analyzed using SPSS software and chi- square test. The sgnifcance level of the differences was less than 0.05

RESULTS AND DISCUSSION: 0f 141 sample , 107 cases (75.89%) had sterilized and 34 cases(24.11%) contaminated .from 141 samples ,18 cases (12.7%) the highest cultivated germ was Staphylococcus coagulase negative (18cases), .the most common isolated bactria include .Staphylococcus coagulase negative ,Staphylococcus coagulase positive, Bacillus subtilis ,E-coli,Klebsiella,Pseudomonas,and Enterobacter spp. Based on the findings of antibiograms among theseven observed germs, Staphylococcus coagulase negative as the highest microbial cultivar was the most susceptible to Coloxacillin and showed the highest resistance to Cotrimoxazole and Penicillin. This study showed that bacterial contamination of operating rooms in hospitals was lower than standard. Therewas no significant relationship between the presence of

Keywords: :Microbial contamination / Hospital equipments /Nosocommial infection/ Operating rooms/microbial sensitivity

Investigation of the frequency of chromosome mediated fluoroquinolone resistance genes in clinical strains of Pseudomonas aeruginosa isolated from urinary tract infections

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BACKGROUND AND OBJECTIVES: The emergence of multidrug-resistant strains of P. aeruginosa is increasing and difficult to treat, and the slow pace of new antibiotic development exacerbates the challenge.

MATERIALS AND METHODS: A total of 100 clinical isolates of P. aeruginosa were collected from university-affiliated hospitals in Tehran and Sanandaj hospitals, Iran. The disk diffusion method was applied to assess the quinolone resistance pattern. The presence gyrA, gyrB, parC, and parE, genes was investigated by the polymerase chain reaction (PCR) method. Fluoroquinolone resistant isolates were subjected to analysis of alterations in their GyrA and ParC subunits of DNA Gyrase and Topoisomerase IV, respectively.

RESULTS AND DISCUSSION: In this study, 100 P. aeruginosa isolates were taken from different wards. The prevalence of antibiotic resistance is including: Imipenem: 48%, Meropenem: 47%, Amikacin: 48%, Gentamicin: 45%, Piperaciclin-Tazobactam: 48%, Ceftolozane-tazobactam: 21%, Levofloxacin: 48%, Azitromicin: 56%, Ciprofloxicin: 55%, Ceftazidim: 34%, Ceftizoxim: 56%. Single mutation in parC (Ser-87-Leu) was also found in 3 of 15 isolates (19%). No additional mutations were observed in the QRDR regions. Sequence data of gyrA and parC from a representative isolate carrying mutations at both sites (PWS10) have been submitted to the GenBank databases under accession numbers PP501828 (gyrA) and PP526740 (parC). In conclusion, the Ceftolozane-tazobactam was the most effective antibiotic. To combat the spread of fluoroquinolone-resistant P. aeruginosa isolates, it is crucial to both reduce the extensive use of fluoroquinolones and accurately identify fluoroquinolone-resistant isolates along with their underlying mechanisms.

Keywords: Pseudomonas aeruginosa, fluoroquinolone, chromosome mediated fluoroquinolone resistance, Ceftolozane-tazobactam

Investigation of the frequency of plasmid mediated fluoroquinolone resistance genes in clinical strains of Pseudomonas aeruginosa isolated from urinary tract infections

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BACKGROUND AND OBJECTIVES: Pseudomonas aeruginosa is associated with several human infections, mainly related to healthcare services. In the hospital, it is associated with resistance to several antibiotics, which poses a great challenge to therapy. This study aimed to Investigation of the frequency of plasmid mediated fluoroquinolone resistance genes in clinical strains of Pseudomonas aeruginosa isolated from urinary tract infections

MATERIALS AND METHODS: In this study, a total of 100 clinical isolates of P. aeruginosa were collected from university-affiliated hospitals in Kordestan and Tehran. The disk diffusion method was applied to assess the quinolone resistance pattern. The presence qnrA, qnrB, qnrC, qnrD, qnrS and qepA genes was investigated by the polymerase chain reaction (PCR) method.

RESULTS AND DISCUSSION: In this study, 100 P. aeruginosa isolates were taken from different wards. Outpatient: 48, ICU: 36, CCU: 2, ENT: 1, Pediatrics: 3, Neurology: 2, Internal: 2, Gastroenterology: 4, Orthopedic: 1, Emergency: 1. The prevalence of antibiotic resistance is including: Imipenem:48%, Meropenem: 47%, Amikacin: 48%, Gentamicin:45%, Piperaciclin-Tazobactam:48%,,Imipenem-Relebactam:13%, Levofloxacin:48%, Azitromicin:56%,Ciprofloxicin:55%, Ceftazidim:34%, Ceftizoxim:56%. The occurence of PMQR genes was as follows: qnrS: 46%, qnrA: 43%,qnrC: 33%, qnrB: 28%, qepA: 20% and qnrD: 12%. In conclusion, the Imipenem-Relebactam was the most effective antibiotic against fluoroquinolone resistance Pseudomonas aeruginosa isolates. Lack of evaluation of chromosomal mutations in the QRDR region and failure to use whole-genome sequencing to provide more in-depth data on high-risk clones and other resistance genes (such as extended spectrum beta-lactamases and carbapenemases) often associated with PMQR, were some limitations of this study.

Keywords: Pseudomonas aeruginosa, fluoroquinolone, plasmid mediated fluoroquinolone resistance, Imipenem-Relebactam

Investigation of the frequency of type III secretion system genes in levofloxacin-resistant Pseudomonas aeruginosa strains isolated from urinary tract infections

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BACKGROUND AND OBJECTIVES: P. aeruginosa is one of the most common pathogenic bacteria causing infections and an important cause of morbidity and mortality worldwide. The emergence of multidrug-resistant strains of P. aeruginosa is increasing and difficult to treat, and the slow pace of new antibiotic development exacerbates the challenge

MATERIALS AND METHODS: A total of 100 clinical isolates of P. aeruginosa were collected from university-affiliated hospitals in Tehran and Sanandaj hospitals, Iran. The disk diffusion method was applied to assess the resistance pattern. The presence exoU, exoY, exoT, exoS genes was investigated by the polymerase chain reaction (PCR) method.

RESULTS AND DISCUSSION: In this study, 100 samples from patients with urinary tract infection caused by Pseudomonas aeruginosa were isolated from inpatients and outpatients. Antibiotic resistance against Piperacilin-tazobactam was seen in 87% of the isolates, followed by Ceftizoxime (58%), Aztreonam(57%), Ciprofloxicin(56%), Imipenem and Amikacin(48%), Meropenem and levofloxacin(47%), Gentamycin(45%), Carbenicillin(41%), Ceftazidime(33%) and Aztreonam-avibactam(18%). In this study, out of 47 levofloxacin-resistant strains, 35 strains (74.46%) were susceptible to aztreonam-avibactam. In addition, PCR results showed that among the 47 levofloxacin-resistant strains, the frequency of TTSS genes included exoT, exoS, exoU and exoY with frequency of 55.3%, 48.9%, 46.8%, and 36.1%, respectively. To combat the spread of Levofloxacin-resistant P. aeruginosa isolates, it is crucial to both reduce the extensive use of fluoroquinolones and accurately identify fluoroquinolone-resistant isolates along with their underlying mechanisms

Keywords: Pseudomonas aeruginosa, Urinary tract infection, Antibiotic resistance, TTSS, Polymerase chain

Isolation and Identification of Lead-Resistant Fungi from Lead Mine Tailings in Zanjan Province

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BACKGROUND AND OBJECTIVES: There are several lead mines in Zanjan Province, and the waste produced by these mines poses a potential environmental hazard to both residents and the region's ecosystem. Due to the high costs associated with chemical methods for managing these wastes, biological remediation techniques utilizing indigenous microorganisms are considered an economically viable and environmentally friendly alternative. This study aims to screen native fungi from the tailings of lead mines.

MATERIALS AND METHODS: Six soil samples from various lead mines were collected, and serial dilutions were prepared. Fungi were isolated using Lee minimal medium, and colonies were purified on Sabouraud dextrose agar supplemented with lead concentrations. The plates were incubated at 25°C for eight days, with daily observations recorded. Isolates were identified through microscopic analysis and biochemical characteristics.

RESULTS AND DISCUSSION: A total of 48 fungal isolates were able to grow at a lead concentration of 5 mM. Eight fungal species were identified, with Cladosporium sp. (40%), Penicillium sp. (25%), and Aspergillus sp. (18%) being the most prevalent. The results indicated that these native fungi exhibit increased tolerance to high lead concentrations, suggesting their potential role in bioremediation. Given the significant volume of mine residues in the area, the application of suitable microorganisms for the biosorption of lead represents both an economical approach and a subject worthy of further investigation.

Keywords: Mine tailing, Fungi, Lead, Resistant

Isolation and characterization of a lytic phage against Pseudomonas aeruginosa from the gut microbiota of Tenebrionidae beetles

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BACKGROUND AND OBJECTIVES: This study reports the isolation of a lytic bacteriophage against P. aeruginosa from the gut of Tenebrionidae beetles.

MATERIALS AND METHODS: Gut tissues from Tenebrionidae beetles were homogenized and used for phage isolation using double-layer- agar assays. A clear plaque was purified through serial propagation. The phage was enriched by co-culture with its host and concentrated using polyethylene glycol. Its host range was tested against seven bacterial strains via spot test. Phage stability was evaluated under various thermal conditions(–20°C to 90°C), pH levels(2–12), and UV exposure, with viability measured after treatment. The optimal multiplicity of infection(MOI) was determined by monitoring bacterial growth inhibition across a range from 0.0001 to 100. Adsorption kinetics were assessed by measuring unadsorbed phages at specific intervals. Nucleic acid type was identified through enzymatic digestion. The phage's ability to degrade biofilms was also examined..

RESULTS AND DISCUSSION: Four distinct plaques were observed, with the largest (1mm, transparent) selected for further characterization. The host range showed lytic activity on B. subtilis and P. aeruginosa. The phage demonstrated stability across a broad temperature range(–70°C to 45°C) and a wide pH spectrum(4–11), with thermal inactivation occurring above 60°C and complete loss of infectivity at 90°C. it exhibited sensitivity to UV light exposure. The MOI was 10, resulting in a 36% reduction in bacterial growth after 12h. Adsorption was efficient, reaching complete attachment within 25min. Enzymatic digestion confirmed a double-stranded DNA genome. The phage reduced biofilm biomass by 39.1%. This phage shows significant potential as a candidate for innovative phage therapy.

Keywords: Bacteriophage, Pseudomonas aeruginosa, Tenebrionidae Beetles

Isolation and identification of bacteriophage derived from hospital wastewater and its effect on imipenem-resistant Acinetobacter baumanii bacteria isolated from wounds of burn patients

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BACKGROUND AND OBJECTIVES: Background and Objective: Acinetobacter baumannii is an emerging multidrug-resistant nosocomial pathogen, particularly in intensive care units, with limited therapeutic options due to rapid antibiotic resistance. This study aims to identify effective bacteriophages as alternative therapeutic agents against A. baumannii isolated from wounds of burn patients' infections.

MATERIALS AND METHODS: Materials and Methods: Clinical isolates of A. baumannii were identified by rpoB gene PCR, and antibiotic susceptibility was determined by disk diffusion. Bacteriophage was isolated from hospital sewage. Lytic activity and the titers of phage lysates were measured using the spot test and double-layer plaque assay. The phage characterization was determined through transmission electron microscopy. Adsorption rate, host range, and stability tests were investigated. The latent period and burst size were estimated from a one-step growth curve. The effect of bacteriophage against A. baumannii biofilms was determined.

RESULTS AND DISCUSSION: Results and Discussion: TEM results showed that the phage resembled the Podoviridae family. Its latent period was 20 min, In addition, the burst size was determined to be 7.5 PFU/infected cell. The phage had a broad host range, and it was most stable at 37°C and pH 7. It was resistance to NaCl concentrations. The expressions of the biofilm-associated genes were significantly reduced in the presence of the phage. The isolated phage was effective against imipenem-resistant strains of A. baumannii, and it can be an optional strategy for controlling biofilm development.

Keywords: Acinetobacter baumannii , Bacteriophage , Phage therapy , burn wound

Isolation and screening of microalgae from shrimp breeding ponds for aquaculture feed

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BACKGROUND AND OBJECTIVES: The screening and isolation of microalgae are vital for developing biological processes and enhancing aquaculture. Studying phytoplankton diversity in shrimp farming environments is particularly important, as high densities of certain species can cause poor water quality, toxicity, or even mortality. Conversely, increases in other species can improve oxygenation, water purification, and feeding conditions for aquatic organisms. Obtaining pure cultures is essential for further applications.

MATERIALS AND METHODS: Samples were collected from the Chabahar shrimp ponds. Microalgae were isolated and purified using serial dilution and single-colony cultivation. Morphological characteristics of the strains were examined by optical microscopy, and molecular identification was performed using 18S rRNA gene analysis.

RESULTS AND DISCUSSION: The isolated and purified strains were identified as belonging to the genera Nodosilineaceae, Chlorella sp., Euryhalinema sp., Navicula salinicola, and Chlorellaceae. These strains have been preserved long-term at the Iranian Biological Resources Center. Utilizing microalgae as aquaculture feed offers cost control, investment predictability, reduced operational risks, and improved financial outcomes. The primary challenge remains the selection of optimal species for aquaculture nutrition. Among the isolates, Chlorella sp. and Navicula salinicola are particularly promising for use in aquatic feed formulations and merit further research.

Keywords: Phytoplanktons, screening, identification, aquaculture

Isolation and Characterization of Bacteriophages Targeting Salmonella enterica serovar Pullorum

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BACKGROUND AND OBJECTIVES: Salmonella enterica serovar Pullorum (SP) is the causative agent of pullorum disease, a severe bacterial infection affecting domestic poultries. Although Salmonella Pullorum occurrence has significantly decreased in modern poultry production systems, its potentials for vertical/horizontal transmission and documented outbreak history include substantial economic risks through flock mortalities and productivity losses. Due to the growing problem of antibiotic resistance, phage therapy is emerging as a promising alternative for targeted bacterial control. In this study, Salmonella Pullorum-specific bacteriophage were isolated from wastewater of a poultry farm.

MATERIALS AND METHODS: In this study, bacteriophages targeting Salmonella Pullorum were isolated using enrichment protocol and double-agar layer method. The host ranges of the bacteriophage were investigated through spot assessment of multiple bacterial strains, including various bacterial genera, species, serovars.

RESULTS AND DISCUSSION: The bacteriophage demonstrated a narrow host range, with lytic activity exclusively against Salmonella Pullorum isolates. The isolated bacteriophages produced clear lytic plaques exclusively on Salmonella Pullorum and showed no visible lysis on the other biovars. This signifies presence of a phage receptor that may be specific to Salmonella Pullorum. The bacteriophage stability within a temperature range of 4–40 °C shows its environmental resistance, supporting its potential roles in controlling Salmonella Pullorum infections in poultries under field and physiological conditions. This preliminary investigation reveals that the isolated environmental bacteriophages include strong host specificity against Salmonella Pullorum. Such specificity highlights their potentials as novel candidates for phage therapy in poultries. However, further studies are necessary to comprehensively verify the bacteriophage host range.

Keywords: Salmonella Pullorum, Bacteriophage Therapy, Poultry Disease, Host Specificity, Antibiotic

Isolation and identification of Brucella abortus and melitensis isolates circulating in industrial dairy cows in Isfahan (1401

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BACKGROUND AND OBJECTIVES: Isolation and identification of Brucella abortus and melitensis isolates circulating in industrial dairy cows in Isfahan (1401

MATERIALS AND METHODS: Lymph node samples were cultured separately on Farrell's medium (Brucella agar containing antibiotics) and kept in a 37°C incubator under CO2 for 10 days. For this purpose, 23 tissue samples from cows infected with brucellosis were collected from Isfahan province in 1401

RESULTS AND DISCUSSION: In studies conducted in Isfahan province, 23 samples of lymph nodes of reactor-positive animals were isolated for brucellosis, and 5 positive isolates were isolated, of which 2 samples of Brucella abortus Bivar 3 and 3 samples of Brucella melitensis Bivar 1 were isolated In studies conducted in Isfahan province, 23 samples of lymph nodes of reactor-positive animals were isolated for brucellosis, and 5 positive isolates were isolated, of which 2 samples of Brucella abortus Bivar 3 and 3 samples of Brucella melitensis Bivar 1 were isolated

Keywords: Brucella abortus, Brucella melitensis, Biovar, Lymph node, Multiplex PCR

Isolation and identification of Pediococcus spp. with probiotics properties from Iranian sour fruits

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BACKGROUND AND OBJECTIVES: According to the definition of WHO and 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.

MATERIALS 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 Pediococcus 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 Pediococcus strains with probiotic properties were confirmed.

RESULTS AND DISCUSSION: 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, Lactobacillus, LAB

Isolation and identification of Streptococcus agalactiae efflux pump genes in women with recurrent miscarriage

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BACKGROUND AND OBJECTIVES: Streptococcus agalactiae can be considered as one of the effective factors in miscarriage. The aim of the present study was to study the efflux pump genes of Streptococcus agalactiae isolated from women with recurrent miscarriage.

MATERIALS AND METHODS: In this descriptive-cross-sectional study, 350 samples were collected from pregnant women with an average age of 20-40 years who referred to Umm Leila Hospital in Bandar Abbas in 1403. Sampling of vaginal discharge from the middle third of the vagina was performed by a midwife. The swabs were immediately transferred to the laboratory in Todd Hewitt broth and, after incubation, were cultured on blood agar under anaerobic conditions. Antibiotic sensitivity to penicillin, ampicillin, vancomycin, clindamycin, erythromycin, and tetracycline was evaluated by disk diffusion method, and then the ermA, ermB, and mefA genes were identified using specific primers with the Multi Plex PCR technique.

RESULTS AND DISCUSSION: 60 samples (30%) were confirmed as Streptococcus agalactiae. In this study, a significant relationship was shown between the rate of vaginal GBS colonization with the number of previous pregnancies (P=0.032) and history of abortion (P=0.029). The isolates showed the highest resistance to the antibiotics erythromycin (100%), clindamycin (85%) and tetracycline (30%), while no resistance was observed to penicillin, amoxicillin and vancomycin. The results of Multi Plex PCR showed the highest frequency to the mefA (98%), ermB (48%) and ermA (21%) genes, respectively. Screening pregnant women can significantly increase preventive measures against miscarriage and improve fertility outcomes.

Keywords: Streptococcus agalactiae, Drug Resistance, Molecular Diagnostic Techniques, Polymerase Chain Reaction

Isolation of a Lytic Tectiviridae Bacteriophage against MDR E. coli

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BACKGROUND AND OBJECTIVES: The emergence of antibiotic-resistant bacteria has escalated to a worldwide crisis. Alternative treatments are critically needed. One potential solution is bacteriophages (phages) which are viruses that specifically infect and lyse bacteria. Urinary tract infections caused by antibiotic-resistant Escherichia coli are of particular interest as treatment can be difficult. The objective of this study was to isolate a lytic bacteriophage that infects multi-drug resistant (MDR) E. coli.

MATERIALS AND METHODS: Environmental samples were screened for isolation lytic phages against MDR E. coli using the double-layer agar method. After isolation and purification, the phage was propagated and its host-range was determined. The pH stability (5 to 9) and thermal stability (50, 60, 70, and 80°C) of the phage were determined. Morphology was determined by TEM.

RESULTS AND DISCUSSION: The lytic phage was isolated from soil contaminated with livestock fecal. The phage had a narrow host-range because did not lyse Lactobacillus spp. (casei, acidophilus, bulgaricus, plantarum). Initial phage titers remained stable at pH 6-8, but decreased 70% and 80% at pHs of 5 and 9, respectively. There was no titer decline at 50°C, and the titer decreased by 20%, 60% and 100% when heated at 60°C, 70°C and 80°C, respectively. Morphological micrograph showed the isolated phage belongs to the family Tectiviridae. The isolated phage exhibited effective lytic activity against MDR E. coli without impacting probiotic strains while showing moderate pH and thermal stability. These features support its potential as a candidate for phage therapy

Keywords: Bacteriophage. Multi-drug resistance, Infection, E. coli

Isolation of Clostridium perfringens toxinotype F from antibiotic-associated diarrhoeal (AAD) patients in Kerman hospitals of Iran

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BACKGROUND AND OBJECTIVES: Clostridium perfringens (C. perfringens) is divided into seven toxinotypes (A, B, C, D, E, F, and G) based on producing of CPA, CPB, ETX, IAP, CPE and NetB toxins. C. perfringens toxinotype F (cpa and cpe genes positive) is known as the cause of 2-15% of all antibiotic-associated diarrhoea (AAD) cases. This study investigated the prevalence of C. perfringens toxinotype F isolated from AAD patients in different hospitals of Kerman, Iran.

MATERIALS AND METHODS: A total of 151 stool specimens from AAD patients were bacteriologically investigated for C. perfringens, and the suspected isolates were analyzed for C. perfringens toxin genes (cpa, cpb, etx, iap, cpe, and netb) by PCR.

RESULTS AND DISCUSSION: C. perfringens isolation ratio was 30.5% (46 of 151 patients) after the bacteriological and molecular examinations, which was significant among different hospitals (p=0.03). The isolation ratio for toxinotype F was 22.5% (34/151). A total of 116 C. perfringens isolates were obtained from patients. The cpa genes was detected in all isolates and cpe gene was detected in 64 isolates (55.1%), thus they belonged to toxinotype F. While C. perfringens is a part of human microbiota, C. perfringens-associated AAD in humans is an important gastrointestinal disease in the nosocomial patient that has been frequently attributed to C. perfringens toxinotype F. This study persists in considering toxinotype F in AAD patients in different hospitals of Kerman, Iran.

Keywords: Clostridium perfringens; Type F; Antibiotic-associated diarrhoea; Hospital; Kerman, Iran

Isolation of lactic acid bacterial strains with probiotic properties from fermented product in eastern Mazandaran

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BACKGROUND AND OBJECTIVES: Probiotic microorganisms provide a wide range of benefits, such as: alleviating digestive disorders, maintaining microbiota balance, preventing both the onset and recurrence of infectious diseases modulating immune system functions, and providing numerous other advantages has been established. Research into traditional and locally fermented products has resulted in the identification of lactic acid bacteria which are typically recognized as probiotics. In present investigation, a local cow yogurt sourced from Sari city was utilized to isolate probiotics.

MATERIALS AND METHODS: The probiotic characteristics assessed included tolerance to simulated digestive conditions such as acid and bile salt resistance, antimicrobial properties, and resistance to pepsin and trypsin. Ultimately, the selected isolates underwent molecular identification evaluation.

RESULTS AND DISCUSSION: Among the three traditional products examined, five isolates were analyzed, with four belonging to the Lactobacilli genus and one to Streptococcus. Most isolates exhibited probiotic potential across two or three characteristics; however, two isolates demonstrated superior results in the majority of probiotic evaluation tests conducted using PCR for 16SrRNA gene analysis. The results confirmed that both isolates were Lactobacillus rhamnosus.

Keywords: probiotic bacteria, traditional fermented products, Lactobacillus, Streptococcus.

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 OBJECTIVES: Staphylococcus aureus is one of the most common hospital-acquired infections. Today, reports of the prevalence of methicillin resistance in Staphylococcus aureus are increasing in different parts of the world. The aim of this study was to isolate and genotype Staphylococcus aureus strains from patients hospitalized in intensive care units.

MATERIALS 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 Geno species S.aureus.The mecA and LukS/F-PV genes were also evaluated by multiplex PCR

RESULTS AND DISCUSSION: Among 60 lung secretion samples, 20 strains of S.aureus were identified by biochemical tests according to standard microbiological methods (morphology,gram staining,catalase test,coagulase test, and mannitol salt fermentation).S. aureus isolates was confirmed and compared to DNA extraction and the PCR test using specific primers.for the identification of S. aureus species the 16S rRNA gene was positive as a reference gene.The frequency of LukS/F-PV and mecA genes were reported in 12 (20%) and 8 (13.33%) isolates, respectively.The 4 (6.66%) isolates showed to have both LukS/F-PV and mecA genes. Discussion Considering the ability of PVL and LukS/F-PV-producing MRSA isolates to cause life-threatening diseases, and prevalence of pulmonary MRSA isolates,rapid diagnosis,direct, simple and cost-effective tests can help reduce MRSA infections.in order to limit the spread of MRSA,maximum aseptic practices for health care professionals and better training in hygiene practices are needed

Keywords: : Staphylococcus aureus; MRSA; mecA; LukS ; LukF

Isolation of Streptomyces isolates and investigation the effect of their potential antimicrobial agents

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BACKGROUND AND OBJECTIVES: Streptomyces strains have a medical importance mainly for their synthesis of a wide range of new antimicrobial agents. Nearly 50% of them normally produce more than 500 distinct antibiotics. Accordingly, the aim of this study was to isolate of Streptomyces strains for evaluation of their potential antimicrobial agents.

MATERIALS AND METHODS: The different strains of Streptomyces were isolated from soil samples using serial dilution and nutrient agar and ISP2 media. All isolates were identified by physiological and biochemical tests. The antimicrobial activity of the isolates was also determined by disc diffusion and cross streak tests against selected human pathogens such as Pseudomonas aeruginosa, Staphylococcus aureus, Escherichia coli, and Candida albicans.

RESULTS AND DISCUSSION: Fifteen isolates were identified as Streptomyces. They were non-motile, positive for catalase, oxidase ,urease tests and positive for H2S production, but negative for nitrate reduction, MR test and VP test. Under a light microscope, they exhibited a filamentous, branching hyphae. They also developed spore chains aerial hyphae. Two isolates showed the highest antimicrobial potential against some nosocomial infections according to the disc diffusion test as well as cross streak method and they were selected for further in vivo analyses. Our findings about new agents with antimicrobial potential from natural sources such as Streptomyces is urgently necessary to address the growing cases of antibiotic-resistant pathogens. Accordingly, our isolated Streptomyces in the present study are good candidates for further supplementary tests and may hopefully promise for future biotechnological and pharmaceutical exploration.

Keywords: Antimicrobial activity, Streptomyces, Hospital infections, Novel antimetabolites.

Isolation of toxigenic Clostridioides difficile isolates from C. difficile-associated disease (CDAD) patients in Kerman, Iran

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BACKGROUND AND OBJECTIVES: Clostridioides difficile (C. difficile) is caused C. difficile-associated disease (CDAD) among hospitalized patients. This study investigated the prevalence of toxigenic C. difficile isolates from CDAD patients in Kerman province of Iran.

MATERIALS AND METHODS: A total of 80 stool specimens from CDAD patients were investigated for C. difficile, and the suspected C. difficile isolates were analyzed for tcdA, tcdB and binary CDT (cdtA and cdtB) toxin genes by PCR. Only strains with both cdtA and cdtB genes were considered as CDT+ strains.

RESULTS AND DISCUSSION: A total of 77 C. difficile isolates were obtained from CDAD patients, which 53 isolates (68.8%) were toxigenic and 24 isolates (31.2) were characterized as nontoxigenic. Six different toxin gene profiles were found: A+B+CDT+ (7/77), A+B+CDT- (29/77), A-B+CDT+ (4/77), A-B+CDT- (12/77), A+B-CDT- (1/77), A-B-CDT- (24/77). Most of toxigenic isolates showed the A+B+ (67.9%; 36/53) and A-B+ (30.2%; 16/53) genotypes (p0.05). C. difficile as the leading cause of nosocomial infections has high threat to public health. In this study toxigenic profiles of C. difficile isolates were characterized in CDAD patients in Kerman province of Iran.

Keywords: Clostridioides difficile, Toxigenic, C. difficile-associated disease (CDAD), Kerman, Iran

Isolation, purification and identification of indigenous bacteria producing polyhydroxyalkanoates

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BACKGROUND AND OBJECTIVES: Today, the production of bio-based products is considered one of the world's research priorities. In the meantime, microorganisms have a high potential in the production of biological products, especially polymers, due to their excellent capabilities. Some bacteria like B.megaterium, C.nector, R.eutropha, etc.can produce polyhydroxyalkanoates, which are natural substitutes for chemical plastics.

MATERIALS AND METHODS: In the present study, with the aim of isolating and identifying bacteria with this ability from various samples, including alfalfa soil, three soil samples from Kharak Island, regional soil in Chalus city and Tepe Silk in Kashan, various bacteria were cultivated, isolated and purified. Then, two strains were selected as strains to confirm polymer production in the culture medium using the Sudan Black staining method. After extracting the white film of polymer from bacterial biomass the film was evaluated by FT-IR. The two top isolates were identified using 16S sequencing method and complementary biochemical experiments.

RESULTS AND DISCUSSION: The isolates were bacteria from the soil sample of Khark Island, which were identified as strains of Priestia megaterium and registered in the NCBI database with the names STH1 and STH2. The FT-IR results matched the control sample, which was polyhydroxybutyrate, and confirmed the presence of the polymer. Finally, it can be concluded that the bacteria isolated from a Khark Island soil sample had the ability to produce polyhydroxyalkanoates optimally, but additional studies and research are needed to optimize the growth condition and polymer extraction from bacterial biomass.

Keywords: Polyhydroxyalkanoates, Priestia megaterium, Microorganisms, Biopolymer

Lactoferricin: A molecule with broad antimicrobial potential against Gram-positive bacteria.

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BACKGROUND AND OBJECTIVES: Antimicrobial peptides are small biomolecules that have antimicrobial properties against a wide range of microorganisms. Lactoferricin is an antimicrobial peptide derived from the Lactoferrin protein, whose broad-spectrum effects against various microbes have been proven. In this study, Pichia Pastoris was used to produce the recombinant mutant lactoferricin and its impact on Gram-positive bacteria was assessed.

MATERIALS AND METHODS: Thermodynamic analysis was applied to design the lactoferricin nucleotide sequence. Following optimization, the final sequence was placed into the pPIC9 vector and expressed in Pichia pastoris. Then, the inducer concentration, peptide extraction buffer pH, and induction duration were adjusted to optimize the conditions for the production of recombinant protein in this expression host. The production of the recombinant antimicrobial peptide was confirmed by SDS-PAGE and its purification was performed by Ni-NTA chromatography. Finally, the antibacterial activity of this peptide against human pathogenic Gram-positive bacterial species was examined by the well diffusion method.

RESULTS AND DISCUSSION: The recombinant production of the antimicrobial peptide Lactoferricin with a molecular weight of 3 kDa was confirmed. The maximum extractable concentration of the peptide was estimated to be 18.71 mg/ml, and the results obtained from the well diffusion method showed that the Lactoferricin peptide, with an average diameter of the inhibition zone of 9.25 ± 2.90, was able to inhibit the growth of 8 human pathogenic Gram-positive bacterial species. The results showed that recombinant Lactoferricin has a high potential to inhibit the growth of various bacteria and can be used as a suitable antimicrobial compound in future studies.

Keywords: Lactoferricin, Antimicrobial peptides, Antibiotic Resistance

Lentinula edodes Polysaccharides And Antibacterial Activity

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BACKGROUND AND OBJECTIVES: Polysaccharides from medicinal and edible mushrooms are natural and biocompatible components that have potential in antimicrobial properties. Purified polysaccharides from Lentinula edodes (shiitake) extract was evaluated for its antimicrobial effects.

MATERIALS AND METHODS: Polysaccharide purification was done by DEAE-cellulose ion exchange and monosaccharide composition of polysaccharide was analysed by HPLC. MIC of purified polysaccharide was determined against Staphylococcus aureus and Pseudomonas aeruginosa.

RESULTS AND DISCUSSION: HPLC analysis revealed the presence of glucose, glucuronic acid, galacturonic acid in varing ratios. Polysaccharide fractions exhibited measurable inhibitory effects against Pseudomonas aeruginosa and Staphylococcus aureus. Natural polysaccharides demonstrated notable antibacterial activity and potential to reduce pathogenic virulence. These results suggest their applicability in developing new antimicrobial agents or adjunct therapies. These findings support further studies into its mode of action and potential clinical applications

Keywords: Polysaccharides, Antimicrobial Activity, MIC, Natural Products, Bacterial Pathogens

Linear epitope prediction of Clostridium perfringens beta toxin using bioinformatics approach

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BACKGROUND AND OBJECTIVES: Clostridium perfringens beta toxin (CPB) is a critical virulence implicated in enterotoxemia and necrotic enteritis in humans and animals. Identifying linear B-cell epitopes on this toxin is essential for developing effective vaccines and immunodiagnostic tools. This study employs bioinformatics tools, including BepiPred-2.0 to predict linear B-cell epitopes of the C. perfringens beta toxin. Four epitopes were identified. Validation of these epitopes presents promising candidates for peptide-based vaccine development against Clostridium perfringens infections.

MATERIALS AND METHODS: Sequence Retrieval The amino acid sequence of Clostridium perfringens beta toxin was retrieved from the UniProt database (UniProt ID: E3VN36). This sequence served as the basis for subsequent structural and immunoinformatics analyses. Linear B-Cell Epitope Prediction Linear B-cell epitopes were predicted using BepiPred-2.0 to determine potential immunogenic regions within the target proteins based on sequence data.

RESULTS AND DISCUSSION: Results Four linear B-cell epitopes were identified as shown in Table 1. peptide length
ANDIGKTTTITRNKTSDGYTIITQNDKQIISYQSVDSSSKNEDGFTAS 48 FIDDKYSSE 9
MSSKKEDVIKKYNLHDVTNST 21 LNESINENVKIVDSIPKNTISQKTVSNTIG 30

Keywords: Key words: Clostridium perfringens, Beta toxin, Linear epitope

Linear epitope prediction of Clostridium septicum alpha toxin using bioinformatic tool and computational approaches

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BACKGROUND AND OBJECTIVES: The Gram-positive, spore-forming bacterium Clostridium septicum is a key etiological agent of gas gangrene and necrotizing infections in humans and animals. The alpha toxin (CSA), a key virulence factor, exhibits pore-forming and cytotoxic activities, making it a prime target for immunological interventions. The identification of immunogenic epitopes is critical for the vaccine development against this toxin. In this study we employed BepiPred-2.0 bioinformatics tool to predict linear B-cell epitopes within the alpha toxin of C. septicum, aiming to identify immunodominant regions suitable for vaccine and diagnostic development. 11 high-probability linear epitopes were identified. The identified epitopes are proposed as promising candidates for synthetic peptide vaccine development and monoclonal antibody production.

MATERIALS AND METHODS: Protein Sequence Retrieval The amino acid sequence of Clostridium septicum alpha toxin was retrieved from the UniProt database (UniProt ID: Q53482). This sequence served as the basis for subsequent structural and immunoinformatics analyses. Linear B-Cell Epitope Prediction Linear B-cell epitopes were predicted using BepiPred-2.0 to determine potential immunogenic regions within the target proteins based on sequence data.

RESULTS AND DISCUSSION: BepiPred-2.0 identified 11 high-confidence linear epitopes (Table 1). peptide lenght 1 HVQAYALTNLEEGGYANHNNASSIKIFGYEDNEDLKAK 38 2 NPNVGQGFEFKREVGAGGKVS 21 3 LLSARYNPNDPYASGYRAK 19 4 TPKVKK 6 5 SKTESKLS 8 6 KTDNFKFGEKIGVKTSFKV 19 7 LEAIADS 7 8 FEFNAEQGWSNTNSTTE 17 9 GNAREDHTEDRPTVKLKFGKNGMSAEEHLKDLYSHKNINGYSEWDWKWV 49 10 ALTSRK 6 11 EGKEIPLPDKKRRGKRSVDSLDARLQNEGIRIENIETQDVPGFRLNSITYNDKKLI 56

Keywords: Clostridium septicum, alpha toxin, linear B-cell epitope, bioinformatics, vaccine design,

Machine Learning Approaches for Design and Process Optimization of Microbial Bioreactors in Chemical Engineering

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BACKGROUND AND OBJECTIVES: Machine learning (ML) is revolutionizing microbial bioprocessing by enabling advanced modeling, monitoring, and optimization beyond the capabilities of conventional mechanistic approaches. ML algorithms have been successfully applied to improve bioreactor design, optimize media composition, enhance metabolic pathway engineering, and enable real-time process control through IoT and digital twin technologies. Hybrid modeling strategies that combine mechanistic and data-driven methods further enhance predictive accuracy and interpretability, facilitating scalability from laboratory to industrial applications Industrial case studies, including bioethanol production and wastewater treatment, demonstrate ML's ability to improve yield, reduce environmental impact, and support sustainable biomanufacturing Despite challenges in data quality, interpretability, and scalability, ongoing research in explainable AI and Industry 4.0 integration highlights ML's potential to drive ethical, economic, and environmentally responsible innovation in microbial and chemical engineering.

MATERIALS AND METHODS: Types of Bioreactors & Critical Design Parameters Microbial bioreactors are fundamental units in chemical industries for producing bio-based chemicals, fuels, and pharmaceuticals. The most widely used type is the stirred tank bioreactor (STBR), valued for its operational flexibility and capability to handle batch, fed-batch, and continuous processes. STBRs are particularly suitable when high oxygen transfer and efficient mixing are required.

RESULTS AND DISCUSSION: Conclusion Machine learning (ML) has emerged as a transformative tool for microbial bioprocess engineering, providing advanced predictive and optimization capabilities beyond what conventional models offer. By leveraging large datasets and identifying nonlinear interactions among multiple variables, ML models enable improved bioreactor design, process control, and product yield (Liu, Feng, Fang, & An, 2025; Srivastava & Atri, 2025).

Keywords: Machine Learning, Microbiology, bioreactor, chemical engineering, AI

Metabolite Identification from degradation of pyrene by a marine bacterium

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BACKGROUND AND OBJECTIVES: Pyrene is a type of polycyclic aromatic hydrocarbon (PAH) that is commonly found in polluted areas. It is known to be a major threat in the environment and can cause toxicity, genotoxicity and carcinogenicity for humans. It is important to study the biodegradation of pyrene and identify intermediate metabolites. This study aimed to identify metabolites during pyrene degradation by a marine bacterium.

MATERIALS AND METHODS: Marine sediments were collected from 10 meters deep in the southern coasts of the Caspian Sea. The enrichment and isolation of bacterial strain was done in basal salt medium (BSM) containing 200 mg/l of pyrene. The biodegradation rate of pyrene was measured after 7 days by gas chromatography-Flame Ionization (GC-FID).The metabolites produced during degradation of pyrene were analyzed using gas chromatography–mass spectrometry (GC–MS).

RESULTS AND DISCUSSION: The results have revealed that isolated strain showed degradation of pyrene 38.32% after 7 days. An intermediate metabolite was detected during the biodegradation of pyrene by bacterial strain using GC-MS analysis. During the analysis, a significant peak was observed at a retention time of 24.642 minutes. Its mass spectrum confirmed the presence of a molecular ion (M+) at m/z of 204.1. A significant ion at m/z 101 (M+-103) strongly indicates that this metabolite is 4,5-dihydropyrene.This study shows that this isolated strain has significant potential for bioremediation of environments contaminated with polycyclic aromatic hydrocarbons (PAHs). The commercial potential of this strain for the bioremediation of pyrene in contaminated wastewater must be assessed through further research.

Keywords: Biodegradation, Gas chromatography–mass spectrometry (GC–MS), Polycyclic aromatic hydrocarbons, Pyrene

Microbial Imbalance and Fecal Microbiota Transplantation in Neurological Diseases

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BACKGROUND AND OBJECTIVES: Dysbiosis, or an imbalance in gut microbial communities, has been associated with the development and progression of several neurological conditions, including Parkinson's disease, multiple sclerosis, and autism spectrum disorders. Recently, fecal microbiota transplantation (FMT) has emerged as a potential therapy to restore gut microbial balance and may offer neuroprotective benefits by modulating the gut-brain axis.

MATERIALS AND METHODS: This article presents a review of existing literature, systematically searching Scopus, PubMed, and Embase databases for studies published between 2016 and 2024. The search used keywords such as "fecal microbiota transplantation," "microbiome," and "neurological diseases." A total of 78 articles that met the inclusion criteria were selected for detailed analysis.

RESULTS AND DISCUSSION: Studies show a strong connection between gut-brain axis dysfunction and neurological disorders. Fecal microbiota transplantation FMT) can alter gut bacteria, reduce inflammation, and ease neurological symptoms, particularly in conditions like Parkinson's disease and autism. However, results across studies vary due to differences in both disease types and FMT methods. Although FMT is a promising supplementary treatment, its use in neurology is still emerging. More rigorous clinical trials are needed to determine its long-term safety and effectiveness.Additionally, the mechanisms by which gut microbes influence the brain remain unclear and require further investigation. Standardizing FMT procedures, such as donor selection and transplantation techniques, is also crucial for achieving reliable results. In summary, while FMT may offer an innovative approach to treating neurological diseases linked to gut dysbiosis, more research is needed to fully understand and harness its therapeutic potential.

Keywords: Fecal microbiota transplantation, Microbiome, Neurological Diseases.

Microbial Quality Assessment of Ultra-High Temperature (UHT) Milk by Bioluminescence Method

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BACKGROUND AND OBJECTIVES: According to the Iranian National Standard No. 1528, UHT milk refers to milk that has been subjected to a temperature of about 136 to 142 degrees Celsius for 1 to 4 seconds during the sterilization process. in order to ensure the quality and safety of the UHT milk , the samples are quarantined at two temperatures of 37 degrees and 55 degrees for 7 to 10 days .

MATERIALS AND METHODS: We incubated 600 samples of plain and flavored UHT milk (from 7 different production batches) for 48, 72, 96, 120, 144 and 168 hours at two temperatures of 30 and 55 °C, and then subjected the samples to microbial testing using both pour plate and bioluminescence methods. PCA medium was used for the total count test(Merk Company), a Lumine TestTM brand kit(Bahar Zist Azma PajouhTM) and a TianlongTM company luminator were used for the ATP-bioluminescence test

RESULTS AND DISCUSSION: The results obtained showed A very high correlation was observed between the microbial culture method and the ATP-bioluminescence technique, and it was determined that if the RLU level is lower than 50 after the third day of production and storage of the sample in a 30 and 55 °C incubator, it can be ensured with a high percentage that the sterilization process was carried out well and no microbial quality problems will arise during the shelf life of the milk (6 months)., to ensure the accuracy of the results, a larger number of samples and testing in one year are needed.

Keywords: Keywords: milk, bioluminescence, , RLU,ATP

Microbial Signatures and Pathogen Variation in Traditional Iranian Lighvan Cheese: A Multi-Producer Comparative Metataxonomic Study

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BACKGROUND AND OBJECTIVES: Lighvan cheese, a traditional raw sheep milk cheese from Tabriz, Iran, has diverse microbial communities. This study analyzed seven aged samples from multiple producers using 16S rRNA sequencing and QIIME. Streptococcus was dominant, followed by Streptococcaceae, Macrococcus, Enterococcus, and Enterobacteriaceae. Other minor taxa included Staphylococcus and Citrobacter. Microbial composition aligned with physicochemical traits. The findings reveal complex microbiomes and potential pathogen presence, highlighting next-generation sequencing's value for safety and quality control.

MATERIALS AND METHODS: Seven Lighvan cheese samples, aged over one year and collected from different traditional producers, were analyzed. Microbial DNA was extracted and the 16S rRNA gene's V1–V3 hypervariable regions were amplified using barcode-indexed primers enabling multiplex sequencing. Libraries were sequenced using the illumina sequencing platform. Bioinformatic processing and taxonomic assignment of Operational Taxonomic Units (OTUs) were performed with QIIME software. Relative abundance of taxa was quantified and cross-referenced against physicochemical data of the samples to explore correlations in microbial community shifts.

RESULTS AND DISCUSSION: Analysis revealed Streptococcus species dominated across all producers, followed by Streptococcaceae, Macrococcus, Enterococcus, and Enterobacteriaceae. Lower abundance taxa included Staphylococcus, Citrobacter, and Gammaproteobacteria. Microbial profiles varied among producers, reflecting production differences. The community structure correlated with physicochemical parameters, supporting consistent cheese maturation. This multi-producer study using 16S rRNA sequencing highlights key bacteria crucial for maturation and safety, showcasing next-generation sequencing's role in monitoring artisanal dairy products.

Keywords: Lighvan Cheese, , Microbiome Profiling, , Pathogenic Bacteria, Next-Generation Sequencing

Microbiome and Infertility: A Paradigm Shift in Reproductive Endocrinology

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BACKGROUND AND OBJECTIVES: There is a growing body of evidence implicating the human microbiome as a key modulator of reproductive function. Recent advances in microbiome research have revealed its influence on endocrine signaling, immune regulation, and reproductive outcomes in both sexes. To explore the role of the microbiome in infertility through the lens of reproductive endocrinology, integrating current findings from ASRM, ESHRE, and high-impact journals. The panel will address microbial contributions to female and male infertility, with a focus on endometriosis, hormonal dysregulation, and assisted reproductive technologies (ART).

MATERIALS AND METHODS: A comprehensive review of recent literature (2022–2025), including ESHRE's Unexplained Infertility guideline, ASRM committee opinions, and peer-reviewed studies from Human Reproduction, Fertility and Sterility, and Nature Reviews Endocrinology. Topics include: • Vaginal and endometrial dysbiosis in female infertility and endometriosis • Seminal microbiota and sperm quality in male infertility • Gut microbiome's role in estrogen metabolism and PCOS • Microbiome profiling as a predictive tool in ART outcomes

RESULTS AND DISCUSSION: There is a growing body of evidence implicating the human microbiome as a key modulator of reproductive function. Recent advances in microbiome research have revealed its influence on endocrine signaling, immune regulation, and reproductive outcomes in both sexes. To explore the role of the microbiome in infertility through the lens of reproductive endocrinology, integrating current findings from ASRM, ESHRE, and high-impact journals. The panel will address microbial contributions to female and male infertility, with a focus on endometriosis, hormonal dysregulation, and assisted reproductive technologies (ART).

Keywords: infertility, microbiome, Reproductive Endocrinology,

Molecular Characterization of Vaccine Serovars of Leptospira based on the adk Gene

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BACKGROUND AND OBJECTIVES: Leptospira species are the etiological agents of leptospirosis, a globally distributed zoonotic disease with substantial public health and veterinary significance. Vaccinal serovars of Leptospira play a pivotal role in immunization programs, and detailed knowledge of their genetic diversity is crucial to improve vaccine efficacy. The adk (adenylate kinase) housekeeping gene, commonly used in multilocus sequence typing (MLST), provides valuable data for molecular typing and phylogenetic studies.This study aimed to characterize the genetic diversity of the adk gene among prevalent vaccinal Leptospira serovars in order to elucidate their phylogenetic relationships.

MATERIALS AND METHODS: Genomic DNA was extracted from five vaccinal Leptospira serovars, including L. canicola, L. grippotyphosa, L. hardjo, L. icterohaemorrhagiae, and L. pomona. PCR amplification of the adk gene yielded a 531 bp fragment, which was sequenced and analyzed by MegAlign and MEGA software to evaluate genetic variation, construct phylogenetic relationships, and compare the isolates with global reference sequences.

RESULTS AND DISCUSSION: The adk locus demonstrated high discriminatory power, enabling clear differentiation among the studied vaccine serovars. Considerable genetic heterogeneity was observed within the panel. Phylogenetic analyses revealed that three serovars clustered with Leptospira interrogans, while the remaining two corresponded to Leptospira kirschneri and Leptospira borgpetersenii. Molecular characterization of the adk gene among circulating leptospiral vaccinal serovars revealed considerable genetic diversity and distinct phylogenetic affiliations. These findings offer valuable insights for optimizing vaccine formulations and may contribute to improved surveillance and control strategies for leptospirosis.

Keywords: Leptospira, Leptospirosis, Bacterial Vaccines , Phylogeny

Molecular cloning and expression of a glutaminase gene from a halotolerant bacterium Bacillus mojavensis

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BACKGROUND AND OBJECTIVES: Glutaminase is considered one of the key enzymes in pharmaceutical and food industries due to its ability to produce glutamate and its anticancer properties. Accordingly, recombinant cloning and expression of this enzyme in E. coli BL-21 provides a suitable platform for the production of active and purified enzymes. This study was designed to clone, express, and evaluate the antimicrobial properties of glutaminase derived from Bacillus mojavensis.

MATERIALS AND METHODS: Bacillus mojavensis was cultured under optimal conditions. Specific forward and reverse primers were designed for the glutaminase gene, and following DNA extraction, PCR was carried out to amplify the target gene. The PCR product was inserted into TA vectors for cloning, and sequencing was performed to confirm gene integrity. New primers containing restriction sites and a histidine tag were designed; the gene was re-amplified and cloned into the pET-21a expression vector, which was then transformed into E. coli BL-21. Protein expression was induced using IPTG, and the recombinant enzyme was purified using nickel affinity chromatography and confirmed via SDS-PAGE. The antimicrobial activity of the purified glutaminase was subsequently assessed.

RESULTS AND DISCUSSION: The glutaminase gene from Bacillus mojavensis was successfully cloned and expressed in E. coli BL-21. The recombinant enzyme was purified and exhibited a distinct band at 36 kDa on SDS-PAGE. Antibacterial assays demonstrated that the enzyme possesses significant antimicrobial activity, highlighting its potential for biomedical applications.

Keywords: Glutaminase, cloning, gene expression, recombinant protein, affinity chromatography, gene expression

Molecular Detection of Brucella spp. in Ardabil's Milk Supply

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BACKGROUND AND OBJECTIVES: Microorganisms transmitted through food are significant pathogens that impact food safety and contribute to human illnesses worldwide. These infections often arise from consuming contaminated food, particularly animal products such as raw milk. This cross-sectional study was conducted to assess the prevalence of Brucella spp. in bulk milk samples collected from Ardabil province, Iran.

MATERIALS AND METHODS: A total of 281 unpasteurized bulk milk samples were collected from cattle, sheep, and goats in Ardabil province, Iran, between April and August 2024. The samples were hygienically transported and kept at -20 °C. DNA extraction was conducted on 15 mL of milk, followed by pathogen identification using the polymerase chain reaction (PCR) and sequencing methods.

RESULTS AND DISCUSSION: The overall prevalence of Brucella spp. in 281 bulk milk samples was 11.3%. Pathogen detection rates in cattle, sheep, and goat milk samples were 10.8% (15/138), 12.3% (14/113), and 10% (3/30), respectively. These findings highlight the presence of Brucella spp. in unpasteurized bulk milk samples from cattle, sheep, and goats in Ardabil province, emphasizing the potential risk of brucellosis transmission. The prevalence rates underscore the need for enhanced surveillance, preventive measures, and public health interventions to mitigate infection risks and ensure the safety of dairy products for consumers.

Keywords: Milk, Brucella, PCR

Molecular detection of Helicobacter bizzozeronii in human Duodenal Ulcers: A retrospective study

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BACKGROUND AND OBJECTIVES: Helicobacter bizzozeronii (H. bizzozeronii) is originally a zoonotic agent that implicated in gastrointestinal pathology, yet its prevalence in human populations remains largely unexplored in many regions. Determining the accurate prevalence of this less-studied species is essential for understanding its potential clinical significance and guiding future therapeutic strategies.

MATERIALS AND METHODS: We conducted a retrospective analysis of 156 archived antral biopsy samples collected from patients undergoing gastrointestinal evaluation between 2018 and 2024 and stored at -80°C. Genomic DNA was extracted using standardized commercial kits. The presence of H. bizzozeronii was assessed using polymerase chain reaction (PCR) assays with species-specific primers under optimized cycling conditions.

RESULTS AND DISCUSSION: H. bizzozeronii DNA was detected in 11 out of 156 analyzed biopsy samples (prevalence: 7%), indicating a notable presence within the studied cohort. Significantly, all PCR-positive samples were derived from patients diagnosed with duodenal ulcers (DUs). The PCR methodology demonstrated high sensitivity and specificity, confirming the reliability of these findings. This study reveals a significant prevalence (7%) of H. bizzozeronii in antral biopsies taken from patients with duodenal ulcers. These findings highlight the potential role of H. bizzozeronii in pathogenesis of duodenal ulcer and underscore the importance of routine molecular screening for emerging non-H. pylori Helicobacter species, particularly in patients with unexplained gastroduodenal pathology. Further studies are warranted to elucidate the clinical implications of H. bizzozeronii infection in human and inform diagnostic and therapeutic approaches.

Keywords: H. bizzozeronii , PCR, DU, emerging infections, zoonotic diseases

Molecular detection of verotoxin producing genes (stx1, stx2) in Enterohemorrhagic E. coli

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BACKGROUND AND OBJECTIVES: Background: Shiga-toxin-producing Escherichia coli can cause mild watery diarrhea to more serious complications of hemorrhagic colitis, and hemolytic uremic syndrome to even death. Present study was conducted to detect Shiga toxin-producing Escherichia coli from grounded meat in Ilam city.

MATERIALS AND METHODS: Materials and methods: In this survey a total of 865 samples of grounded meat were collected in Ilam city, and transferred to microbiology laboratory in Ilam University. All samples were detected for microbial contamination, and all E. coli isolates were selected foe further studies. Antibiotic susceptibility test of isolates was done by Kirby-Bauer method, and molecular detection of stx1, and stx2 genes was carried out by PCR.

RESULTS AND DISCUSSION: Results: In this survey a total of 100 E. coli species were isolated, antibiogram results showed that, the highest rate of resistance was related to ampicillin in 93 isolates (93%), and the lowest rate of resistance was seen to meropenem in 4 isolates (4%). Molecular detection of frequency rate of stx1, and stx2 genes by PCR, showed that, a total of 16 isolates (16%) harbored stx1 gene, while the frequency rate of stx2 gene was 6%, and only 1 isolate (1%) was harbored stx1 and stx2 genes spontaneously. Discussion: We found that, grounded meats, harbored Shiga-toxin-producing E. coli and could be a component of Shiga-toxin-producing E. coli transmission from lambs to the humans and can pose a risk to human health in the region.

Keywords: Shiga toxin, E. coli, stx1, stx2, grounded meat, PCR

Molecular detection of virulence genes gelE, cylA in Enterococcus species, isolated from patients referred to Ilam hospitals

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BACKGROUND AND OBJECTIVES: Background: Multi-drug-resistant enterococci are important nosocomial pathogens that are shown to have high prevalence in recent years. In this study, the pattern of antibiotic resistance and frequency rate of virulence genes (gelE, and cylA) in uropathogenic enterococcus species, were investigated.

MATERIALS AND METHODS: Materials and methods: In this survey a total of 684 clinical urine samples were collected from patients referred to Ilam hospitals. All isolates were diagnosed by biochemical tests, and Enterococcus species were selected for antibiogram by using Kirby-Bauer method, and finally the frequency rate of some virulence genes (gelE, and cylA) were detected by PCR.

RESULTS AND DISCUSSION: Results: In this study a total of 100 Enterococcus species consist of 70 E. faecalis and 30 E. faecium were diagnosed by biochemical tests. Results of antibiogram showed that, the highest rate of resistant was related to ampicillin in 95 isolates (95%), and the minimum rate of resistant was related to nitrofurantoin in 8 isolates (8%). Results of PCR showed that, the frequency rate of gelE, and cylA virulence genes was 64%, and 14% respectively. Discussion: Due to the multidrug resistance enterococci and also increasing resistance of enterococcus to most common antibiotics, there is a need for preventive and control measurements. Therefore, antibiotic susceptibility testing is recommended for all patients before prescription of appropriate antibiotics.

Keywords: Enterococcus faecalis, E. faecium, gelE, cylA, PCR

Molecular detection of carbapenem resistance genes in clinical strains of Klebsiella pneumoniae isolated from urinary tract infections

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BACKGROUND AND OBJECTIVES: Klebsiella pneumoniae is an opportunistic pathogen. The carbapenems are effective therapeutic choice for the treatment of Klebsiella pneumoniae infections. This study aimed to investigate the carbapenem resistance genes in K. pneumoniae strains isolated from urinary tract infections.

MATERIALS AND METHODS: In this study, 80 clinical K. pneumoniae strains were isolated from urine samples. Antimicrobial susceptibility tests for 11 different antibiotics were performed using the disk diffusion method. Phenotypic detection of carbapenemase enzymes was performed by modified Hodge test. PCR assay further investigated resistant isolates forcarbapenemase-encoding genes.

RESULTS AND DISCUSSION: In this study, out of 80 examined isolates, 42 isolates (52.5%) were resistant to imipenem. The MHT showed that among 42 imipenem resistant strains, 30 strains (71.4%) were phenotipically carbapenemase producers. Additionally, the results of PCR method showed that 15 strains (35.7%), 12 strains(28.5%), 10 strains(23.8%) and 5 strains(11.9%) of imipenem resistant Pseudomonas aeruginosa isolates contained blaOXA-48, blaVIM, blaNDM and blaIMP genes respectively. No blaSPM gene was found in the examined samples. The study's findings reveal the alarming prevalence of beta-lactamase enzymes in K. pneumoniae strains. Early detection of carbapenem-resistant isolates and effective infection control measures are necessary to minimise further spread, as carbapenem resistance has become a public health concern.

Keywords: Klebsiella pneumoniae, UTI, MHT; antibiotic resistance; carbapenemase enzymes

Molecular Docking Discovery of Potent Anti-Clostridium perfringens Agents: Hexamethoxychalcone vs. Morin

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BACKGROUND AND OBJECTIVES: Lethal and pore-forming ε-toxin of Clostridium perfringens is associated with dysentery, enteritis, and enterotoxaemia, which can infiltrate vital organs, including the brain, kidneys, and lungs, potentially causing fatal outcomes. Early-stage toxin inhibition thus represents a promising therapeutic strategy to prevent mortality. Therefore, this study aims to evaluate and compare the potential of two anti-toxin candidates via molecular docking analysis.

MATERIALS AND METHODS: The 3D structure of ε-toxin and inhibitory ligands 2,2',4,4',6,6'-Hexamethoxychalcone and Morin were obtained from RCSB PDB (PDB ID: 1uyj) and PubChem databases, respectively. Protein and ligands were prepared and docked using Molegro Virtual Docker6.0. The best interaction was analyzed via Molegro Molecular Viewer. Finally, pharmacokinetic properties were investigated using SwissADME site.

RESULTS AND DISCUSSION: Molecular docking analysis revealed that 2,2',4,4',6,6'-Hexamethoxychalcone exhibited a significantly higher binding affinity to ε-toxin residues compare to Morin (–111.63kcal/mol vs. –74.33 kcal/mol). The interaction profile of Hexamethoxychalcone included six steric interactions, one hydrogen bond, and eight hydrophobic interactions, surpassing Morin's five steric, three hydrogen bonds, and seven hydrophobic interactions. ADME profiling further indicated that Hexamethoxychalcone possesses better water solubility (LogS:–4.19 vs. –3.16), higher lipophilicity (LogP:3.52 vs. 1.54), and lower polarity (TPSA:72.45Å² vs. 131.36Å²), making it more suitable for drug development. Overall, 2,2',4,4',6,6'-Hexamethoxychalcone demonstrated a more favorable pharmacological profile compared to Morin, indicating its potential as a better lead compound for drug development. Our findings showed that 2,2',4,4',6,6'-Hexamethoxychalcone is a more promising inhibitor of Clostridium perfringens ε-toxin compared to Morin. Further in vitro and in vivo studies are necessary to validate their therapeutic potential.

Keywords: Clostridium perfringens, Molecular Docking, Morin, Hexamethoxychalcone

Molecular Docking Evaluation of Neu5Ac2en and its Analogues as Potent Inhibitors of Klebsiella aerogenes N-acetylneuraminate Lyase

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BACKGROUND AND OBJECTIVES: Klebsiella aerogenes, an opportunistic pathogen for causing diverse hospital-acquired infections, is increasingly demonstrating resistance to conventional treatments. A critical factor in its pathogenicity is N-acetylneuraminate lyase, which facilitates the reversible cleavage of N-acetylneuraminic acid, a process integral to bacterial virulence. Addressing multidrug resistance by targeting such virulence factors holds promising therapeutic potential. This study aims to identify potent N-acetylneuraminate lyase inhibitors through molecular docking analysis.

MATERIALS AND METHODS: The 3D structure of N-acetylneuraminate lyase of Klebsiella aerogenes (PDB ID:8u93) was obtained from RCSB PDB database. The structures of Neu5Ac2en (PubChemCID:65309) and its 30 analogs were retrieved in SDF format from PubChem database. After preparing protein and ligands, 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 AND DISCUSSION: The compound (2R)-3-acetamido-2-[(1R)-1-[ethyl(propyl)carbamoyl]oxy-3-hydroxypropyl]-3,4-dihydro-2H-pyran-6-carboxylic acid (PubChemCID:166676962) emerged as the most promising inhibitor, with a molecular weight of 372.4g/mol and the most negative ΔGbind (-125.371kcal/mol). This ligand formed three hydrogen bonds with Ile206, Tyr137, and Thr48 residues, and 13 steric interactions. ADME profile indicated that this ligand had a water solubility score of -1.91, a lipophilicity score of 0.88, and a polarity score of 125.40, suggesting good drug-likeness. These findings position this compound as an inhibitor candidate against N-acetylneuraminate lyase of Klebsiella aerogenes, although further in vivo and in vitro analysis are necessary.

Keywords: N-acetylneuraminate lyase, Klebsiella aerogenes, Molecular Docking, Neu5Ac2en.

Molecular Docking Insights into 5,3',4'-Trihydroxy-3,6,7,8-Tetramethoxyflavone as a Novel IcaR inhibitor in Staphylococcus epidermidis

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BACKGROUND AND OBJECTIVES: Staphylococcus epidermidis frequently causes nosocomial infections by forming biofilms. These biofilms protect the bacteria from immune defenses and resist antibiotic treatments, making the infections difficult to treat and control effectively. A crucial protein that manages biofilm formation is IcaR (intercellular adhesion regulator). This study aims to explore new promising inhibitory candidates against IcaR via molecular docking analysis.

MATERIALS AND METHODS: The 3D structure of IcaR of S.epidermidis (PDB ID: 2zcn) was received from the RCSB PDB database. The structure of Isookanin (PubChemCID: 91196552) and its 15 analogs were retrieved in SDF format from the PubChem database. After preparing protein and ligands, molecular docking was done by Molegro Virtual Docker v.6, and only the top 1 pose of each ligand was selected through Molegro Virtual Viewer v.7. The best ligand with the lowest energy binding was chosen. Lastly, the pharmacokinetic properties were obtained via the SwissADME database.

RESULTS AND DISCUSSION: Among the evaluated analogs, the most effective inhibitor was identified as 5,3',4'-Trihydroxy-3,6,7,8-Tetramethoxyflavone (PubChemCID:54799), with a ΔGbind of -102.299 kcal/mol and molecular weight of 390.34 g/mol. Interaction analysis shows 7 hydrogen bonds with Tyr95(A), Glu149(A), Ser158(B), Ile163(B), Ser167(B), and Arg170(B) residues and 13 steric interactions with Tyr95(A), Asn117(A), Glu149(A), Arg154(B), Ser158(B), Gly162(B), Ile163(B), Ser167(B), and Arg170(B). ADME analysis revealed acceptable water solubility (LogS: -4.09), lipophilicity (XLOGP3: 2.76), polarity (TPSA: 127.82), 9 hydrogen acceptors, and 3 hydrogen donors. These findings suggest PubChemCID:54799 as a new promising IcaR inhibitor, warranting further in vivo and in vitro validation.

Keywords: Staphylococcus epidermidis, 5,3',4'-Trihydroxy-3,6,7,8-Tetramethoxyflavone, Molecular Docking, SwissADME.

Molecular identification and antifungal susceptibility pattern of Candida species isolates from HPV-positive and -negative patients with vulvovaginal candidiasis

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BACKGROUND AND OBJECTIVES: Candida species has been recovered principally as a causative agent of vulvovaginal candidiasis (VVC) from different countries. Although inflammation caused by Candida species has been shown to facilitate oncogenesis, the interactions between HPV and Candida species remain unclear. This study aimed to determine the prevalence of candida species between HPV-positive and -negative individuals with VVC.

MATERIALS AND METHODS: Samples were taken from 150 participants aged 21–67 years who applied to Firoozgar Hospital, Iran University of Medical Sciences, Iran. For detection of HPV presence and HR-HPV genotyping, PCR/direct cycle sequencing was used. The presence of Candida species in specimens of women suspected of VVC was investigated by molecular and culture methods.

RESULTS AND DISCUSSION: 86 isolates of Candida species, including C. albicans (34.9%) and non-Candida albicans species (65.1%), were obtained from 78 of 150 patients. 48 (61.5%) were HPV positive and 37 (10.5%) were found to be high- risk HPV type, including types HPV16 (67.6%), HPV51 (32.4%) and HPV31 (29. 7%). Based on the conventional and PCR-RFLP techniques, 56 isolates of non-Candida albicans species (65.1%), were obtained, including C. glabrata (n=28; 50%), C. tropicalis (n= 15; 26.8%), C. parapsilosis (n = 12, 21.4%) and C. krusei (n= 1; 1.8%). The prevalence of Candida species isolates differed in HPV-positive and -negative patients. The pattern of Candida species isolates in various HPV types were also different. Therefore, knowing the presence of Candida infection in HPV-positive women is essential to plan the treatment and prevent the risk of secondary disease.

Keywords: Candida species, human papillomavirus (HPV), vulvovaginal candidiasis, susceptibility profiles

Molecular Identification of Campylobacter jejuni in Ardabil's Milk Supply

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BACKGROUND AND OBJECTIVES: Campylobacter jejuni is the primary causative agent of human campylobacteriosis (~90%), with poultry as its most common reservoir. Other sources, such as contaminated water, unpasteurized milk, and fresh produce, have also been linked to infections. This cross-sectional study examines the prevalence of C. jejuni in bulk milk samples collected from Ardabil province, Iran.

MATERIALS AND METHODS: Between April and August 2024, 281 unpasteurized bulk milk samples were collected from cattle, sheep, and goats in Ardabil province, Iran. The samples were hygienically transported and stored at -20 °C. DNA extraction was performed on 15 mL of milk, followed by pathogen identification using the polymerase chain reaction (PCR) and sequencing methods.

RESULTS AND DISCUSSION: C. jejuni was detected in 7.8% of the 281 bulk milk samples. Prevalence rates varied by source: 5.7% in cattle (8 of 138 samples), 10.6% in sheep (12 of 113 samples), and 6.6% in goats milk (2 of 30 samples). This study confirms the presence of C. jejuni in bulk milk samples from Ardabil province, Iran, highlighting a potential public health risk. The highest prevalence was found in sheep milk. Strengthened monitoring and pasteurization efforts are essential to reduce contamination and prevent infections associated with unpasteurized dairy consumption.

Keywords: Milk, Campylobacter jejuni, PCR

Molecular Identification of the icdA Gene in Vaccine Serovars of Leptospira

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BACKGROUND AND OBJECTIVES: Leptospira species cause leptospirosis, a zoonotic disease with significant health and economic impacts worldwide. Vaccinal serovars prevent infections in livestock, but their genetic characterization is crucial to ensure vaccine efficacy and monitor strain stability. The icdA gene, a conserved housekeeping gene encoding isocitrate dehydrogenase, is a reliable molecular marker for genetic differentiation and phylogenetic analysis. This study aimed to characterize vaccine serovars of Leptospira at the molecular level using the icdA gene as a genetic marker.

MATERIALS AND METHODS: Genomic DNA was extracted from five reference strains of vaccinal serovars, including Leptospira canicola, L. grippotyphosa, L. hardjo, L. icterohaemorrhagiae, and L. pomona. The icdA gene was amplified with specific primers, producing a 674 bp PCR fragment that was subsequently sequenced. The obtained sequences were aligned and analyzed to assess allelic variation and infer phylogenetic relationships among the strains.

RESULTS AND DISCUSSION: Sequence analysis demonstrated that the icdA gene possesses high discriminatory power. The results showed a percentage similarity ranging from 86.6% to 100% among vaccinal Leptospira serovars. Several single nucleotide polymorphisms (SNPs) were detected in the icdA gene, enabling clear known discrimination between serovars. Phylogenetic analysis revealed clustering patterns consistent with serogroup classifications, confirming the reliability of icdA as a molecular marker for accurate identification of vaccine strains. The icdA gene thus serves as a robust and informative tool for the molecular characterization of Leptospira vaccinal serovars. These findings enhance our understanding of their genetic diversity and support continued surveillance and vaccine development efforts.

Keywords: Leptospira, Leptospirosis, Phylogeny, Vaccines, Genes

Molecular Identification of Ureaplasma urealyticum Infections in Semen Sample of Men Referred to Infertility Treatment Center

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BACKGROUND AND OBJECTIVES: Ureaplasma urealyticum infection is considered as one of the most important bacterial infections of reproductive system and causes changes in the volume, pH, motility, morphology and sperm count in men. This bacterium can lead to reduction in level of fertility or infertility. The aim of this study were to investigate biological parameters and the frequency of Ureaplasma urealyticum in semen samples.

MATERIALS AND METHODS: In this descriptive-analytic study, a total of 150 semen samples were collected from infertile men referred to Qom Jihad Daneshgahi Infertility Treatment Center. Semen analysis was assessed according to the guideline of World Health Organization. After the extraction of genomic DNA of semen samples, detection of Ureaplasma urealyticum was performed by PCR method using 16SrRNA specific primers and the results were analyzed using SPSS software and Pearson's correlation test.

RESULTS AND DISCUSSION: From a total of 150 semen samples 38 sample (% 25.33) were positive for Ureaplasma urealyticum The results of statistical analysis showed that there was statistically significant association between bacterial infection and in situ sperm motility(P=0.005). The results of the present study showed that Ureaplasma urealyticum seems to play an important role in infertility and infections of reproductive system in infertile mens and it is necessary to adopt appropriate strategies for the control and treatment of Ureaplasma urealyticum infections to prevent the spread of these.

Keywords: Ureaplasma urealyticum, infertility, PCR

Molecular Investigation of Aminoglycoside-modifying Enzymes among Acinetobacter baumannii Isolated From Qom

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BACKGROUND AND OBJECTIVES: Aminoglycoside antibiotics are widely used for the treatment of infections caused by Acinetobacter baumannii. Unfortunately, today the effectiveness of aminoglycosides has decreased due to the dissemination of aminoglycoside-modifying enzymes (AMEs) in clinical isolates. The aim of this study was to investigate the presence of the genes encoding aminoglycoside-modifying enzymes (phosphotransferase type) in clinical isolates of A. baumannii and evaluation of its relationship with aminoglycosides resistance.

MATERIALS AND METHODS: A total of l00 isolates of A. baumannii were collected from hospitalized patients in hospitals in Qom, Iran. The aminoglycoside resistance pattern of isolates of A. baumannii was determined by disk diffusion method and prevalence of aph(3')IIb, Aph(3')Ib and Aph(3')v genes was investigated by PCR methods. The results were analyzed using SPSS software and Pearson's chi-squared test.

RESULTS AND DISCUSSION: In the present study, the rates of resistance to amikacin, gentamicin, netilmicin, kanamycin and tobramycin were observed to be 77.6%, 73%, 63%, 100% and 63%, respectively. The results of PCR analysis of phosphotransferase type genes in A. baumannii isolates showed that 45% isolates carried Aph(3')v gene, 11.11% isolates carried aph(3')IIb gene and 7.3% isolates carried Aph(3')Ib gene. The rates of resistance to gentamicin and kanamycin were statistically higher in isolates with Aph(3')v gene than in isolates without the gene (P 0.05). The results of this study showed that the rates of resistance to aminoglycoside for treatment of infection caused by A. baumannii was high in the study region and the Aph(3')v gene was the most prevalent types of phosphotransferase among A. baumannii isolates.

Keywords: Aminoglycoside, PCR, Phosphotransferase

Molecular Investigation of TEM and CTX-M9 Genes in Escherichia coli Isolated from Hospitalized Patients in Azerbaijan Hospital, Urmia, Iran

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BACKGROUND AND OBJECTIVES: Escherichia coli belongs to the Enterobacteriaceae family and causes nosocomial infections, urinary tract infections, meningitis, and diarrhea in children. This bacterium is also capable of producing the beta-lactamase enzyme, leading to resistance against beta-lactam antibiotics. The aim of the present study was to investigate the molecular presence of beta-lactamase genes in Escherichia coli isolated from hospitalized patients.

MATERIALS AND METHODS: In this study, 360 urine and blood samples from hospitalized patients in Azerbaijan Hospital in Urmia city were examined. After culturing, isolating, and performing antibiotic susceptibility tests on the strains, DNA was extracted using the boiling method, and the presence of resistance genes was assessed by the molecular PCR method.

RESULTS AND DISCUSSION: The study results showed that out of 360 samples, 98 samples were contaminated with Escherichia coli. Antibiotic susceptibility testing revealed that the highest resistance was to amoxicillin and ampicillin at 100%, while the highest sensitivity was recorded for ciprofloxacin (63%) and gentamicin (52%). In the molecular method, among 38 positive blood samples, 29 samples (76.31%) contained the CTX-M9 gene. In 50 positive urine samples, all isolates (100%) possessed both the CTX-M9 and TEM genes. Considering the over-the-counter sale of antibiotics and their uncontrolled use, resistant strains continue to spread, and with this pace, drug resistance will render infectious diseases fatal in the coming years.

Keywords: Escherichia coli, Nosocomial infections, Drug resistance, Beta-lactamase

Molecular Screening of BK and JC Viruses in Fertile and Infertile Females Using Real-Time PCR

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BACKGROUND AND OBJECTIVES: Viral infections are recognized as significant risk factors contributing to female infertility. Polyomaviruses are small, non-enveloped viruses known to cause urinary tract infections. However, no studies have yet examined their relationship with female infertility. This study aims to investigate a possible association between female infertility and infections caused by the JC and BK polyomaviruses.

MATERIALS AND METHODS: In this cross-sectional study, vaginal swab samples were collected from 50 fertile and 50 infertile women attending the Yazd Reproductive Sciences Institute Infertility Center in 2024. The samples were analyzed using Real-Time PCR to identify the presence of BK and JC polyomaviruses. Subsequently, the association between viral infection and reproductive health parameters was evaluated.

RESULTS AND DISCUSSION: None of the women in either the fertile or infertile groups tested positive for the BK virus. The JC virus was identified in three infertile participants (6%), whereas no cases were detected among the fertile women. Despite this observation, the difference in JC virus prevalence between the two groups was not statistically significant. Among the JC virus-positive infertile individuals, one participant (33.3%) exhibited ovulatory dysfunction. No other reproductive abnormalities were recorded among either the infected or uninfected infertile women. Overall, analysis revealed no statistically significant differences across any evaluated reproductive health parameters between JC virus-infected and uninfected infertile participants ($P = 1.000$). Although no statistically significant association was observed, the possibility remains that JC virus infection may be associated with ovulatory dysfunction and contribute to infertility.

Keywords: Female infertility, Polyomavirus, BK virus, JC virus, Ovulatory dysfunction

Molecular typing of Shigella flexneri using MLVA method

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BACKGROUND AND OBJECTIVES: Background: Multiple locus variable number tandem repeat (VNTR) analysis (MLVA) is a great method for typing with numerous advantages. Dissemination of Shigella is very important in developing countries. Also, the rise of drug resistance in Shigella strains is a worrying. Despite the rising importance of Shigella in Iran, there is limited knowledge about the genetic diversity among the local strains.

MATERIALS AND METHODS: The purpose of this study was to characterize the genetic diversity of Shigella strains isolated in Ahvaz Jundishapur, Iran. A total of 49 S. flexneri samples were isolated from 500 stool samples of patients, routine biochemical tests were used to identify all isolates. Antimicrobial susceptibility tests and molecular detection of resistance genes were also performed.

RESULTS AND DISCUSSION: Results: From 49 positive isolates, ESBL, Carbapenemase and Metallo-β-Lactamases were detected respectively in 93.87% (n= 46), 28.57% (n= 14), and 44.89% (n= 22) isolates. Based on the results of VNTR from 49 isolates of S. flexneri were classified into 21 distinct MLVA types with 10 clusters and 12 singleton genotype. Conclusion: The present study has offered important findings about the genetic diversity of Shigella species in Ahvaz, Iran. Our findings demonstrated that MLVA is a viable method for investigating Shigella species as it is cost-effective, provides quick results, and allows for easy sharing of numerical data between laboratories.

Keywords: MLVA, Shigella, Resistance genes

Nanoparticles as a Novel Alternative to Antibiotics for Combating Bacterial Biofilms

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BACKGROUND AND OBJECTIVES: Antimicrobial resistance (AMR) poses a significant challenge in veterinary medicine, global health, and zoonotic pathogens, threatening animal welfare, food security, and public health through direct transmission between animals and humans. According to the World Health Organization, the overuse of antibiotics in livestock, particularly in immunocompromised animals, has led to the emergence of multidrug-resistant (MDR) pathogens, including Salmonella enterica, Clostridium difficile, Klebsiella pneumoniae, Pseudomonas aeruginosa, Escherichia coli, and Streptococcus pneumoniae, accelerating the global AMR crisis.

MATERIALS AND METHODS: Consequently, there is an urgent need for effective alternatives to address this issue. Nanoparticles, with their unique properties, have emerged as a promising alternative, demonstrating reduced toxicity in laboratory settings. They combat antibiotic resistance and microbial activity by disrupting cell membranes, generating reactive oxygen species, and inhibiting biofilm formation, which impedes drug resistance pathways. This systematic review evaluates the mechanisms of action of metallic nanoparticles, such as silver and zinc oxide, and polymeric nanoparticles as alternatives to antibiotics in veterinary medicine. It examines their efficacy against MDR pathogens, applications in treating veterinary infections, and potential in managing foodborne intoxications. The review also explores challenges in combating biofilm formation and discusses therapeutic strategies, including composite materials, hydrogels, and biological approaches.

RESULTS AND DISCUSSION: Recent studies highlight the promise of nanoparticles in future pharmacotherapy as a replacement for traditional approaches. By synthesizing current research, this review offers valuable insights into addressing AMR and biofilm-associated infections, outlining future directions and conclusions for advancing nanoparticle-based solutions in veterinary medicine.

Keywords: novel compounds, nanomaterials, foodborne zoonotic pathogens, antimicrobial resistance, reduced susceptibility

Naso-oropharyngeal Colonization by Candida Species in Laboratory-Confirmed COVID-19 Patients

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BACKGROUND AND OBJECTIVES: Candida colonization of oral mucosa is a key factor in opportunistic oropharyngeal candidiasis, common in hospitalized COVID-19 patients, especially those in ICUs on ventilators. Immune suppression, mineral deficiencies, and hospital transmissions increase vulnerability. This colonization worsens COVID-19 by causing inflammation and immune impairment, potentially leading to ventilator-associated pneumonia. The study examined colonization in COVID-19 patients and its links to viral load, demographics, and health factors.

MATERIALS AND METHODS: This study examined 457 COVID-19 patients in Semnan, Iran. The patients' COVID-19 diagnosis was confirmed using the COVITECH Multiplex rqPCR kit. A questionnaire was used to gather demographic, medical, and laboratory data. Candida colonization was assessed using CHROMagar Candida medium and identified using polymorphism-polymerase chain reaction. Statistical analysis was conducted using SPSS software, including the Chi-square test and t-test to assess group differences and associations.

RESULTS AND DISCUSSION: Results: In a study of 457 COVID-19 patients, 35.5% had Candida colonization, with the highest rate in the 40-49 age group and 59.2% of colonized patients being male. Six Candida species were identified, most commonly C. albicans followed by C. glabrata. A significant association was found between certain factors and naso-oropharyngeal Candida colonization. Conclusion: Candida colonization in the naso-oropharynx is linked to early COVID-19, especially in patients with Ct ≤ 20. The risk increases with older age, lower education levels, and occupations such as housewives and workers. Further prospective studies are needed to determine if COVID-19 is an independent risk factor for Candida colonization in this region.

Keywords: Candida colonization, COVID-19, Nasopharynx, Oropharynx, associated factors

National and International Microbiological Standards for Food: From Theoretical Framework to Operational Implementation

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BACKGROUND AND OBJECTIVES: National and international food microbiology standards are fundamental pillars for ensuring food quality and safety. These standards include international requirements such as ISO 16140 (validation of microbiological methods), ISO 22000 (food safety management systems), Codex Alimentarius guidelines, and recommendations from the World Health Organization (WHO) and the World Organization for Animal Health (WOAH), all of which play a critical role in reducing microbial hazards and preventing foodborne illnesses .

MATERIALS AND METHODS: The theoretical section analyzes the scientific and methodological frameworks underpinning these standards, including applied microbiology principles, sampling strategies, identification and quantification of pathogenic agents (e.g., Salmonella, Listeria monocytogenes, E. coli O157:H7, and Campylobacter), and key concepts such as microbiological criteria, acceptance limits, and risk-based approaches to food safety assessment. The focus then shifts to the operational implementation of these standards across the food supply chain. This includes applying standards in diagnostic laboratories, food production units, hygiene inspection systems, and national surveillance programs.

RESULTS AND DISCUSSION: Challenges such as discrepancies in standard implementation between countries, the need for trained personnel, equipment calibration, and laboratory accreditation are also examined. Case studies from countries with advanced microbiological standard implementation are presented to extract practical lessons from successes and limitations. Finally, recommendations are provided for greater harmonization between national and international standards, strengthening laboratory infrastructures, and integrating advanced technologies—such as Real-time PCR, Next-Generation Sequencing (NGS), and biosensors—into microbial monitoring systems. By emphasizing the transition from theoretical frameworks to effective practical actions, this paper offers strategies to enhance national and global food safety surveillance systems.

Keywords: standards, food safety,

National Surveillance of Antimicrobial Consumption in Iran: Trends and AWaRe Classification (2020–2023)

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BACKGROUND AND OBJECTIVES: Background: Antimicrobial resistance (AMR) is a growing global health concern, driven largely by inappropriate antibiotic use. In response, Iran has implemented a national surveillance system to monitor antibiotic consumption and promote rational prescribing.

MATERIALS AND METHODS: Methods: Data were collected from national pharmaceutical distribution records and analyzed using the Defined Daily Dose per 1000 inhabitants per day (DID) metric. Antibiotics were classified according to the WHO AWaRe framework (Access, Watch, Reserve) and ATC codes. Trends from 2020 to 2023 were evaluated at the total global level.

RESULTS AND DISCUSSION: Results: Iran's total antibiotic consumption showed an upward trend, with significant increases in macrolides (J01F), penicillins (J01C), and cephalosporins (J01D). Azithromycin, amoxicillin, and cefixime were among the most consumed agents. The proportion of Watch and Reserve antibiotics increased over time, raising concerns about resistance. Compared to European countries, Iran's DID values were notably higher. Hospital data revealed high usage of cefazolin, ceftriaxone, and meropenem. Conclusion: Iran's antibiotic consumption patterns highlight the urgent need for strengthened stewardship programs. The AWaRe classification provides a strategic framework to guide rational use and reduce AMR risks. National policies should prioritize Access antibiotics and regulate the use of Watch and Reserve agents.

Keywords: Antibiotic consumption, AWaRe classification, Iran, Defined Daily Dose

Need for Complementary Specific Tests Accompanied by Tuberculin Testing for the Control of Bovine Tuberculosis in Iran

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BACKGROUND AND OBJECTIVES: Non-tuberculous Mycobacteria (NTMs) increasingly complicate the control and eradication of bovine tuberculosis (BTB) in Iran. While the Mycobacterium tuberculosis complex (MTBC) remains the primary focus of BTB programs, NTMs—especially the Mycobacterium avium complex (MAC)—pose growing concerns due to their impact on surveillance outcomes. On a farm in Qazvin, tuberculin testing showed about 30% positivity among heifers. This study aimed to isolate and identify Mycobacteria from tuberculin-positive cattle, rodents on infected premises, and other suspect samples, including sputum from tuberculin-positive workers.

MATERIALS AND METHODS: Specimens were collected from abattoir-positive cattle and rodents, and human sputum. Cultures were performed, and isolates were examined using Ziehl–Neelsen staining and fluorescence microscopy. Confirmatory identification employed PCR, with species-level resolution achieved through sequencing and long-amplicon 16S rRNA analysis. MTBC members (e.g., M. bovis, M. tuberculosis) were distinguished via RD typing or PCR-RFLP.

RESULTS AND DISCUSSION: Mycobacterium thermoresistibile, an NTM, was identified among isolates. Some human and animal samples yielded negative results after intervention. MTBC members (M. bovis, M. microti) were detected in cattle isolates, and rodent reservoirs emerged as potential challenges to eradication. Co-infections of BTB with Paratuberculosis persisted, with M. bovis often acting as the primary pathogen on affected farms. NTMs can disrupt BTB control and may interact with established infections on farms. Relying solely on MTBC diagnostics risks missed detections and hindered eradication. Rodent reservoirs and co-infections complicate control strategies, underscoring the need for broader diagnostics. So, expanding surveillance to NTMs, notably MAC and Paratuberculosis, is essential for improving diagnostic accuracy.

Keywords: Mycobacterium tuberculosis complex, Non-tuberculous Mycobacteria, Bovine tuberculosis, Tuberculin test

New findings in human phage therapy till 2025

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BACKGROUND AND OBJECTIVES: Antibiotic resistance has become a global health threat, complicating the treatment of different clinical infections. Its rise has rendered many antibiotics ineffective, increased mortality rates, and elevated healthcare costs. Meanwhile, the development of new antimicrobials lags due to scientific, economic, and regulatory barriers. Phage therapy, which employs lytic bacteriophages that specifically target and destroy bacterial hosts without harming human cells, offers a promising alternative.

MATERIALS AND METHODS: This study analyzed peer-reviewed literatures published between 2020 and 2025, including systematic reviews, clinical trials, and genomic/transcriptomic studies. Different studies about combatting clinical bacteria especially multidrug resistant isolates using bacteriophages were investigated. The last studies in human phage therapy, their administration routes, used doses of phages and also challenges are needed to be solved for expanding therapeutic use of bacteriophages in humans were reviewed.

RESULTS AND DISCUSSION: Variuos studies highlighted the promising potential of phage therapy as a novel approach to combat multidrug-resistant pathogens. Treatment of cystic fibrosis infections, as a severe and life-threatening cases, with multi drug-resistant p. aeruginosa isolates were performed successfully using a phage cocktail. In addition, in different cases of diabetes with severe multi drug resistant foot infections, these patients saved from diabetic foot amputation using appropriate phage cocktails. Also, according to a new study in Belgium on 100 different cases treatment using phage therapy, they declare good and critical treatment in human infections occurred. For widespread implementation still faces challenges related to standardization, safety, and legal frameworks. Continuous research and clear rules enable wider clinical use.

Keywords: phage therapy, antibiotic resistance, lytic bacteriophages, clinical trials

New Roles for Non-antibiotic Drugs: Antidepressants vs. Multidrug-resistant Pseudomonas aeruginosa

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BACKGROUND AND OBJECTIVES: Antibiotic resistance has emerged as one of the most pressing global health challenges, leading to increased mortality rates and escalating healthcare costs. Antidepressants, widely prescribed across the globe, may effect on susceptibility bacteria to antibiotics and biofilm formation. This study aimed to evaluate the effect of antidepressants including sertraline (SER), amitriptyline (AMT), and fluoxetine (FLX) on antibiotic resistance and biofilm formation in P. aeruginosa clinical isolates, focusing on changes in MIC and MBIC in the presence of meropenem, ciprofloxacin, amikacin, and cefepime.

MATERIALS AND METHODS: This study was performed on five clinical isolates and two standard strains of Pseudomonas aeruginosa PAO1 and ATCC 27853. The minimum inhibitory concentrations (MICs) and minimum biofilm inhibitory concentrations (MBICs) of the antidepressants and antibiotics were determined and then the MIC and MBIC of bacteria to antibiotics were determined in the with/without of sub-inhibitory concentrations of antidepressants.

RESULTS AND DISCUSSION: All clinical isolates were resistant to MEM, CIP, AMK and FEP. The antidepressants alone exhibited weak antibacterial activity (MICs: 64–512 µg/mL), but in combination with antibiotics, they significantly (0.0001) reduced the MIC and MBIC values in some isolates. The greatest MIC reductions were observed with SER+MEM and AMT+CIP combinations. Antidepressants such as SER+FEP also significantly (0.0001) inhibited biofilm formation, as reflected by decreased MBIC values. Antidepressants may potentiate the activity of selected antibiotics against MDR P. aeruginosa isolates. These findings highlight the potential of drug repurposing strategies in combating antibiotic resistance and emphasize the need for further investigation into the underlying mechanisms.

Keywords: Pseudomonas aeruginosa, Antibiotic resistance, Antidepressants drugs, Biofilm

Nitrate removal from contaminated subsurface water using technologies based on denitrifying bacteria

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BACKGROUND AND OBJECTIVES: One important concern in drinking water consumption is its quality with respect to nitrate content. According to World Health Organization standards, the maximum permissible concentration of nitrate, expressed as nitrogen (NO3-N), in water is 10 mg/L. Nitrate typically enters water sources due to agricultural activities or the discharge of sanitary wastewater

MATERIALS AND METHODS: Among industrial methods for nitrate removal, biotechnology stands out as one of the most effective. Nitrate-reducing bacteria can eliminate nitrate from water under anoxic conditions. This article reviews the biological technologies employed to remove nitrate from contaminated water.

RESULTS AND DISCUSSION: While biological denitrification research in the country remains largely at the laboratory stage, other countries have successfully implemented these technologies. For example, fluidized bed reactors (FBR) can treat large volumes of nitrate-contaminated water at low cost, achieving removal efficiencies over 99%, and reducing nitrate levels to below 0.1 mg/L. This method has received health authority approval for groundwater treatment. Granular activated carbon (GAC) filters are another common approach, adsorbing nitrate ions and supporting denitrifying bacteria to convert nitrate into nitrogen gas, often lowering nitrate concentrations below 5 mg/L in treatment plants. Moving Bed Biofilm Reactor (MBBR) systems also offer effective nitrate removal by using biofilm carriers with high surface area. Employed especially for agricultural runoff treatment, MBBRs utilize molasses as a carbon source, achieving nitrate removal efficiencies between 75% and 94%.

Keywords: Nitrate removal, denitrifying bacteria, nitrate-contaminated water, Moving Bed Biofilm Reactor

Novel Therapeutic Approaches for the Treatment of Diabetic Foot Infections Caused by Bacterial Biofilms

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BACKGROUND AND OBJECTIVES: Diabetic foot ulcers (DFUs) are a major complication of diabetes, often becoming chronically infected due to bacterial biofilm formation. These biofilms shield pathogens from antibiotics and immune responses, leading to poor wound healing and increased risk of amputation. Addressing biofilm-associated resistance has become a critical focus in advancing diabetic wound care.

MATERIALS AND METHODS: A comprehensive literature review was performed using databases such as PubMed, ProQuest, Scopus, Embase, Google Scholar, ScienceDirect, and Wiley to identify recent developments in antibiofilm therapies

RESULTS AND DISCUSSION: The study highlights several innovative approaches targeting biofilm-related infections in DFUs. These include sonocatalytically activated C_3N_4 nanosheets and gold-silver nanoparticles used in photodynamic therapy, both of which generate reactive oxygen species to disrupt biofilms. Antimicrobial peptides like nisin Z effectively combat biofilms formed by Pseudomonas aeruginosa and Staphylococcus aureus. Natural compounds such as Ginkgo biloba extract, phloretin, and eugenol inhibit biofilm formation by downregulating genes involved in adhesion and quorum sensing. Furthermore, the synthetic peptide AMP 108 targets signaling molecules like ppGpp, significantly reducing biofilm formation, drug resistance, and bacterial virulence in pathogens including Acinetobacter baumannii, P. aeruginosa, and S. aureus. These emerging therapies offer promising alternatives for managing treatment-resistant DFUs. By targeting biofilms and their underlying molecular pathways, they have the potential to enhance healing outcomes and improve patients' quality of life

Keywords: Diabetic foot ulcer, Bacterial biofilm, Antibiofilm therapy, Novel treatments

Occurrence of Biofilm-Associated Genes and Biofilm Production Capacity in Clinical Pseudomonas aeruginosa Strains

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BACKGROUND AND OBJECTIVES: Pseudomonas aeruginosa is a significant opportunistic pathogen in healthcare settings, responsible for severe infections. Its pathogenicity is largely attributed to various toxin secretion systems, including the Type III secretion system effectors. These toxins contribute to virulence and antibiotic resistance, complicating treatment outcomes. This study aimed to determine the prevalence of toxin-related genes and the antibiotic resistance profiles of clinical P. aeruginosa isolates.

MATERIALS AND METHODS: A total of 100 clinical isolates of P. aeruginosa were collected from diverse clinical specimens. Antibiotic susceptibility testing was performed according to CLSI guidelines to assess resistance patterns against commonly used antibiotics such as ceftazidime, ciprofloxacin, meropenem, and others. Polymerase Chain Reaction (PCR) was used to detect the presence of toxin genes exoS, exoT, exoU, and exoY.

RESULTS AND DISCUSSION: The antibiotic resistance analysis revealed high resistance rates to ceftazidime and ciprofloxacin, while meropenem showed the highest susceptibility . Among the toxin genes, exoT was the most prevalent, detected in 85% of isolates, followed by exoS (75%), exoY (65%), and exoU (40%). Notably, isolates harboring exoU exhibited higher multidrug resistance rates compared to those lacking this gene, suggesting a link between toxin gene carriage and antibiotic resistance. The high prevalence of toxin system genes among clinical P. aeruginosa isolates, coupled with significant antibiotic resistance, underscores the critical role of these virulence factors in infection severity and treatment challenges. Continuous surveillance and targeted therapeutic strategies are essential to manage infections caused by these MDR and highly virulent strains in hospital settings.

Keywords: Pseudomonas aeruginosa, toxin genes, antibiotic resistance, PCR, nosocomial infections

Occurrence of fluoroquinolone resistance genes in clinical isolates of EAEC from patients suffering diarrhea in Bushehr

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BACKGROUND AND OBJECTIVES: Enteroaggregative Escherichia coli (EAEC) is a major diarrheagenic pathotype of E. coli, known to cause acute and persistent diarrhea. Fluoroquinolones are among the most commonly prescribed antibiotics for bacterial gastrointestinal infections. However, the emergence and spread of fluoroquinolone-resistant E. coli strains pose a growing public health threat. This study aims to determine the prevalence of qnrA, qnrB and qnrD genes in EAEC obtained from diarrheal patients in Bushehr.

MATERIALS AND METHODS: A total of 16 EAEC isolates were obtained from stool samples of diarrheal patients by multiplex PCR for aggR and pCVD432 genes from November 2021 to April 2022 from two hospitals in Bushehr. Total DNA was extracted by boiling method. The isolates were analyzed to detection antibiotic resistance through susceptibility test according to CLSI recommendations. EAEC isolates were evaluated by PCR for presence of qnrA, qnrB, and qnrD fluoroquinolones resistance genes.

RESULTS AND DISCUSSION: Antimicrobial susceptibility testing revealed the high susceptibility rate to Ciprofloxacin (68.75%). Ciprofloxacin Resistance was detected in 12.5% of isolates, and 18.75% of isolates showed intermediate. Out of these isolates, qnrB gene was detected in 9 (56.25%) samples by PCR, and none of the isolates were found to carry the qnrA or qnrD genes. Our findings indicate a notable presence of fluoroquinolone resistance genes among EAEC isolates obtained from patients in Bushehr. Understanding the distribution of these resistance determinants can help guide effective treatment strategies and support local antimicrobial resistance monitoring efforts.

Keywords: .Enteroaggregative E. coli, Diarrhea, Ciprofloxacin, PCR, Qnr

On the presence of nosF gene in the four aquatic and terrestrial Neowestiellopsis strains revealing antifungal and trypsin inhibitor activity

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BACKGROUND AND OBJECTIVES: Cyanobacteria are one of the most widespread microorganisms on earth, and they are found in almost all ecosystems, from fresh and marine waters to terrestrial environments. Neowestiellopsis strains received a great deal of attention as prolific producers of bioactive secondary metabolites which are highly toxic to humans and other animals. Discovery of several dead dogs, mice, ducks, and fish around paddy fields, prompted us to study the toxic compounds and characterize novel bioactive natural products from four Neowestiellopsis strains isolated from aquatic and terrestrial paddy fields of Gilan province.

MATERIALS AND METHODS: To determine if the Neowestiellopsis strains are a potential producer of toxins, genomic DNA was amplified by conventional PCR using primers targeting a specific gene of the biosynthetic gene cluster of the toxin to be detected. In addition, extracted compounds of the Neowestiellopsis strains were examined for bioactivity against the yeast Candida albicans and the fungus Aspergillus flavus.

RESULTS AND DISCUSSION: Results of molecular analysis, demonstrated that the only two aquatic strains contain the nosF gene and a remarkable antifungal activity was identified in the methanolic extracts. While trypsin inhibitor was detected from two terrestrial strains. Based on the results, this study suggests that methylproline-containing compounds in two aquatic strains might account for the death of these animals. This case is the first documented incident of toxicity from aquatic cyanobacteria related intoxication in dogs, mice, and aquatic organisms in Iran.

Keywords: Natural bioactive compound, Neowestiellopsis, Toxicity, Antifungal, nosF gene

One Health Approach, Antimicrobial Residues in Foods and its Impact on Public Health

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BACKGROUND AND OBJECTIVES: The emergence of AMR in food-borne pathogens is one of the most important aspects of preharvest food safety, which is mainly attributed to the irrational (Illogical) use of antimicrobials in food animals. Prolonged use of sub-therapeutic doses of antimicrobials in food animals for growth promotion and disease prevention results in the development of multi-drug resistance in bacterial pathogens. Antimicrobials in low doses kill the majority of the gut microbiota, but some resilient bacteria are able to survive and become resistant over time. Extensive usage of important antibiotics in production animals speeds up this process and creates selective pressure on bacteria that eventually develop resistance to survive. These farms become a reservoir for the selection of new AMR bacteria that can be exchanged between animals and humans.

MATERIALS AND METHODS: The resistant bacteria originating from production systems can travel to surrounding human dwellings (habitation) and slaughter and processing units and transfer antimicrobial-resistant determinants to the native microbial population. The major public health significance of antimicrobial residues include: 1- the development of antimicrobial drug resistance, 2- hypersensitivity reaction, 3- carcinogenicity, 4- mutagenicity, 5- teratogenicity, 6- bone marrow depression, 7- and disruption of normal intestinal flora.

RESULTS AND DISCUSSION: Conclusion: Food safety efforts and monitoring are required by international standards set by the joint Food and Agriculture Organization of the United Nations and the World Health Organization (FAO/WHO) Codex Alimentarius Commission (CAC).

Keywords: Keywords: Antimicrobial Residues, Foods, One Health, Public Health.

Optimization of fibrinolysin production by Bacillus mycoides strain 30

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BACKGROUND AND OBJECTIVES: Fibrinolysin is a enzyme involved in fibrin clots breakdown. The formation of these clots can contribute to various cardiovascular conditions, including hypertension and acute myocardial infarction. Additionally, fibrin accumulation on medical devices like stents can lead to ischemia and the development of thrombi. The aim of this study was to optimize the fibrinolysin production by the Bacillus mycoides strain 30.

MATERIALS AND METHODS: The isolate was cultured in Nutrient broth and incubated at 30, 37 and 43˚C and the optimum temperature was obtained based on the growth curve analysis. Subsequently, it was cultured in Nutrient broth at pH 6,7 and 8 and incubated at optimum temperature from previous step for 24h and optimum pH was obtained. Following bacterial culture at optimum pH and temperature, sterile blank discs were saturated with the supernatant of isolates (10000 rpm, 5 min) and placed for 24h at 37˚C on plasma plate (1ml of plasma, 4ml agar and 1ml of thromboplastin D) and the amount of fibrin digestion was determined based on the diameter of formed halo zone.

RESULTS AND DISCUSSION: As a result of this study, optimum temperature and pH for Bacillus mycoides strain 30 were obtained as 30˚C and 8, respectively. In these conditions it was led to an increase in fibrinolysin production which was identified with 9mm clear halo zone. Based on the results obtained, it can be concluded that Bacillus mycoides strain 30 can efficiently produce fibrinolysin under optimal temperature and pH conditions, indicating its potential for large-scale enzyme production.

Keywords: Bacillus mycoides strain 30, Fibrinolysin, Plasma plate

Optimization of Saccharomyces cerevisiae cultivation conditions for bioethanol production using the Taguchi experimental design method

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BACKGROUND AND OBJECTIVES: Due to the environmental consequences of consuming non-renewable energy resources, achieving clean and sustainable energy sources has become a global priority. Bioethanol represents one of these alternatives, generated via the fermentation of sugars found in sugar beet molasses by Saccharomyces cerevisiae. Enhancement of ethanol production yield via this pathway can be achieved by optimizing the culture medium composition through the use of macro elements and employing the Taguchi statistical approach for experimental design.

MATERIALS AND METHODS: In the present study, an experimental design based on the Taguchi statistical approach was employed to optimize the culture medium for bioethanol production. The investigated factors included ammonium sulfate, magnesium sulfate, yeast extract, molasses Brix, and yeast inoculum level, each examined at four distinct levels. A total of sixteen treatment combinations were formulated based on varying levels of the selected factors. Following 72 hours of anaerobic incubation, ethanol production was quantitatively determined through spectrophotometric and colorimetric analysis using sodium dichromate.

RESULTS AND DISCUSSION: The experimental results indicated that Treatment 14, comprising 20g/L ammonium sulfate, 8g/L magnesium sulfate, 10g/L yeast extract, and 1g/L yeast inoculum in a medium with a Brix of 22, achieved the highest ethanol yield at 10.5%. This yield corresponds to a 15% improvement in bioethanol production efficiency compared to the non-optimized treatment, which produced 9%. Conclusion: The improvement in bioethanol production efficiency achieved in this study holds industrial relevance, as bioethanol is recognized as a sustainable and economically viable alternative to non-renewable energy sources.

Keywords: Key words: Optimization, Saccharomyces cerevisiae, Ethanol, Taguchi.

Oral Dysbiosis and Its Role in Periodontal Disease Progression

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BACKGROUND AND OBJECTIVES: Periodontal disease is a chronic inflammatory condition marked by irreversible destruction of the supporting structures of the teeth. The disease is driven by a dysbiotic shift in the oral microbiome, wherein health-associated microbial communities are disrupted, leading to enrichment of pathogenic species and dysregulated host immune responses. This study aims to review the microbiome-host interactions involved in the pathogenesis and progression of periodontal disease.

MATERIALS AND METHODS: A comprehensive literature review was performed using PubMed, Scopus, and Web of Science databases, covering studies from 2015 to 2025. Inclusion criteria were peer-reviewed original and review articles discussing microbiome composition, host immune modulation, and microbial mechanisms in periodontitis. Studies lacking sufficient data were excluded.

RESULTS AND DISCUSSION: Biofilm maturation involves coaggregation of early colonizers (e.g., Streptococcus, Actinomyces, Neisseria) with late colonizers (P. gingivalis, T. forsythia, F. nucleatum), resulting in spatially organized communities. Dysbiosis promotes immune evasion and tissue destruction through genotoxins, oxidative stress, and immune modulation. Pathogens such as P. gingivalis degrade complement and subvert neutrophil function. Socransky's red and orange complexes are enriched in periodontitis, while yellow, green, and purple complexes are associated with health. Host responses, particularly Th17-driven inflammation and reduced Treg-mediated regulation, amplify bone loss via IL-17–mediated osteoclastogenesis. Genetic, lifestyle, and environmental factors such as diet and smoking exacerbate microbial imbalance. Periodontitis results from a breakdown in oral microbial and immune homeostasis. Future studies should focus on host-microbiome-targeted therapies and early biomarkers to guide preventive and personalized interventions.

Keywords: Periodontitis, Microbiota, Biofilms, Dysbiosis, Th17 Cells

Oral Egg-Derived IgY as a Novel Adjunct Therapy for Helicobacter pylori-Associated Peptic Ulcers: A Randomized Clinical Trial

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BACKGROUND AND OBJECTIVES: The routine antibiotic regimens for treating Helicobacter pylori-associated peptic ulcers are increasingly ineffective due to rising antibiotic resistance. In recent years, egg-derived IgY antibodies have emerged as a potential alternative or complementary therapeutic approach. This randomized clinical trial aimed to evaluate the clinical efficacy of IgY antibodies as a novel adjunct therapy for H. pylori-associated peptic ulcers.

MATERIALS AND METHODS: One hundred chickens were immunized with whole-cell preparations of multiple H. pylori strains isolated from patients. IgY antibodies were extracted and purified from egg yolks. Following preclinical validation in a murine model infected with H. pylori, a randomized, double-blind clinical trial was conducted involving 60 patients with H. pylori-associated peptic ulcers. Participants were randomly assigned to receive either IgY in combination with standard therapy (intervention group) or placebo with standard therapy (control group). Clinical symptoms—including stomach pain, nausea, anorexia, belching, and bloating—were assessed using standardized indicators.

RESULTS AND DISCUSSION: The intervention group showed a significant reduction in urea breath test scores. H. pylori eradication rates were higher in the intervention group (66.7%) compared to the placebo group (40%). Symptomatic relief—particularly in terms of stomach pain, nausea, and bloating—was observed more rapidly in the intervention group. Adjunct therapy with IgY antibodies appears to be a safe and effective strategy for reducing bacterial load and improving clinical symptoms in patients with H. pylori-associated peptic ulcers. This approach may offer a promising alternative for patients with antibiotic-resistant infections

Keywords: Helicobacter pylori, IgY antibody, clinical symptoms, Randomized Clinical Trial

Overcoming drug resistance: thymol and cefotaxime synergy against Acinetobacter baumannii and Klebsiella pneumoniae

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BACKGROUND AND OBJECTIVES: This research evaluates the combined antimicrobial effects of thymol and cefotaxime against Acinetobacter baumannii and Klebsiella pneumoniae.

MATERIALS AND METHODS: The antimicrobial effects of thymol and cefotaxime were evaluated individually and in combination against K. pneumoniae ATCC 100031 and A. baumannii ATCC 19906 using the MIC-MBC method. Subsequently, the synergistic antimicrobial effects of these compounds were tested on ten clinical strains employing the MIC-MBC method. Chemical bonds, functional groups, and molecular interactions were analyzed using an FTIR device. Additional experiments included the checkered method, biofilm inhibition assays targeting K. pneumoniae and A. baumannii, as well as cytotoxicity tests on RBCs through hemolysis and Ffk using the MTT method. Synergistic effects of thymol and cefotaxime investigated, and the outcomes of the tests were compared between the two bacterial species.

RESULTS AND DISCUSSION: The antimicrobial effects of thymol/cefotaxime were more effective against K. pneumoniae compared to A. baumannii in both clinical and ATCC strains. FTIR analysis revealed the presence of bonds. A unique band, C=C conjugated and C≡C, highlighted the interaction between thymol and cefotaxime. The biofilm inhibition efficacy of thymol/cefotaxime was higher for K. pneumoniae than for A. baumannii. The cytotoxicity assessment revealed that the synergistic compounds demonstrated comparable effects on RBCs and human Ffk cells, with lower toxicity compared to Triton X-100. This study found that thymol/cefotaxime demonstrated superior antimicrobial and anti-biofilm effects against K. pneumoniae compared to A. baumannii. With further research, this compound holds potential to be developed into a novel therapeutic option for patients.

Keywords: Klebsiella pneumoniae, Acinetobacter baumannii, Thymol, cefotaxime, Synergistic

Overcoming drug resistance: thymol and ceftazidime synergy against Acinetobacter baumannii and Klebsiella pneumoniae

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Keywords: bsiella pneumoniae, Acinetobacter baumannii, Thymol, Ceftazidime, Synergistic

Overview of Human Microbiome Diversity and Their Impact to Health

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BACKGROUND AND OBJECTIVES: The term microbiome refers to the collection of microorganisms such as bacteria, viruses, and fungi that live in symbiosis in the human body including the gut, skin, mouth, and the respiratory tract. The human microbiome has been shown to be actively involved in metabolism, immunomodulation, vitamin synthesis, and the modulation of nervous system functions

MATERIALS AND METHODS: The review was done by using articles from 2018-2025 alongside the descriptive sections of scientific papers, as sources of information.

RESULTS AND DISCUSSION: Different organs of the body have varying composition and diversity of microbiomes. As an example, gut microbiomes are primarily comprised of Firmicutes and Bacteroidetes while skin microbiomes consist mostly of Staphylococcus and Corynebacterium. The outcomes suggest that the microbiome is involved in the control of metabolism, boosting immunity, and vitamin and important metabolite synthesis. Moreover, an unbalanced gut microbiome (dysbiosis) is linked to a number of health conditions like obesity, diabetes, cancer, inflammatory bowel diseases, and diseases of the nervous system. In broad terms, preserving the balance of microbiota is crucial to a person's wellbeing, and its disturbances can affect the body seriously. understanding the microbiome, as well as the factors that affect it, could lead to novel approaches in disease prevention, early detection, and treatment, thereby advancing research in medicine and microbiome therapies.

Keywords: Microbiome, Human, Health, Microbial Variation, Bacteria

Overview of Microbiome and Oral Cancer

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BACKGROUND AND OBJECTIVES: The oral microbiome refers to the genomes of microorganisms that inhabit the oral cavity. After the gut, the oral cavity is the second largest and most diverse microbial communities. human microbiome members contribute to chronic inflammation in multiple cancers. There is also evidence that other types of cancer are related to changes in the human microbiome.

MATERIALS AND METHODS: The search was conducted using articles from 2018-2025 as well as the narrative sections of scientific papers, for information.

RESULTS AND DISCUSSION: The Results demonstrated that, as one of the most complex and diverse microbial communities within the human body, the oral microbiome is pertaining to oral health and its disruption directly is correlated with oral cancer development and progression. The oral microbiome can mediate the process of carcinogenesis by causing chronic inflammation, releasing carcinogens, disrupting gene expression, and suppressing immunity. Furthermore, environmental factors such as smoking, unhealthy diet and antibiotic use, can interfere with the balance of the oral microbiome and contribute to cancer risk. The oral microbiome is related to oral cancer. The balance in the oral microbiome may be critical in prevention of oral cancer. It has been suggested that microbiome modulation at different phases of the disease and therapy should be addressed in future studies.Furthermore, employing state-of-the-art methodologies such as next-generation sequencing on microbiome metabolic pathways may provide new insights on the contribution of particular species on carcinogenesis.

Keywords: Microbiome, Oral cancer, Probiotics, Chronic inflammation

PA-X Accessory Protein: An Additional Contributor to the Pathogenicity of Avian Influenza Viruses

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BACKGROUND AND OBJECTIVES: The avian influenza A virus subtype H9N2 poses a significant threat to poultry and public health due to its potential for cross-species transmission. The PA-X protein, produced by a frameshift mutation in the PA gene, facilitates the virus's evasion of immune responses by degrading cellular mRNAs. This study examines the genetic and evolutionary characteristics of the PA-X protein in H9N2 viruses from Iran.

MATERIALS AND METHODS: In this descriptive-analytical study, 15 H9N2 avian influenza virus isolates collected from outbreaks in Iran between 2017 and 2024 were examined. Following virus propagation in embryonated chicken eggs and confirmation of their identity through hemagglutination (HA) and hemagglutination inhibition (HI) assays, viral RNA was extracted. The PA-X-encoding gene was amplified using specific primers and RT-PCR. The purified PCR products were then sequenced. Finally, the obtained nucleotide and amino acid sequences were analyzed using bioinformatics tools for alignment, phylogenetic reconstruction, and structural modeling.

RESULTS AND DISCUSSION: Analysis of the PA-X gene showed high genetic and amino-acid conservation (90.5–100% and 96–100%, respectively), with all isolates forming a distinct clade related to Middle Eastern strains, particularly from Turkey. While minor mutations were observed, key motifs, such as the endonuclease active site, remained conserved. Structural modeling supported the stability of PA-X's functional domains. These findings indicate intense selective pressure on PA-X for viral pathogenicity, driven by host shutoff and immune evasion. The clustering of Iranian isolates indicates stable circulation of H9N2 in the Middle East. Continued surveillance is essential for tracking potential evolutionary changes.

Keywords: Avian influenza virus, H9N2, sequencing, genetic analysis, phylogenetic analysis, PA-X

Pathogenic Escherichia coli O-serogroups: A Link Between Virulence Gene, and Antimicrobial Resistance

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BACKGROUND AND OBJECTIVES: Escherichia coli (E. coli) is a common intestinal commensal that includes pathogenic strains responsible for sepsis, gastrointestinal infections, and urinary tract infections (UTIs). Its diverse pathotypes, virulence factors, and O-serogroups contribute to its clinical significance. The emergence of multidrug-resistant (MDR) strains has complicated treatment strategies, representing a critical global health concern.

MATERIALS AND METHODS: A literature search was conducted on PubMed, Scopus, and Google Scholar using the keywords E. coli, pathogenicity, O-serogroups, immune evasion, and antibiotic resistance. Included were studies focusing on E. coli virulence, immune evasion, and MDR, while non-English studies, case reports, and editorials were excluded.

RESULTS AND DISCUSSION: Results: Our analysis indicates that O-serogroups O25, O78, O145, and O157 are predominantly associated with MDR profiles, especially against β-lactams and aminoglycosides. This high prevalence of MDR in these serogroups significantly complicates clinical management, often leading to prolonged hospital stays, increased treatment failures, and higher rates of severe complications such as hemolytic uremic syndrome (HUS) in EHEC infections or recurrent UTIs in UPEC cases. For instance, resistance of O25 to β-lactams, observed in 92% of isolates for piperacillin, limits the efficacy of first-line therapies and necessitates the use of last-line antibiotics. This study underscores the clinical significance of O-serogroup diversity in E. coli infections and its impact on therapeutic challenges. Understanding the distribution of virulence factors and resistance genes among key serogroups provides critical insights for developing effective management strategies for E. coli infections. Future research should prioritize innovative therapeutic approaches targeting serogroup-specific resistance mechanisms.

Keywords: Escherichia coli, O-serogroups, Virulence factors, Antibiotic resistance

Phage Therapy for Multidrug-Resistant Bacterial Infections Following Lung Transplantation in Cystic Fibrosis Patients

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BACKGROUND AND OBJECTIVES: Cystic fibrosis (CF) is an autosomal recessive disorder caused by mutations in the CFTR gene, leading to defective chloride transport and the accumulation of thick mucus primarily in the lungs (1). As the disease progresses, chronic infections and inflammation cause significant lung damage, often necessitating lung transplantation (2). However, post-transplant infections with multidrug-resistant (MDR) bacteria, notably Pseudomonas aeruginosa and Burkholderia cepacia, severely compromise patient outcomes (3). Rising antibiotic resistance further limits therapeutic options (4). Phage therapy has emerged as a targeted and promising intervention for MDR infections in CF post-transplant patients, though further clinical validation is required (5).

MATERIALS AND METHODS: A systematic review of PubMed, Scopus, and Web of Science (2010–2024) was performed focusing on phage therapy in CF lung transplant recipients with MDR infections. Included studies comprised clinical trials, case reports, and preclinical investigations addressing phage therapy for P. aeruginosa and B. cepacia (3,5). Evaluated outcomes included bacterial eradication, clinical improvement, and safety (4,6).

RESULTS AND DISCUSSION: Results: Phage therapy demonstrated reductions in bacterial load and improvements in clinical symptoms such as fever resolution and pulmonary function recovery. Adverse events were infrequent and mild (4). Treatment efficacy depended on precise phage-bacterium matching, and the emergence of phage-resistant bacterial strains indicated the need for phage cocktails or combination therapies (5). Conclusion: Phage therapy offers a promising approach as a safe and targeted treatment for MDR infections in CF patients after lung transplantation. Further standardized clinical trials are essential to validate efficacy and optimize protocols.

Keywords: Cystic Fibrosis, Lung Transplantation, Multidrug-Resistant Infections, Phage Therapy, Pseudomonas aeruginosa

Phage-Antibiotic Synergy Against Salmonella enteritidis: Combating Antibiotic Resistance

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BACKGROUND AND OBJECTIVES: Salmonella enteritidis is a major cause of foodborne gastrointestinal infections. The rise of multidrug-resistant (MDR) strains has also made treatment increasingly difficult and has prompted the need for alternative strategies. This study aimed to investigate the synergistic antibacterial effect of a lytic phage combined with common antibiotics against the standard S. enteritidis strain (ATCC 13076).

MATERIALS AND METHODS: The phage was combined with three widely used antibiotics: ciprofloxacin, azithromycin, and ampicillin. Minimum inhibitory concentrations (MICs) were determined using the microbroth dilution method. Viable cell counts (CFU/ml) were measured at 0-, 6-, 12-, and 24-hours post-treatment.

RESULTS AND DISCUSSION: The combination of phage and ciprofloxacin exhibited the most significant synergistic effect, leading to a 5.8-log reduction in bacterial count compared to the control group. Phage alone resulted in a 3.2-log reduction. No notable improvement was observed with the addition of azithromycin or ampicillin alone.Combining phage therapy with antibiotics—particularly ciprofloxacin—offers a promising approach for addressing MDR Salmonella infections. Further investigations using clinical isolates, biofilm-associated infections, and animal models are recommended to confirm these findings

Keywords: Salmonella enteritidis, Bacteriophages, Drug Resistance, Drug Synergism, Anti-Bacterial Agents, Ciprofloxacin

Phages on the Menu: Friends or Foes in Food Safety?

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BACKGROUND AND OBJECTIVES: Bacteriophage (Phages) are viruses that infect only bacteria and are naturally widespread. Their high specificity makes them useful in the food industry, where they are applied in three main areas: primary production, biosanitization, and biocontrol. Phages are useful in plant and animal production stages. In biosanitization, phages or their enzymes are used to prevent biofilm formation on food-processing surfaces. As biocontrol agents, they extend the shelf life of food by reducing harmful bacteria.

MATERIALS AND METHODS: Commercial phage products are now applied across the entire food production chain. Products like AgriPhage™ protect crops from bacterial diseases, while feed additives like BAFASAL® and hide-wash preparations reduce Salmonella and E. coli in poultry and cattle. Phage-based sprays and enzyme preparations prevent biofilm formation on food-processing equipment. FDA- and EFSA-approved products such as ListShield™, EcoShield™, SalmoFresh™, and PhageGuard™ target Listeria, E. coli, and Salmonella, enhancing safety and shelf life.

RESULTS AND DISCUSSION: Despite these benefits, challenges remain. Phages can unintentionally destroy beneficial starter cultures in dairy production or transfer antimicrobial resistance genes. Bacteria can also become resistant to phages by altering their surface receptors or producing protective biofilms. In addition, regulations are not yet uniform worldwide, and guidelines for long-term monitoring are limited. This review explores the dual role of phages in the food industry. It discusses both the benefits and risks of phages in food safety and highlights strategies such as combining phages with antibiotics, CRISPR-based engineering, and using phage-resistant bacterial strains to ensure safe and effective use in the food industry.

Keywords: Bacteriophage, biosanitization, Biocontrol, food safety

Phenotypic and Genotypic Analysis of Antibiotic Resistance in Staphylococcus aureus strains Isolated from Patients and Healthcare Workers at Salahuddin General Hospital, Baghdad

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BACKGROUND AND OBJECTIVES: The rise of methicillin-resistant Staphylococcus aureus (MRSA) poses a serious public health risk, particularly in healthcare settings. In Iraq, limited data on resistance patterns hampers effective control measures. This study assessed phenotypic and genotypic resistance in S. aureus isolates from patients and healthcare workers (HCWs) at Salahuddin General Hospital, Baghdad, to support improved surveillance and stewardship.

MATERIALS AND METHODS: In 2024, a cross-sectional study analyzed 100 S. aureus isolates (50 each from patients and HCWs). Samples underwent standard microbiological testing. Resistance was evaluated using disk diffusion (12 antibiotics), and PCR was used to detect mecA, blaZ, aac(6')-Ie-aph(2")-Ia, and tetK genes. Data were analyzed using chi-square tests ($\alpha = 0.05$).

RESULTS AND DISCUSSION: MRSA was detected in 72% of isolates—80% from patients and 64% from HCWs. Resistance was highest to oxacillin, ciprofloxacin, and erythromycin. Multidrug resistance (MDR) was found in 78% of isolates, more prevalent among MRSA strains. Genotypically, mecA was most common (89% in patients, 72% in HCWs), followed by blaZ, aac(6')-Ie-aph(2")-Ia, and tetK. MRSA strains showed stronger associations with MDR and multiple resistance genes than MSSA. HCWs may act as MRSA reservoirs, contributing to hospital transmission. High MDR and gene-based resistance emphasize the need for antimicrobial stewardship, HCW screening, and enhanced infection control. These findings can guide regional policy and support genomic surveillance efforts.

Keywords: methicillin-resistant S. aureus, antimicrobial resistance, Iraq, healthcare workers, resistant genes,

Phenotypic and Genotypic Analysis of Carbapenemase Enzyme Prevalence in Clinical Isolates of Multidrug-Resistant Klebsiella pneumoniae

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BACKGROUND AND OBJECTIVES: Klebsiella pneumoniae is one of the most important human opportunistic pathogens and is an important factor in causing nosocomial infections. This bacterium is inherently resistant to a number of antimicrobial agents. The aim of this study was to determine the antibacterial resistance and phenotypic determination of carbapenemase production in clinical isolates of Klebsiella pneumoniae and detection of frequency of metallo beta-lactamses encoding IMP, VIM and KPC genes.

MATERIALS AND METHODS: In this study, isolates (n=60) of Klebsiella pneumoniae were recovered from different laboratories in Rasht. After identification of Klebsiella isolates by biochemical tests, disk diffusion method was used to determine the antibacterial susceptibility of isolates. Combined disk method was used to indentify Extended- spectrom beta-lactamase and metallo-beta-lactamases producing isolates. Frequency of of bla IMP,bla VIM and bla KPC genes in test isolates was investigated by PCR.

RESULTS AND DISCUSSION: Results. Of the 60 isolates of Klebsiella pneumoniae, 19 isolate (31.6 %) were resistant to imipenem. In total, 17 (28.33%) carbapenemase producer and 23 (38.33%) extended-spectrum beta-lactamase producer isolates were identified. The frequency of bla VIM,bla IMP, bla KPC genes in tested isolates were 18.33, 16.66 and 23/33 percent , respectively. All isolates carring the studied genes were carbapenemase producer in the phenotypic assay. Conclusion. Due to importance of presence of carbapenemase producing stains in clinical isolates of Klebsiella pneumoniae, identifiying and tracking these strains is an importantstep in trating and controling infection caused by these bacteria.

Keywords: Carbapenemase, Klebsiella pneumoniae , bla IMP,bla VIM , bla KPC

Phenotypic and genotypic detection of efflux pumps in multidruge-drug resistant clinical isolates of Klebsiella pneumoniae

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BACKGROUND AND OBJECTIVES: The increasing emergence of antimicrobial resistance among gram negative bacteria especially Enterobacteriaceae has become a globa problem. Klebsiella pneumoniae is an opportunistic pathogen which has been lionized recently,due to causing broad spectrum of disease and antibiotic resistance.Efflux pumps are one of the most important antibiotic resistance mechanism, which were introduced in this bacteria. So,the present study was aimed to determine antibiotic resistance patterns among K.pneumonia isolates and phenotypic and genotipic evaluation of effluxe pump in multidruge-drug resistant clinical isolates of this bacterium.

MATERIALS AND METHODS: in this study ٦٠ K.pneumonia isolates were isolated and identified by culturing and biochemical tests.The antibiotic susceptibility pattern was investigated by ditsc diffusion method according to CLSI.Phenotypic identification of efflux pump has been done byusing cartwheel method and the frequency of oqxA, oqxB, AcrAB genes was analyzed by PCR.

RESULTS AND DISCUSSION: In this study,colistin was the most potent antibiotic against K. pnemoniae isolates. In total,46 K. Pneumoniae isolates showed multiple antibiotic resistance. In phenotypic evaluathion of frequency of effluxe pump in clinical isolates of K.pneumonia, ٥٢ isolates (٨٦.٦%) showed active efflux pump.The prevalence of oqxA,oqxB and AcrAB genes among resistant isolates was75,٧٥ and ٩٣,٢ percent respectively. Conclusion:The results showed high rate of multiple antibiotic resisatance in Klebsiella pneumonia. The presence of oxqA,oxqb and AcrAB genes of the efflux pumps in this bacterium and antibiotic resistance reduction in the presence of efflux pump inhibitor shows the importance of examining these genes' presence to suggest a suitable treatment model for the patients infected with K.pneumonia.

Keywords: Klebsiella pneumonia,Efflux pump,OqxAB,AcrAB,Antimicrobial resistance

Phenotypic and genotypic fluoroquinolone resistance in UPEC isolates from UTIs of kidney transplant patients in Tehran

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BACKGROUND AND OBJECTIVES: Preventing the dissemination of drug-resistant bacteria is a critical public health concern. Escherichia coli is one of the most prevalent drug resistant pathogens isolated from both community acquired and hospital associated urinary tract infections (UTIs). Fluoroquinolones are one of the most useful antibiotics during E. coli UTIs. The aim of this study was to characterize the phenotypic and genotypic patterns of fluoroquinolone resistance in uropathogenic E. coli (UPEC) isolates obtained from kidney transplant recipients in Tehran.

MATERIALS AND METHODS: In this study, 50 clinical E. coli isolates from UTIs among kidney transplant patients referred to some diagnostic laboratories were collected during 2023-2025. Isolate identification was confirmed using standard biochemical methods. Antibiotic susceptibility (AST) was determined by the disk diffusion method based on CLSI 2025. The presence of the plasmid quinolone resistance genes including qnrA, qnrB, and qnrS was assessed molecularly by PCR method after DNA extraction. Statistical analysis was done by SPSS software.

RESULTS AND DISCUSSION: Based on AST, the highest resistance rate was observed against cefuroxime (84.0%), while the lowest resistance was to imipenem (6.0%). Among ciprofloxacin-resistant isolates (48.0%), the prevalence of resistant genes including qnrA, qnrB, and qnrS genes were 4.2%, 20.8%, and 75.0%, respectively. Statistical analysis revealed a significant association between ciprofloxacin resistance and the presence of the qnrA, qnrB, and qnrS genes. Treatment should be guided by local susceptibility tests beside determining of the resistance patterns is recommended to prevent the emergence of antimicrobial resistance and therapeutic failures, which can lead to complicated infections.

Keywords: Antibiotic Resistance, Kidney Transplant, E. coli

Phenotypic and Genotypic Identification of Nocardia Isolates from Suspected Tuberculosis Patients

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BACKGROUND AND OBJECTIVES: Nocardia, a genus of Actinomycetes bacteria, is Gram-positive, rod-shaped, catalase-positive, partially acid-fast, and strictly aerobic. They infect humans mainly via inhalation or wounds, causing nocardiosis. The current study employed molecular techniques alongside biochemical methods due to challenges in accurate phenotypic and genotypic identification of Nocardia isolates from tuberculosis-suspected patients in Iran.

MATERIALS AND METHODS: Clinical specimens from patients suspected of tuberculosis at the Pasteur Institute were cultivated on blood agar, Löwenstein-Jensen, and BCYE media. Gram and Ziehl-Neelsen staining, phenotypic testing, DNA extraction, genotypic identification via RFLP-PCR targeting five genes (hsp65, 16S rDNA, rpoB, secA1, gyrB), and phylogenetic analysis using MEGA software were performed.

RESULTS AND DISCUSSION: Among 54 clinical isolates, 45 (83.3%) were from sputum, 5 (9.3%) from bronchoalveolar lavage, 3 (5.6%) from biopsy, and 1 (1.8%) from wound. Twelve isolates were classified as Nocardia asteroides complex, while others remained identified as clinical Nocardia isolates. These findings indicate that diverse Nocardia species can cause disease in vulnerable Iranian populations. Larger future studies are needed for precise species-level identification and antimicrobial susceptibility profiling, which may also uncover novel species.

Keywords: Nocardia, drug resistance, genotypic characterization, phenotypic analysis, antimicrobial susceptibility

Phenotypic and Genotypic Identification of Nontuberculous Mycobacteria Isolates from Clinical Samples of Patients Suspected of Tuberculosis

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BACKGROUND AND OBJECTIVES: Nontuberculous mycobacteria (NTM) are today prevalent opportunistic pathogens of pulmonary infections, while they were previously considered harmless environmental saprophytes. One of the therapeutic problems is the difficulty of differentiating NTM from Mycobacterium tuberculosis, which has become a serious threat and challenge in the global health system. Therefore, the use of accurate techniques can be one of the necessary solutions for their timely and effective diagnosis and treatment. This study aimed to use phenotypic and genotypic methods to accurately differentiate nontuberculous Mycobacteria from M. tuberculosis in patients' clinical samples suspected of tuberculosis (TB) disease.

MATERIALS AND METHODS: After collecting clinical samples from patients suspected of tuberculosis, they were prepared with N-acetyl-1-cysteine. Then, selective culture medium, Ziehl-Neelsen staining, and biochemical tests were used for NTM screening. Following DNA extraction, the NTM species were accurately identified using the MLST method, along with the sequences of the hsp65, roB, and 16S rRNA genes. Finally, the MEGA software was used to analyze the data and draw phylogenetic trees.

RESULTS AND DISCUSSION: Among 1650 clinical samples, 50 species of NTM were identified using molecular techniques. On the other hand, the observation of more than 99% sequence similarity with standard strains and high bootstrap values indicated significant accuracy and confidence in species determination. Therefore, given the importance of diagnosing NTM and differentiating it from M. tuberculosis, the use of simultaneous phenotypic and genotypic methods can play a significant role in the accurate identification and rapid treatment of patients with pulmonary infections.

Keywords: Nontuberculous Mycobacteria, Multilocus Sequence Typing, Phylogenetic Analysis, Pulmonary Disease

Phenotypic and Genotypic Resistance Pattern Analysis of the KPC Gene in Klebsiella pneumoniae Isolates from ICU Patients at a Tertiary Care Hospital

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BACKGROUND AND OBJECTIVES: Klebsiella pneumoniae is a Gram-negative opportunistic pathogen that produces the KPC enzyme, leading to widespread resistance to carbapenem antibiotics. In recent years, the increasing prevalence of carbapenem-resistant K. pneumoniae strains has emerged as a significant challenge in healthcare, particularly in hospital settings. This study aimed to investigate the phenotypic and genotypic resistance patterns of the KPC gene in K. pneumoniae isolates obtained from patients admitted to a Tertiary Care Hospital's Intensive Care Unit (ICU).

MATERIALS AND METHODS: In a cross-sectional study, 143 K. pneumoniae isolates were collected from patients hospitalized in a government teaching hospital's intensive care unit (ICU) in 2024. Bacterial identification was performed using phenotypic tests and confirmed by genotypic methods. The isolates' antibiotic susceptibility was assessed using the antibiogram (disk diffusion) method. DNA extraction and analysis were conducted using the PCR technique to identify resistance genes.

RESULTS AND DISCUSSION: Among the 143 isolates, 122 (85.3%) were found to carry the KPC gene based on genotypic testing. In contrast, 21 isolates (14.7%) tested negative for the KPC gene. In phenotypic assays, 95 isolates (66.4%) were identified as resistant to carbapenems. To accurately identify and monitor patterns of antibiotic resistance in pathogenic bacteria—particularly K. pneumoniae— periodic implementation of phenotypic and especially genotypic testing is recommended. This strategy may play a critical role in the early detection of resistant strains and in guiding more effective therapeutic and infection control interventions.

Keywords: Klebsiella pneumoniae, KPC gene, ICU, Tertiary hospital

Phenotypic Detection of Efflux Pumps in ESBL-Producing and Fluoroquinolone-Resistant Escherichia coli and Klebsiella pneumoniae Isolates from Clinical Samples in Gonbad-e Kavus, Iran

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BACKGROUND AND OBJECTIVES: Introduction: Antibiotic resistance in Escherichia coli and Klebsiella pneumoniae, especially against fluoroquinolones, is rapidly increasing. One key mechanism contributing to this resistance is the activity of efflux pump systems. This study aimed to assess antibiotic resistance patterns and determine the phenotypic prevalence of efflux pumps in ESBL-producing and fluoroquinolone-resistant *E. coli* and *K. pneumoniae* isolates from clinical specimens in Gonbad-e Kavus, Iran.

MATERIALS AND METHODS: Method: In this cross-sectional study, 35 E. coli and 21 K. pneumonia isolates were collected from clinical samples. Antimicrobial susceptibility testing was performed using the disk diffusion method (CLSI guidelines) on Mueller-Hinton agar. ESBL production was assessed via the combination disk method using cefotaxime and cefotaxime-clavulanic acid disks. Phenotypic detection of efflux pumps was conducted using the Cart-Wheel method.

RESULTS AND DISCUSSION: Results: Resistance rates in E. coli isolates to ciprofloxacin, nalidixic acid, norfloxacin, levofloxacin, ofloxacin, cefotaxime, and ceftazidime were 14%, 17%, 9%, 10%, 9%, 15%, and 10%, respectively. In K. pneumonia , corresponding rates were 16%, 15%, 12%, 13%, 13%, 15%, and 16%. Efflux pump activity was detected in 23 (60%) E. coli and 3 (14.28%) K. pneumonia isolates. ESBL production was confirmed in 4 (11.42%) E. coli and 3 (14.28%) K. pneumonia isolates. Conclusion: A high proportion of clinical isolates exhibited multidrug resistance, with significant involvement of efflux pumps and ESBL production. Ciprofloxacin and nalidixic acid resistance was notably higher, emphasizing the need for careful antibiotic prescription to limit resistance spread

Keywords: Efflux pump , Escherichia coli , Klebsiella pneumonia , Antibiotic

Phenotypic versus Genotypic Detection of VIM-1 and VEB-1 Metallo-β-Lactamases in Clinical Acinetobacter baumannii Isolates from Tehran

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BACKGROUND AND OBJECTIVES: Acinetobacter baumannii has emerged as a global priority pathogen due to its remarkable ability to acquire resistance determinants, including carbapenemases like NDM-1, VIM-1, and OXA-type enzymes, along with extended-spectrum β-lactamases such as VEB-1. The rapid spread of pandrug-resistant (PDR) clones carrying these resistance genes, particularly in ICUs, underscores the urgency for novel antimicrobial approaches targeting biofilm formation and horizontal gene transfer. Recent advances in CRISPR-based diagnostics for detecting blaVIM-1/blaVEB-1 and phage therapy against these resistant strains have been reported.

MATERIALS AND METHODS: During 2017, seventy-five Acinetobacter baumannii clinical isolates were collected from hospitals in Tehran, Iran. Phenotypic detection of metallo-β-lactamase (MBL) production was performed using combined disk diffusion test (CDDT) with imipenem (10 µg) and imipenem-EDTA (10/750 µg) discs according to CLSI guidelines (M100-S27). For genotypic analysis, PCR amplification was conducted to detect blaVIM-1 and blaVEB-1 resistance genes using specific primers. Discordant results between phenotypic and genotypic methods were resolved by repeat testing and sequencing validation. The agreement between CDDT and PCR results was analyzed using Cohen's kappa coefficient .

RESULTS AND DISCUSSION: The observed discrepancy between genotypic (PCR) and phenotypic (CDDT) results may stem from several factors: 1) potential silent genes not being expressed phenotypically, 2) limitations of disk diffusion in detecting low-level resistance, and 3) uncharacterized resistance mechanisms. The higher detection rate of blaVEB-1 (54.66%) compared to blaVIM-1 (38.66%) suggests varying dissemination patterns of these resistance determinants in Tehran hospitals. These findings emphasize the necessity of combining both methods for accurate resistance surveillance and treatment decisions.

Keywords: Acinetobacter baumannii , Antibiotic resistance , Metallo-β-lactamase

Phylogenetic Distribution of Extraintestinal Pathogenic Escherichia coli in Poultry Colibacillosis and Human UTIs: A One Health Perspective

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BACKGROUND AND OBJECTIVES: Extraintestinal pathogenic Escherichia coli (ExPEC) strains are major agents of colibacillosis in poultry and urinary tract infections (UTIs) in humans. Evidence of shared lineages between avian and human reservoirs raises concerns about zoonotic transmission. This study compared the phylogenetic distribution of ExPEC isolates from both hosts to assess cross-species transmission risks.

MATERIALS AND METHODS: A total of 98 Escherichia coli isolates were analyzed, including 46 avian isolates recovered from the viscera of poultry with confirmed colibacillosis (obtained from veterinary diagnostic laboratories in Semnan, Iran) and 52 clinical isolates from human urinary tract infections (UTIs) (collected from a tertiary care hospital in Semnan, Iran). Isolates were confirmed via standard bacteriological tests (MacConkey agar, urease, TSI, Simmons citrate, indole tests, EMB agar). Genomic DNA was extracted by phenol-chloroform, and phylogroups (A, B1, B2, D) were determined via triplex PCR targeting chuA, yjaA, and TSPE4.C2.

RESULTS AND DISCUSSION: Phylogroup B2 predominated in both poultry (78.3%) and human (63.5%) isolates. Poultry distribution was B2 (78.3%), B1 (15.2%), A (6.5%), and D (2.2%); human isolates were B2 (63.5%), B1 (19.2%), A (11.5%), and D (5.8%). Statistical analysis confirmed significantly higher prevalence of B2 in both hosts (p 0.05), suggesting shared phylogenetic lineages. The dominance of phylogroup B2 in avian and human ExPEC strains indicates potential cross-host transmission. These findings highlight the need for integrated One Health surveillance to monitor zoonotic risks associated with multidrug-resistant ExPEC clones.

Keywords: Extraintestinal pathogenic Escherichia coli (ExPEC), urinary tract infections (UTIs), phylogenetic

Plant-Based Prebiotics and Probiotics in Modulating Gut Microbiota: A Review

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BACKGROUND AND OBJECTIVES: The gut microbiome plays a vital role in maintaining human health, influencing digestion, immune regulation, and metabolic homeostasis. In recent years, there has been growing interest in plant-derived compounds with prebiotic and probiotic properties for modulating the composition and function of the gut microbiota.

MATERIALS AND METHODS: This review aims to summarize current knowledge on plant-based prebiotics and probiotics and their impact on gut microbial balance, based on selected recent studies published between 2018 and 2025.

RESULTS AND DISCUSSION: Plant-based prebiotics such as inulin, fructooligosaccharides (FOS), and galactooligosaccharides (GOS), found in foods like garlic, chicory root, green bananas, and Jerusalem artichoke, have been shown to stimulate the growth of beneficial bacteria such as Bifidobacterium and Lactobacillus. These changes are often associated with increased production of short-chain fatty acids (SCFAs), especially butyrate, which contribute to improved gut barrier integrity and reduced inflammation. In addition, certain fermented plant products—like kimchi, kombucha, and tempeh—may serve as natural sources of probiotic bacteria, offering complementary benefits. Plant-based prebiotics and probiotics offer a promising, natural approach to promoting gut health and microbial balance. They may be especially valuable in preventive health strategies and as supportive agents in managing gut-related disorders. However, further clinical trials are needed to standardize doses and assess long-term effects.

Keywords: Prebiotics; Probiotics; Gut Microbiota; Plant Extracts

Post-intravitreal injection endophthalmitis following intravitreal anti-VEGF injection worldwide: A systematic review and meta-analysis

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BACKGROUND AND OBJECTIVES: We conducted a systematic review and meta-analysis to determine the global prevalence of post-intravitreal injection endophthalmitis after intravitreal anti-vascular endothelial growth factor (anti-VEGF) injections.

MATERIALS AND METHODS: We searched PubMed, Scopus, Web of Science, and Google Scholar to identify relevant research published until June 2024. The search terms employed were "Endophthalmitis", "Intravitreal injection", "anti-VEGF", "Bevacizumab", "Avastin", "Aflibercept", and "Ranibizumab". We only included studies that examined endophthalmitis patients treated solely with intravitreal injections of anti-VEGF.

RESULTS AND DISCUSSION: Our systematic review and meta-analysis included a total of 163 publications after evaluating 1,563 sources. Reasons for exclusion included duplicate reports on the same group, an incorrect methodology for measuring prevalence, and a failure to evaluate eligibility. A total of 136 studies met the inclusion criteria. Out of 23,809,816 people who got intravitreal injections of bevacizumab, Avastin, aflibercept, or ranibizumab, 0.0382 (95% CI: 0.034 to 0.042) tested positive for post-intravitreal injection endophthalmitis. We concluded that the incidence of endophthalmitis following intravitreal anti-VEGF injection is minimal.

Keywords: Endophthalmitis, Intravitreal injection, anti-VEGF, Bevacizumab, Avastin, Aflibercept, and Ranibizumab.

Postbiotics from Gastric Microbiota-Derived Probiotics: A Novel Strategy to Combat Salmonella Infections

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BACKGROUND AND OBJECTIVES: Initially, it was believed that the stomach was sterile, but it is now known to host a microbiome that may be beneficial. Probiotic bacteria from this microbiome can produce postbiotics, which have gained attention for their potential therapeutic effects. Salmonella is a harmful foodborne pathogen, and the postbiotics derived from the stomach microbiome could be effective in combating this gastrointestinal pathogen, offering a novel approach to treatment.

MATERIALS AND METHODS: Twenty gastric biopsy samples were collected via endoscopy from patients with gastritis and atrophic gastritis. Samples were enriched in BHI broth under aerobic and anaerobic conditions at 37°C for 48–72 hours. Serial dilutions were plated on MRS and TSA agar to isolate strains, which were purified and characterized morphologically. Among 65 isolates, two strains (Q3 and M2) were selected for probiotic potential based on non-hemolytic activity, acid and bile salt tolerance, adhesion to Caco-2 cells, and antibiotic susceptibility. Postbiotics were extracted, lyophilized, and functionally analyzed. Molecular identification confirmed the strains as Lacticaseibacillus and Ligilactobacillus species.

RESULTS AND DISCUSSION: Antimicrobial activity was assessed via MIC and MBC using microdilution methods. Antibiofilm effects were evaluated through Crystal Violet staining and absorbance measurement at 595 nm. The postbiotics showed strong antimicrobial activity (MIC: 0.062 mg/mL; MBC: 0.125 mg/mL) and dose-dependent biofilm inhibition (18–49%) against Salmonella, with the highest effect at 1 mg/mL. These results highlight the potential of Lacticaseibacillus and Ligilactobacillus-derived postbiotics as effective, safe alternatives for controlling antibiotic-resistant and biofilm-forming Salmonella strains in clinical and food industry settings.

Keywords: Postbiotics, Salmonella, Biofilm, Antibiotic resistance, Lacticaseibacillus, Ligilactobacillus, Foodborne pathogen, Probiotic

Prevalence and Antimicrobial Resistance Patterns of Escherichia coli, Salmonella spp., and Staphylococcus aureus Isolated from Broiler Chickens

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BACKGROUND AND OBJECTIVES: Antimicrobial resistance (AMR) is a critical global health issue, affecting humans, animals, and the environment, mainly due to excessive antibiotic use in medicine and agriculture. The WHO and WOAH warn that this trend could make simple infections untreatable again. The poultry industry significantly contributes to AMR through antibiotic use for growth and disease prevention, posing public health risks via food and direct contact

MATERIALS AND METHODS: This descriptive cross-sectional study was conducted in 2024 at an industrial poultry slaughterhouse in Kerman. Feces, liver, and trachea samples were collected from 40 healthy broiler chickens. Bacteria were isolated using selective culture media and identified. The antibiotic resistance pattern was assessed using the disk diffusion method according to CLSI guidelines (2023), examining antibiotics including ampicillin, tetracycline, gentamicin, cephalexin, ciprofloxacin, and chloramphenicol. Data were analyzed using descriptive statistics

RESULTS AND DISCUSSION: In this study, researchers isolated 28 Escherichia coli, 15 Salmonella spp., and 10 Staphylococcus aureus from broiler chicken samples. The highest antibiotic resistance was found in E. coli and Salmonella against ampicillin and tetracycline, while S. aureus showed the most resistance to tetracycline and chloramphenicol. Ciprofloxacin and gentamicin had the lowest resistance rates. Many isolates also displayed multidrug resistance (MDR). These results indicate that excessive antibiotic use in poultry farming leads to resistant bacterial strains, which threaten both animal and public health. The study highlights the importance of continuous antimicrobial resistance monitoring, responsible antibiotic use, and enhanced biosecurity measures in poultry farms.

Keywords: Antibioticresistance,broilerchickens,Salmonellaspp, Staphylococcus aureus, E. coli, public

Prevalence and Genetic Basis of High-Level Aminoglycoside Resistance in Enterococci Isolated from Healthy Horses

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BACKGROUND AND OBJECTIVES: The gut microbiome of horses, as animals with a close connection to humans, can serve as a source of antibiotic-resistant enterococci. These organisms not only contribute to infections that are challenging to treat but also facilitate the dissemination of antibiotic resistance genes via horizontal gene transfer mechanisms. This study seeks to determine the prevalence of high-level aminoglycoside resistance (HLAR) among enterococcal isolates obtained from the fecal samples of clinically healthy horses.

MATERIALS AND METHODS: A total of 100 enterococcal isolates obtained from the fecal samples of healthy horses in Gorgan (n = 38) and Sabzevar (n = 62) were included in the study. High-level aminoglycoside resistance (HLAR) was assessed phenotypically via the disc diffusion method employing streptomycin (300 µg) and gentamicin (120 µg) antibiotic discs. The presence of the streptomycin resistance gene ant(6')-Ia was evaluated using polymerase chain reaction (PCR) analysis.

RESULTS AND DISCUSSION: High-level resistance to gentamicin was detected in 1% of the enterococcal isolates, whereas 72% exhibited high-level resistance to streptomycin. Comparative analysis revealed no statistically significant differences in the prevalence of HLAR between isolates from the two geographical regions. The ant(6')-Ia gene was identified in 39% of the isolates, of which 71.8% also demonstrated phenotypic resistance to streptomycin.

Keywords: Enterococcus, high-level aminoglycoside resistance, horse

Prevalence of OXA-Type Carbapenemase Genes in Acinetobacter baumannii Isolates from Clinical Specimens

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BACKGROUND AND OBJECTIVES: Acinetobacter baumannii is a critical nosocomial pathogen with rising resistance to carbapenems, primarily mediated by oxacillinase enzymes (OXA-type) Carbapenemases. This resistance represents a growing threat to global health and necessitates urgent surveillance of resistance mechanisms. This study aimed to assess the prevalence of key OXA-type genes—bla-OXA-23, bla-OXA-24, and bla-OXA-58—in clinical isolates collected over two consecutive years (1402–1403), to better understand the local epidemiology of resistance.

MATERIALS AND METHODS: This study analyzed A. baumannii isolates from hospitalized patients with confirmed biochemistry tests. Antimicrobial susceptibility testing was conducted based on Clinical Laboratory Standards Institute (CLSI) guidelines. This study used PCR to investigate the antibiotic resistance genes mentioned.

RESULTS AND DISCUSSION: A total of 110 A. baumannii isolates were analyzed. In 1402 among 48 isolates, bla-OXA-23 was detected in 89.5% and bla-OXA-24 in 87.5%, with co-expression in 81.2%. In 1403, among 62 isolates, bla-OXA-23 prevalence significantly declined to 33.8%, while bla-OXA-24 remained high at 80.6%; co-expression dropped to 22.5%. Notably, bla-OXA-58 was absent in all isolates during both years, suggesting a negligible role in regional resistance dynamics. The high and persistent prevalence of bla-OXA-24 and the decline of bla-OXA-23 over time suggest dynamic shifts in resistance patterns, potentially influenced by antibiotic selective pressure. The absence of bla-OXA-58 highlights regional variability in gene dissemination. These findings reinforce the need for continuous molecular surveillance and tailored antimicrobial stewardship strategies.

Keywords: Acinetobacter baumannii, Carbapenem Resistance Genes, Antibiotic Resistance

Predicting Linear B-cell Epitopes of Clostridium perfringens Alpha Toxin Using a Bioinformatics Approach

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BACKGROUND AND OBJECTIVES: Clostridium perfringens is a Gram-positive, spore-forming anaerobic bacterium responsible for food poisoning, gas gangrene, and enterotoxemia. Its pathogenicity is attributed to the production several toxins and enzymes. CPA can lead to tissue necrosis and inflammation. Due to the hyperacute nature of the disease , prevention is preferable to treatment. Vaccination stands as one of the most effective strategies to prevent these infections. However, traditional vaccine often encounter obstacles such as poor immunogenicity and safety concerns. Traditional vaccine development approaches are costly and time-consuming. Consequently, identifying epitopes of CPA capable of eliciting immune responses is crucial for the vaccine development . The primary aim of this study is to identify potential B-cell of of the CPA toxin using bioinformatics tools.

MATERIALS AND METHODS: Several linear B-cell epitopes were identified, which are presented in table1. peptide length HVQAYALTNLEEGGYANHNNASSIKIFGYEDNEDLKAK 38 NPNVGQGFEFKREVGAGGKVS 21 LLSARYNPNDPYASGYRAK 19 TPKVKK 6 SKTESKLS 8 KTDNFKFGEKIGVKTSFKV 19 LEAIADS 7 FEFNAEQGWSNTNSTTE 17 GNAREDHTEDRPTVKLKFGKNGMSAEEHLKDLYSHKNINGYSEWDWKWV 49 ALTSRK 6 EGKEIPLPDKKRRGKRSVDSLDARLQNEGIRIENIETQDVPGFRLNSITYNDKKLI 56

RESULTS AND DISCUSSION: B-Cell Epitope Prediction HVQAYALTNLEEGGYANHNNASSIKIFGYEDNEDLKAK 38 NPNVGQGFEFKREVGAGGKVS 21 LLSARYNPNDPYASGYRAK 19 TPKVKK 6 SKTESKLS 8 KTDNFKFGEKIGVKTSFKV 19 LEAIADS 7 FEFNAEQGWSNTNSTTE 17 GNAREDHTEDRPTVKLKFGKNGMSAEEHLKDLYSHKNINGYSEWDWKWV 49 ALTSRK 6 EGKEIPLPDKKRRGKRSVDSLDARLQNEGIRIENIETQDVPGFRLNSITYNDKKLI 56 The identification of immunogenic epitopes within CPA provides a foundation for designing peptide-based vaccines. B-cell epitopes can be used to generate neutralizing antibodies. Previous studies have focused on whole-toxin vaccines, which carry risks of toxicity and adverse reactions.

Keywords: Clostridium perfringens, alpha toxin, epitope prediction

Prediction of Novel Therapeutic Targets from Hypothetical Proteins in Multidrug-Resistant Pseudomonas aeruginosa

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BACKGROUND AND OBJECTIVES: Pseudomonas aeruginosa (P. aeruginosa) is an opportunistic, multidrug-resistant, aerobic, gram-negative bacterial pathogen. This bacterium plays an important role in nosocomial infections and related mortality, particularly among immunocompromised patients. Despite extensive research over the past 50 years, no effective vaccine has yet been approved against P. aeruginosa. The present study aims to predict novel therapeutic targets for drug and vaccine development against multidrug-resistant strains of P. aeruginosa.

MATERIALS AND METHODS: Multidrug-resistant strains of P. aeruginosa, particularly those resistant to carbapenems, were retrieved from the databases, and eleven common hypothetical proteins (HPs) were selected for further analysis. Several comprehensive bioinformatics approaches were employed to assess the physicochemical and structural properties, subcellular localization, signal peptide presence, functional domains, pathogenicity, toxicity, antigenicity, allergenicity, and immunoinformatic analysis of these proteins.

RESULTS AND DISCUSSION: Two common HPs (Gene IDs: 2877781505 and 2877781551) were predicted as promising candidates for drug and vaccine development, based on their structural, functional, and immunoinformatic profiles. This study predicts novel therapeutic targets against multidrug-resistant P. aeruginosa, providing a basis for the effective drug and vaccine development through experimental validation.

Keywords: Pseudomonas aeruginosa, Multidrug-resistant, in silico analysis, hypothetical proteins, vaccine development

Preliminary Evaluation of the Antibacterial Properties of TiO_2 Nanoparticles Against Staphylococcus aureus: Toward Novel Approaches for Infection Control

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BACKGROUND AND OBJECTIVES: Staphylococcus aureus is a common Gram-positive bacterium that can cause a wide range of health concerns. Due to increasing interest in nanomaterials with biomedical applications, evaluating their antibacterial properties has become a major research focus. Titanium dioxide (TiO_2) nanoparticles, known for their high chemical stability, oxidative potential, and biocompatibility, have shown promise in this regard. This study aims to investigate the antibacterial activity of TiO_2 nanoparticles against a standard S. aureus strain, providing a basis for broader studies on various bacterial species

MATERIALS AND METHODS: TiO_2 nanoparticles were synthesized using the chemical precipitation method and characterized for their physicochemical properties. Antibacterial efficacy was evaluated by determining the minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) a against Staphylococcus aureus

RESULTS AND DISCUSSION: TiO_2 nanoparticles exhibited noticeable antibacterial activity. Both MIC and MBC were found to be 0.75 mg/mL, indicating their ability to inhibit bacterial growth and exert bactericidal effects at this concentration. The results demonstrate that TiO_2 nanoparticles have significant antibacterial activity against Staphylococcus aureus, a representative Gram-positive organism. These findings suggest their potential for broader application and encourage further evaluation of their antibacterial effects on a wider range of bacterial species, including Gram-negative organisms.

Keywords: Staphylococcus aureus, Titanium dioxide nanoparticles, Antibacterial, Nanoparticles

Preliminary Quality Evaluation of a Quadrivalent Inactivated Enterotoxemia Vaccine with Different Alum Concentrations

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BACKGROUND AND OBJECTIVES: Clostridium perfringens causes several forms of enteric disease in animals that the most important of them is enterotoxemia that often occurs in young sheep and goats..vaccination is considered to be a critical tool for controlling these diseases This study evaluated the sterility, safety, toxicity, and residual formalin content of a quadrivalent inactivated enterotoxemia vaccine formulated with varying concentrations of aluminum hydroxide adjuvant. Three formulations containing 0.6%, 1.2%, and 2.4% Alum were tested.

MATERIALS AND METHODS: Sterility tests were performed according to pharmacopeial guidelines and.Residual formalin content was measured using spectrophotometry based on standard operation guideline. Additionally, Safety in sheeps and residual toxicity in mice evaluations included clinical observation, gross pathology, and local reaction assessment post-injection.

RESULTS AND DISCUSSION: Results of sterility test confirmed the absence of microbial contamination in all batches and the Formulations with 0.6% and 1.2% Alum were safe and well-tolerated, showing no systemic toxicity or significant local reactions. In contrast, the 2.4% Alum formulation caused local tissue lesions in both mice and sheep, including swelling and necrosis at the injection site. These findings suggest a dose-dependent adverse effect at higher adjuvant concentrations. Residual formalin levels in all formulations were within acceptable limits, in compliance with international guidelines. No correlation was observed between formalin content and adverse effects. In conclusion, while all vaccine formulations were sterile and contained acceptable formalin levels, only the 0.6% and 1.2% Alum concentrations were considered safe. The 2.4% Alum group induced local tissue damage and is therefore not recommended for further development

Keywords: adjuvant, sterility, safety, toxicity, formalin ,enterotoxemia vaccine

Preparation of a specific bacteriophage cocktail against Escherichia coli strains isolated from raw milk

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BACKGROUND AND OBJECTIVES: Escherichia coli is one of the most important food-borne pathogens that causes significant financial losses worldwide. Raw milk is considered a potential source of E. coli transmission, and its consumption without proper pasteurization may result in serious foodborne illnesses, such as abdominal pain, diarrhea, and nausea. The increasing antibiotic resistance observed in E. coli strains isolated from both clinical samples and food products — including raw milk — highlights the necessity of eliminating this bacterium before consumption. One of the most promising approaches is the use of lytic bacteriophages,which can completely destroy E. coli cells. The present study aimed to isolate anti-E. coli bacteriophages from wastewater, with a focus on controlling strains isolated from raw milk.

MATERIALS AND METHODS: 31samples of raw milk were collected from local dairy shops, and Escherichia coli strains were isolated and confirmed using biochemical and molecular methods. In the next step, wastewater samples were collected, and the isolation and purification of E. coli-specific bacteriophages were performed following standard reference protocols. Transmission electron microscopy (TEM) was employed to examine the morphological characteristics of the bacteriophages.

RESULTS AND DISCUSSION: Of the 31 raw milk samples collected, 18 were susceptible to the bacteriophage extracted from sewage. The morphology of the bacteriophage was observed by electron microscopy as an icosahedral capsid and a short tail. Given the increasing antibiotic resistance, lytic bacteria can be used for milk decontamination because, unlike pasteurization and sterilization methods, they do not cause changes in the quality, color, odor, or taste of this nutrient.

Keywords: Bacteriophage, raw milk, e. Coli

Prevalence and Antibiotic Resistance Patterns of EPEC, EHEC, and EIEC Pathotypes in Pediatric Diarrheal Infections in Ahvaz, Iran

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BACKGROUND AND OBJECTIVES: Diarrheal disease is a leading cause of death in children under five years of age. Among its bacterial causes, three Escherichia coli pathotypes, including Enteropathogenic (EPEC), Enterohemorrhagic (EHEC) and Enteroinvasive (EIEC), are particularly notable. These strains exert their pathogenic effects by targeting intestinal epithelial cells and lead to a range of symptoms from watery to bloody diarrhea, abdominal cramps and, in severe cases, death. In this study, we investigated the presence or absence of microbial contamination with EHEC, EIEC and EPEC pathotypes, according to the gastrointestinal symptoms of patients under five years of age, such as diarrhea, abdominal cramps and blood in the stool.

MATERIALS AND METHODS: In this study, the prevalence of the mentioned pathotypes in children of Ahvaz was investigated for 12 months. At first, diarrheal samples were cultured on EMB culture medium, then polymerase chain reaction (PCR) was used to check the frequency of the mentioned pathotypes, and electrophoresis was used to identify the positive samples obtained, and then to determine the identity The obtained positive samples were subjected to biochemical tests and finally the antibiotic resistance pattern of the positive samples was investigated.

RESULTS AND DISCUSSION: , two EPEC pathotypes, two EHEC pathotypes, and one EIEC pathotype were identified from a total of 200 stool samples. Antibiotic resistance results showed that EHEC pathotype was sensitive to 5 antibiotics and resistant to 6 antibiotics, EPAC pathotype was sensitive to 5 antibiotics and resistant to 7 antibiotics, and EIEC pathotype was sensitive to 6 antibiotics and resistant to 7 antibiotics.

Keywords: EPEC. EHEC. EIEC. Diarrheal

Prevalence and Antibiotic Susceptibility of Filamentous Bacteria in Oral Cavity of HIV-positive Patients, Tehran, Iran

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BACKGROUND AND OBJECTIVES: HIV virus suppresses the immune system, making infected individuals vulnerable to oral infections, including gum inflammations and dental infections. Filamentous bacteria like Actinomyces, Streptomyces, and Nocardia species multiply, causing treatment-resistant infections in these patients. Routine antimicrobial drugs such as penicillin G, amoxicillin and tetracycline are used in treatments; therefore, this study aimed to assess prevalence and antibiotic susceptibility of filamentous bacteria in oral cavity of HIV-positive patients in Tehran, Iran

MATERIALS AND METHODS: oral swabs were collected from 205 HIV-positive patients in a Tehran university HIV clinic and transported under cold chain conditions. Bacterial cultures were prepared on differential media, with primary identification via biochemical and microscopic assays. DNA extraction was performed for molecular identification using 16s rRNA sequencing and PCR. Antimicrobial susceptibility of isolates was assessed using the disk diffusion method.

RESULTS AND DISCUSSION: : Filamentous bacteria were identified in 6.5% of HIV-positive patients, including Nocardia (2.9%) and Streptomyces (2.4%). Molecular and biochemical assessments verified these findings. The highest prevalence was in males (74.1%) aged 41–60. Phylogenetic analysis showed genetic similarities. These bacteria were susceptible to trimethoprim-sulfamethoxazole but resistant to other antimicrobials.

Keywords: Filamentous bacteria, actinomycetes, Nocardia, Streptomyces, HIV

Prevalence and Genetic Mechanisms of Metallo-β-Lactamase Resistance in Pseudomonas aeruginosa Clinical Isolates

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BACKGROUND AND OBJECTIVES: Antibiotic resistance in Pseudomonas aeruginosa poses a significant global health challenge, particularly due to its resistance to metallo-β-lactams, a critical class of antibiotics. This study investigates the prevalence and mechanisms of resistance in clinical isolates, focusing on the presence of resistance genes such as VEB-1 and VIM-1. Understanding these genetic determinants is crucial for developing effective strategies to combat multidrug-resistant infections

MATERIALS AND METHODS: In this descriptive cross-sectional study, 75 isolates of Pseudomonas aeruginosa were collected from hospitalized patients in the internal medicine, surgery, and ICU wards of selected hospitals in Tehran. After phenotypic identification and antibiotic susceptibility testing, the presence of metallo-beta-lactamases (MBLs) was phenotypically assessed using the Combined Disk Diffusion Test (CDDT) with imipenem and imipenem/EDTA disks. Subsequently, the isolates were further evaluated using PCR with specific primers targeting the relevant genes

RESULTS AND DISCUSSION: it was observed that out of a total of 75 Pseudomonas aeruginosa isolates, 54 samples were resistant to imipenem. Among these, 35 samples were found to produce metallo-beta-lactamase enzymes, which was confirmed through phenotypic methods. Using the PCR method to evaluate the VIM-1 and VEB-1 genes, it was determined that 100% of these 35 samples contained the blaVIM-1 gene, while only 30% of the samples had the blaVEB-1 gene.The results indicate that most samples are resistant to beta-lactam antibiotics due to various beta-lactamases, and considering that the prevalence of these enzymes in the future may pose challenges to antimicrobial treatments, it is advisable to prescribe beta-lactam antibiotics with greater care and caution.

Keywords: Pseudomonas aeruginosa, metallo-beta-lactamase, antibiotic resistance.

Prevalence and Molecular Characterization of Carbapenem-Resistant Klebsiella pneumoniae in Clinical Isolates from Iran

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BACKGROUND AND OBJECTIVES: Carbapenem-resistant Klebsiella pneumoniae (CRKP) represents a significant threat to public health worldwide. The emergence of CRKP in Iranian healthcare settings has raised concerns about treatment options and infection control measures.

MATERIALS AND METHODS: In this study, 150 clinical isolates of Klebsiella pneumoniae were collected from major hospitals in Tehran between 2023 and 2024. Carbapenem resistance was confirmed by disk diffusion and minimum inhibitory concentration testing. Molecular detection of carbapenemase genes (blaKPC, blaNDM, blaOXA-48) was performed by PCR.

RESULTS AND DISCUSSION: Of the 150 isolates, 42 (28%) were resistant to carbapenems. The most prevalent carbapenemase gene was blaNDM (52%), followed by blaOXA-48 (38%) and blaKPC (10%). Co-occurrence of multiple carbapenemase genes was detected in 15% of CRKP isolates. The high prevalence of CRKP carrying blaNDM and blaOXA-48 genes highlights the need for robust surveillance and antimicrobial stewardship programs in Iranian hospitals.

Keywords: Klebsiella pneumoniae, carbapenem-resistant, molecular characterization, Iran, antimicrobial resistance, blaNDM

Prevalence and molecular identification of protozoan intestinal parasitic infections in cancer patients and a control group

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BACKGROUND AND OBJECTIVES: Parasitic infections, particularly opportunistic ones, pose significant concerns for patients with weakened immune systems, such as those undergoing cancer treatment. This study aimed to assess the prevalence of intestinal protozoan infections among Iranian cancer patients compared to a control group, utilizing both microscopic and molecular techniques.

MATERIALS AND METHODS: In this cross-sectional study, 158 individuals diagnosed with gastrointestinal and non-gastrointestinal cancers from hospitals affiliated with Iran University of Medical Sciences were analyzed alongside 158 healthy controls. Stool samples were collected from all participants and examined through direct observation and concentration methods. The modified acid-fast staining technique was employed to identify coccidian parasite infections. DNA was extracted from the samples of the patients, followed by PCR amplification and sequencing.

RESULTS AND DISCUSSION: The prevalence of protozoan infections was significantly higher in cancer patients (31.6%) than in controls (12.0%) ($P = 0.0001$). Blastocystis hominies were the most common infection in cancer patients (22.8%), followed by Giardia lamblia (2.5%) and others. Opportunistic infections like Cystoisospora belly and Cryptosporidium sp. Were found in 2.5% and 0.6% of cancer patients, respectively. Significant differences were noted for Cystoisospora belle ($P = 0.044$) and Blastocystis hominies ($P = 0.0013$). PCR confirmed Cryptosporidium parvum and Cystoisospora belli. Chemotherapy and corticosteroid use increase the risk of intestinal protozoan infections in patients with hematological cancers, particularly lymphoma and leukemia. These patients are more susceptible to opportunistic infections like Cystoisospora belli and Cryptosporidium parvum, which can lead to diarrhea compared to healthy individuals

Keywords: Immunosuppression, Chemotherapy, Cancer, Intestinal parasites

Prevalence and Virulence Profiling of Staphylococcus aureus in Bovine Mastitis in East Azerbaijan, Iran

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BACKGROUND AND OBJECTIVES: Bovine mastitis leads to economic losses in dairy production due to lower milk yield and treatment costs, while serving as a reservoir for zoonotic Staphylococcus aureus (S. aureus). This pathogen, frequently isolated from mastitic milk, harbors virulence factors linked to foodborne illness and immune evasion. This study evaluates S. aureus prevalence and virulence genes in mastitic milk from East Azerbaijan, Iran, within a One Health framework.

MATERIALS AND METHODS: In a cross-sectional study (June 2024–March 2025), 138 milk samples from cows with mastitis were collected via convenience sampling from East Azerbaijan, Iran, farms. S. aureus was isolated on Mannitol Salt Agar (MSA) and confirmed using Gram staining and biochemical tests. PCR detected virulence genes (lukE, seA, seI), with DNA extracted by boiling and analyzed via 1% agarose gel electrophoresis. Data were analyzed using Cochran's Q, McNemar and chi-square tests.

RESULTS AND DISCUSSION: Of 138 samples, 58 (42.0%) were S. aureus-positive. Virulence genes were found in 39.7% (lukE), 36.2% (seA), and 17.2% (seI) of isolates, with significant variation (Cochran's Q = 11.76, p = 0.003). seI was less prevalent than lukE and seA (McNemar, p 0.05). Among MSA-positive isolates, 8.6% carried all three genes, 22.4% carried two, 20.7% carried one, and 48.3% carried none, with significant deviation from expected frequencies (χ^2 = 24.35, p 0.001). Detection of virulence-carrying S. aureus in bovine mastitis underscores its zoonotic potential, necessitating molecular surveillance, prudent antibiotic use, and a One Health approach to mitigate cross-species transmission and antimicrobial resistance.

Keywords: Staphylococcus aureus, Mastitis, Bovine, Zoonoses, One Health

Prevalence of Bacterial Infections in Patients with Otitis Externa Referred to ENT Clinic in Fasa university of medical sciences in 2023-2024

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BACKGROUND AND OBJECTIVES: Otitis externa (OE) is a common recurrent inflammation of the external ear canal. Early recognition of these infections is essential to prevent complications and promote prompt recovery. However, empirical treatment has limitations and may delay the initiation of targeted therapy. Therefore, this study was conducted to investigate the most prevalent bacterial otitis and determine the genus and species of bacteria.

MATERIALS AND METHODS: Patients clinically suspected of OE, based on signs and symptoms, were included if they had not received antibacterial drugs and had not been in contact with water within the previous 24 hours. Samples were collected by a physician. Culture and Gram stain were performed on the sample, and bacterial species were detected by biochemical tests and PCR.

RESULTS AND DISCUSSION: Among 111 patients with OE 59.5% were female and 40.5% were male. The highest prevalence was observed in the 31–40-year age group. Biochemical testing revealed bacterial growth in 27 (24.3%) samples and fungal growth in 37 (33.3%) samples. Mixed bacterial and fungal pathogens were detected in 31 specimens (28%), whereas 16 (14.4%) showed no growth. Of 52 PCR-positive bacterial specimens, 38 (34.2%) were positive for Staphylococcus spp., 10 (9%) for Pseudomonas spp., and 4 (3.6%) showed mixed infections, while 6 specimens remained negative. The findings demonstrate that bacterial infections, particularly Staphylococcus spp., as well as mixed bacterial–fungal infections, are common causes of OE. PCR proved more sensitive than culture. Thus, it is recommended to consider both bacterial and fungal organisms in diagnostic and therapeutic protocols.

Keywords: Bacterial otitis externa, PCR, external otitis, Staphylococcus, Pseudomonas

Prevalence of Escherichia coli, Klebsiella, and Proteus strains with extended-spectrum beta-lactamase in urine samples

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BACKGROUND AND OBJECTIVES: Resistance to a wide range of common antimicrobials has made the proliferation of extended-spectrum beta-lactamase (ESBL)--producing strains a serious global health concern, complicating therapeutic strategies.

MATERIALS AND METHODS: A total of 2000 isolates of gram-negative bacilli were isolated by examining more than 5000 Bal culture samples. Then, all the isolated bacteria were identified by microbiology diagnostic methods. The presence of ESBL positivity was detected using a double disc synergy test (DDST). The discs used in this experiment were ceftazidime and ceftazidime clavulanate. After antibiogram analysis, PCR for beta-lactamase (bla) genes of SHV, TEM and CTX-M family was also performed using primers designed in 25 ESBL isolates of each Escherichia coli, Klebsiella and Proteus species.

RESULTS AND DISCUSSION: Among 2000 Gram-negative bacilli isolated, 820 (45.69%) were ESBL producers. The main source of ESBL production was urine samples, with the highest ESBL production in Klebsiella sp. (65.12 %). Resistance to multiple classes of antibiotics was observed among ESBL producers. Among the bacteria that can have EBLS resistance, Proteus was the least of all. Among ESBL-producing genes, the prevalence of bla-CTX-M (70.3%) was the highest, followed by bla-TEM (48.2%) and bla-SHV (56.3%) in the present study. The frequency of ESBL-producing strains among clinical isolates is steadily increasing.

Keywords: Prevalence, Escherichia coli, Klebsiella, Proteus

Prevalence of Extended-Spectrum β-Lactamase Producing Escherichia coli isolated from Dog Feces in Tehran, Iran

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BACKGROUND AND OBJECTIVES: The inappropriate and overuse of antibiotics, especially β-lactams antibiotic, in both veterinary and human medicine has led to the increase in antimicrobial-resistant (AMR) strains and the emergence of extended-spectrum β-lactamase (ESBL)-producing Bacteria. The AMR and, ESBL strains have the ability to spread antibiotic resistance genes via mobile genetic elements and, may be transmitted from animals to humans Methods.

MATERIALS AND METHODS: In the present study, a total of 100 E. coli strains were isolated and, identified from the feces of dogs (50 shelter and, 50 pet dogs) referred to veterinary clinics in Tehran, using conventional microbiological technique, and molecular methods. Extended-spectrum β-lactamase (ESBL)-producing E. coli isolates were phenotypically determined using the double-disk synergy test according to the Clinical and Laboratory Standards Institute (CLSI, 2023) guidelines. Finally, the isolates which identified as ESBL producers E. coli phenotypically, total genomic DNA was extracted by the boiling method, and the presence of β-lactamase encoding genes i. e. blaTEM, blaCTX-M, blaOXA, blaSHV, and blaFOX was investigated using the PCR technique.

RESULTS AND DISCUSSION: Out of 100 E. coli strains, 58 (58%) isolates were phenotypically considered as ESBL producers E. coli. The most prevalent β-lactamase encoding genes in ESBL producers E. coli (n= 58) was blaTEM, (79.31%), followed by blaCTX-M (72.41%), blaOXA (24.14%), and blaSHV (13.79%). The high prevalence of ESBL-producing E. coli recovered from dog feces, along with the high frequency of β-lactamase-encoding genes, underscores the importance of regular monitoring of antibiotic resistance in zoonotic bacteria, particularly in companion animals.

Keywords: Antimicrobial Resistance, Extended Spectrum β-lactamase Producing E. coli (ESBL), Dogs

Prevalence of Human Herpesvirus 6 in Benign Lymphoproliferative Disorders

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BACKGROUND AND OBJECTIVES: The association between human herpesvirus 6 (HHV-6) infection and lymphoproliferative disorders is strongly supported by epidemiological studies. This study aimed to determine the prevalence of HHV-6 among patients with benign lymphoproliferative disorders.

MATERIALS AND METHODS: Twenty-two formalin-fixed, paraffin-embedded tissue samples from patients diagnosed with benign lymphoproliferative disorders were included in this study. DNA was extracted from these samples, and HHV-6 was detected using Nested PCR. The HHV-6 A or B subtypes were characterized based on PCR product size and subsequent sequencing.

RESULTS AND DISCUSSION: Nine out of 22 (40.9%) samples tested positive for HHV-6. Of these nine positive cases, 4 (44.5%) patients were male, and 5 (55.5%) were female (P0.05). All detected HHV-6 strains were identified as HHV-6 variant A.This study suggests that the interaction of the virus with the immune system and its immunomodulatory effects may play a significant role in lymphoproliferative disorders. Furthermore, in benign lymphatic complications, the reactivation of the latent virus might be associated with more severe disease in patients.

Keywords: Nested PCR, HHV-6, lymphoproliferative disorders, Immune system

Prevalence of Methicillin-Resistant Staphylococcus aureus (MRSA) Among Patients Attending Urban Healthcare Centers in Shiraz in 2023

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BACKGROUND AND OBJECTIVES: Staphylococcus aureus is a common pathogen that causes infections from mild skin issues to severe diseases. The rise of methicillin-resistant Staphylococcus aureus (MRSA) is a significant global health concern, as these strains resist many antibiotics, complicating treatment and increasing health risks. This study focused on determining the prevalence of MRSA and its antibiotic resistance patterns among clinical isolates from patients in urban healthcare centers in Shiraz in 2023.

MATERIALS AND METHODS: This cross-sectional descriptive study was conducted in 2023 (1402) across three urban healthcare centers in Shiraz, Iran. A total of 200 clinical samples—including wound, nasal, throat swabs, urine, and blood—were collected from patients with various infections. Samples were cultured on standard media, and Staphylococcus aureus isolates were identified using conventional biochemical tests. Methicillin resistance was determined by the cefoxitin disk diffusion method according to CLSI 2022 guidelines. Antibiotic susceptibility of MRSA isolates to erythromycin, clindamycin, and ciprofloxacin was assessed. Data were analyzed descriptively to determine MRSA prevalence and resistance patterns

RESULTS AND DISCUSSION: Out of 200 clinical samples, 68 Staphylococcus aureus isolates were identified, with 39 (57.3%) being methicillin-resistant (MRSA). The highest prevalence was in wound samples. MRSA isolates showed high resistance to erythromycin, clindamycin, and ciprofloxacin, but remained susceptible to vancomycin. The high MRSA prevalence highlights a significant public health concern, emphasizing the need for strict infection control and antibiotic stewardship.

Keywords: MRSA,Staphylococcusaureusm,Prevalence,Infectioncontrol,Antibiotic resistance,Methicillin resistance

Prevalence of OmpK36 Variants and Their Association with Antibiotic Resistance Patterns in Klebsiella pneumoniae Clinical Isolates

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BACKGROUND AND OBJECTIVES: Klebsiella pneumoniae is an opportunistic pathogen causing hospital-acquired infections worldwide. Increasing resistance to beta-lactams and carbapenems complicates treatment. Outer membrane porins like OmpK36 affect antibiotic entry and resistance. Variations in the OmpK36 gene may change membrane permeability and antibiotic susceptibility. This study examines the prevalence of OmpK36 gene variants, groups C and D, in clinical K. pneumoniae isolates and their association with antibiotic resistance patterns.

MATERIALS AND METHODS: Total of 115 clinical Klebsiella pneumoniae isolates were collected from patients in tertiary hospital. Antibiotic susceptibility was tested using disk diffusion according to CLSI guidelines for imipenem, gentamicin, ciprofloxacin, ceftazidime, aztreonam, and amoxicillin-clavulanic acid. PCR detected OmpK36 gene groups C and D. The distribution of these groups was correlated with resistance profiles. Statistical analysis assessed associations between gene groups and resistance patterns.

RESULTS AND DISCUSSION: Among the 115 Klebsiella pneumoniae isolates, the majority exhibited high resistance rates to amoxicillin-clavulanic acid, while imipenem showed the highest susceptibility. PCR analysis revealed that most isolates carried the OmpK36 gene group C, with a smaller subset belonging to group D. Notably, isolates harboring the OmpK36 group D demonstrated an specefic resistance pattern, particularly increased resistance to ceftazidime, aztreonam, and gentamicin, compared to group C. These findings suggest that OmpK36 variants contribute to differential antibiotic susceptibility profiles in K. pneumoniae. The correlation between OmpK36 groups and resistance patterns highlights the importance of molecular characterization for guiding effective antibiotic therapy and controlling the spread of resistant strains.

Keywords: Klebsiella pneumoniae, OmpK36, antibiotic resistance

Prevalence of OXA-23 and OXA-51 Genes and Antibiotic Resistance in Clinical Acinetobacter baumannii Isolates from Tehran

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BACKGROUND AND OBJECTIVES: Introduction: Acinetobacter baumannii is a Gram-negative, capsulated, non-motile, catalase-positive, oxidase-negative, aerobic, and opportunistic pathogen widely spread in hospitals, representing a major cause of nosocomial infections. Its ability to develop antibiotic resistance poses a serious global health threat. This study aimed to evaluate the antibiotic resistance profile and the prevalence of resistance genes in A. baumannii isolates from hospitalized patients in a Tehran hospital.

MATERIALS AND METHODS: Methods: 30 hospitalized patients were studied. Final bacterial identification was confirmed by biochemical tests. The prevalence of OXA-23 and OXA-51 genes was assessed using PCR. Antibiotic susceptibility patterns were determined by the Kirby–Bauer disk diffusion method. Antibiotics tested included Colistin, Ciprofloxacin, Cefotaxime, Doxycycline, Amikacin, Piperacillin-Tazobactam, Cefepime, Gentamicin, Tetracycline, Imipenem, Ceftazidime, Ampicillin-Sulbactam, and Trimethoprim-Sulfamethoxazole.

RESULTS AND DISCUSSION: Results: Of the patients, 40% were female and 60% male. The prevalence of OXA-23 and OXA-51 genes was 70% and 100%, respectively. Colistin showed the highest sensitivity (100%), while complete resistance (100%) was observed against Cefotaxime, Imipenem, Ciprofloxacin, and Piperacillin–Tazobactam. 20 out of 30 isolates were from sputum samples. Conclusion: Due to the 100% prevalence of OXA-51 in Acinetobacter baumannii, this gene can be introduced as an intrinsic gene. Except for colistin, the high resistance observed against the mentioned antibiotics represents a serious public health warning. To combat this issue, understanding antibiotic resistance patterns, preventing the indiscriminate use of antibiotics, and promoting targeted antibiotic prescription are essential to help prevent the further emergence of resistance to other effective antibiotics.

Keywords: Keywords: Acinetobacter baumannii, beta-Lactam Antibiotics, Anti-Bacterial Agents, Beta-Lactamases

Prevalence of Quinolone and Fluoroquinolone Resistance and Detection of qnr Genes in Escherichia coli Isolates From Urinary Tract Infections

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BACKGROUND AND OBJECTIVES: Introduction: Antibiotic resistance (AR) presents a major challenge in the prevention, treatment, and control of infectious diseases, posing a significant public health threat. Escherichia coli is the primary causative agent of urinary tract infections (UTIs). This study aimed to assess the prevalence of resistance to quinolone and fluoroquinolone antibiotics and to investigate the presence of qnr genes among E. coli isolates from UTI cases.

MATERIALS AND METHODS: Methods: A total of 105 E. coli isolates were collected from UTI patients in Bojnord, northeastern Iran, and confirmed by biochemical tests. Antimicrobial susceptibility to ciprofloxacin, nalidixic acid, and levofloxacin was evaluated using the disk diffusion method. Additionally, the presence of qnrA, qnrB, and qnrS genes, as well as phylogenetic grouping, was determined by conventional polymerase chain reaction (PCR).

RESULTS AND DISCUSSION: Results: Phenotypic resistance to ciprofloxacin, nalidixic acid, and levofloxacin was observed in 47.6%, 44.8%, and 38.1% of isolates, respectively. The qnrS gene was detected in 3 isolates, while qnrA was found in 1 isolate. Seven phylogenetic groups were identified: A0 (18%), A1 (6.7%), B1 (7.6%), B22 (1.9%), B23 (23.8%), D1 (15.3%), and D2 (26.7%).

Keywords: Keywords: Antibiotic resistance, Fluoroquinolones, UTI, Escherichia coli, Phylogenetic background

Prevalence of sarcocystis infection in slaughtered beef in slaughterhouses: A Narrative review

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BACKGROUND AND OBJECTIVES: Sarcocystis species are regarded as significant protozoan parasites that commonly infect both humans and animals. considering the surge in the consumption of fast food and the elevated prevalence of sarcocystis in slaughtered cattle, this issue assumes a substantial magnitude as a potential foodborne hazard. The objective of this study is to examine the prevalence of Sarcocystis infection in beef cattle that have been slaughtered in abattoirs.

MATERIALS AND METHODS: In this review, we examined articles pertaining to the prevalence of Sarcocystis infection among beef cattle slaughtered in abattoirs. The articles were sourced from reputable databases such as Web of Science, PubMed, Scopus, Google Scholar, and others. The review encompassed the period from 2018 to 2024.

RESULTS AND DISCUSSION: 3. Results: In a 2021 study conducted in Sulaimani province, located in northern Iraq, the presence of banana-shaped bradyzoites was observed in 90% and 92.5% of the muscle samples obtained from cattle and sheep, respectively. The peptic digestion method was employed to analyze a total of 130 muscle samples. In a study conducted in China in 2019, the presence of Sarcocystis gene sequencing was identified in 20 out of 62 meat samples. In a study conducted in Tehran in 2020, it was found that out of a total of 180 samples, 94.4% were microscopically positive and 89.44% were molecularly positive for Sarcocystis species. 4. Conclusion: Identifying these protozoa is of utmost importance for the effective management and prevention of diseases. The existing literature clearly indicates a high prevalence of Sarcocystis in beef cattle.

Keywords: Sarcocystis, protozoa, beef

Prevalence of Torque Teno Virus (TTV) among Iranian HIV positive patients in comparison with healthy control

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BACKGROUND AND OBJECTIVES: The Anelloviridae family comprises a diverse group of viruses, among which Torque Teno Virus (TTV) is a notable member. This virus is a member of the Alpha torque virus genus and has a circular single-stranded DNA genome. Elevated TTV load has been observed in the serum of immunocompromised individuals, particularly among HIV patients. Viral coinfections in HIV patients should be monitored as HIV infection can lead to a progressive decline in CD4+ T cell counts occurs, resulting in the compromised capacity of the host to mount effective immune responses against infections. The aim of present study is to determine TTV positivity rate among HIV infected patients in comparison with healthy controls.

MATERIALS AND METHODS: The present study conducts a qualitative assessment of TTV in blood samples of forty-two HIV-positive patients and healthy control subjects. The CD4 count and HIV viral load were determined among HIV positive patients. The samples were extracted and subjected to molecular testing using nested-PCR technique.

RESULTS AND DISCUSSION: Mean age of studied population was 49.07+11.14 years. Among HIV positive patients, HIV viral load and CD4 count were 5.842 log10 Copies/ml and 536.95 cells, respectively. A higher TTV positivity rate (p value=0.03) was observed among HIV patients (19 of 21 HIV-positive samples, 90.4%) in comparison with healthy controls (13 of 21, 61.9% control).Considering the high prevalence of TTV infection among HIV-positive individuals, the effects of this coinfection and the virus's pathogenesis should be assessed longitudinally, particularly during the late stages of HIV infection.

Keywords: Torque Teno Virus, Human Immunodeficiency Virus, Polymerase Chain Reaction

Prevalence of toxA gene in Pseudomonas aeruginosa isolated from hospitals of Sanandaj 1403

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BACKGROUND AND OBJECTIVES: Pseudomonas aeruginosa is a key pathogen commonly linked to infections acquired in healthcare settings. Its clinical significance has been growing due to its ability to resist multiple antimicrobial agents and develop high-level multidrug resistance (MDR), a trait influenced by various virulence factors encoded in its genome. This study aims to determine the frequency of the toxA gene in these bacteria.

MATERIALS AND METHODS: This cross-sectional study was carried out in the Department of Microbiology at Kurdistan University of Medical Sciences. During the summer of 1403, all P. aeruginosa isolates collected from hospitals in Sanandaj were included in this descriptive analysis. Identification of the isolates was done using conventional laboratory methods. DNA extraction from the isolates was performed using the boiling technique. The presence of the toxA gene was detected through polymerase chain reaction (PCR) using specific primers: forward primer GGTAACCAGCTCAGCCACAT and reverse primer TGATGTCCAGGTCATGCTTC.

RESULTS AND DISCUSSION: Out of the 54 isolates confirmed as P. aeruginosa, 10 isolates (18.5%) tested were positive for the toxA gene. Our findings reveal that the toxA gene is present in a notable 18.5% of the P. aeruginosa isolates examined. This relatively high prevalence underscores its potential role in the pathogenicity or resistance mechanisms of these strains. This indicates a measurable presence of this gene within the local strain population. The presence of toxA could contribute to the virulence or antibiotic resistance profiles observed. Understanding its distribution is crucial for targeted surveillance and treatment strategies.

Keywords: Pseudomonas aeruginosa, toxA, virulance factors

Prevalence of β-Lactam Resistance Genes in ESBL K. pneumoniae from UTI Isolates

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BACKGROUND AND OBJECTIVES: Urinary tract infections (UTIs) rank as the second most prevalent infections, while the rise of antibiotic resistance, particularly among extended-spectrum beta-lactamase (ESBL) producing strains such as Klebsiella pneumoniae, presents a critical and growing challenge. These strains reduce the effectiveness of beta-lactams by producing enzymes encoded by genes such as blaSHV, blaCTX-M, and blaTEM. This leads to increased complications, treatment costs, and multidrug resistance (MDR), necessitating innovative therapeutic approaches.

MATERIALS AND METHODS: In a clinical laboratory, isolates of K. pneumoniae MDR were collected from urinary bacterial samples. These isolates were screened for ESBL production. Subsequently, the presence of blaSHV, blaCTX-M, and blaTEM genes in each isolate was confirmed using polymerase chain reaction (PCR).

RESULTS AND DISCUSSION: Results: Among 100 urinary bacterial samples analyzed, a total of 26 K. pneumoniae isolates were identified, with 24 exhibiting MDR. The results indicated that 21 isolates were resistant to at least one beta-lactam antibiotic. Ten isolates were confirmed as ESBL-producing strains using cefotaxime-clavulanic acid and ceftazidime-clavulanic acid combination disks. Nine strains carried the blaSHV gene, 10 carried the blaCTX-M gene, and seven carried the blaTEM gene. Conclusion: This study found High rates of multidrug-resistant K. pneumoniae in UTIs were linked to blaCTX-M, blaSHV, and blaTEM genes. Tracking these genes is key for rapid ESBL strain detection and managing MDR infections, enabling better prevention.

Keywords: Antibiotic, Extended-spectrum-beta-lactamase (ESBL), Infection, Klebsiella pneumonia, Multidrug resistance (MDR)

Prior COVID-19 infection among newly diagnosed tuberculosis patients in a tertiary care center in Tehran: A case-control study

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BACKGROUND AND OBJECTIVES: Since the advent of the COVID-19 pandemic much discussion has been had on the possible role it might play on global efforts to combat TB; most, focusing on the pandemic's impact on health care systems' capabilities to manage TB cases. Mechanisms have also been proposed by which the COVID-19 infection may directly affect individuals' chance of developing TB infection. Cases have been reported with a history of COVID-19 infection preceding a diagnosis of TB, evidencing its possible role as a risk factor for the disease.

MATERIALS AND METHODS: A case-control study was conducted enrolling patients diagnosed with pulmonary TB in the absence of major risk factors previous history of TB, (HIV) human immunodeficiency virus infection), end-stage renal disease, organ transplants, and use of immunosuppressive agents) for developing TB. Each patient was age and sex matched with one healthy control. Data regarding prior COVID-19 infection, diabetes, and smoking status as well as the use of corticosteroids and Tocilizumab for the treatment of COVID-19 infection was obtained. Bivariate analysis was conducted and variables with a likely association with TB status were entered in a multivariate model.

RESULTS AND DISCUSSION: Bivariate analysis demonstrated a significant relationship between prior COVID-19 infection and TB (95% confidence interval = 1.1−22.8, odds ratio [OR] = 5). Among other variables the severity of COVID-19 infection was found to have a likely association with TB status (p = .125). In a multivariate model, prior COVID-19 infection per se, was not found to be significantly associated with TB (p = .12, OR = 4.5).

Keywords: COVID-19, tuberculosis

Probiotics and Gut Microbiota: Therapeutic Potential and Mechanisms

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BACKGROUND AND OBJECTIVES: Probiotics have emerged as key modulators of gut microbiota, influencing host metabolism, immunity, and disease resistance. This review synthesizes recent evidence (2020–2025) on probiotic strains, their mechanisms of action, and clinical applications in gastrointestinal (GI) disorders, metabolic diseases, and mental health. We highlight advances in microbiome engineering, next-generation probiotics (NGPs), and personalized microbial therapies.

MATERIALS AND METHODS: Study Design - Systematic review of PubMed, Scopus, and ClinicalTrials.gov (2020–2025). - Inclusion criteria: Human RCTs, meta-analyses, and mechanistic studies. - Exclusion criteria: Animal-only studies, non-peer-reviewed articles.

RESULTS AND DISCUSSION: Results :Lactobacillus rhamnosus GG Reduces antibiotic-associated diarrhea (AAD) by 50% RCT (n=1,200, 2024) Bifidobacterium longum Improves IBS symptoms (30% reduction) Meta-analysis Akkermansia muciniphila (NGP) Enhances metabolic health in obesity Phase II trial. Discussion: Strain-specific effects are critical; NGPs show promise for metabolic diseases.

Keywords: Probiotics Gut microbiota Next-generation probiotics (NGPs) Dysbiosis Psychobiotics Microbiome engineering

probiotics as an Ethical Intervention to Address the Crisis of Antimicrobial Resistance

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BACKGROUND AND OBJECTIVES: Antimicrobial resistance (AMR) is a serious global health threat, mainly caused by antibiotic overuse. This study evaluates probiotics as a safe and ethical intervention to address AMR. Probiotics, live beneficial bacteria, restore microbiome balance, reduce antibiotic dependency, and limit resistant pathogens. We tested Lactobacillus rhamnosus GG and Bifidobacterium bifidum against drug-resistant Escherichia coli, Staphylococcus aureus, and Pseudomonas aeruginosa. Using standard culturing and Kirby-Bauer disk diffusion, we assessed pathogen growth and antibiotic susceptibility with and without probiotics

MATERIALS AND METHODS: This study assessed the effect of probiotics on antimicrobial resistance in selected bacteria. Clinical isolates of Escherichia coli, Staphylococcus aureus, and Pseudomonas aeruginosa were cultured using standard methods. Probiotic strains Lactobacillus rhamnosus GG and Bifidobacterium bifidum were grown in MRS broth at 37°C anaerobically. Antibiotic susceptibility was tested by Kirby-Bauer disk diffusion with and without probiotics. Co-culture assays were done by incubating equal volumes of probiotic and pathogen at McFarland 0.5 for 24 hours. Colony counts (CFU/mL) were measured before and after incubation. Experiments were done in triplicate. Statistical analysis used GraphPad Prism 9 with significance at p 0.05. Results are shown as mean ± SD.

RESULTS AND DISCUSSION: Both probiotic strains significantly inhibited pathogen growth (p 0.05) and increased antibiotic susceptibility. These results suggest probiotics can suppress harmful bacteria and enhance antibiotic effectiveness. Probiotics present an ethical, natural alternative to reduce AMR, supporting global efforts to limit antibiotic misuse. However, effectiveness varies by strain and pathogen, so further clinical studies are necessary.

Keywords: Probiotics, Antimicrobial Resistance, Ethical Intervention, Antibiotic Alternatives

Protective Effects of Hydroalcoholic Extract of Nigella sativa on Enzymatic Activity and Kidney Histopathology in Mice Infected with Plasmodium berghei

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BACKGROUND AND OBJECTIVES: Nigella sativa is a medicinal plant traditionally used for the treatment of various diseases. The presence of essential fatty acids in N.sativa has contributed to its anticancer properties and its effectiveness in promoting skin health. This study aimed to evaluate the protective effect of the hydroalcoholic extract of N.sativa on enzymatic activity and renal histopathology in mice infected with Plasmodium berghei.

MATERIALS AND METHODS: A total of 35 adult male mice, were divided into 7 groups. The mice were infected with P. berghei to induce malaria. After confirmation of infection, the mice were treated with N.sativa extract for 4 consecutive days. At the end of the treatment period, blood samples were collected to measure serum levels of urea and creatinine. Additionally, kidney tissues were subjected to histopathological examination.

RESULTS AND DISCUSSION: The results demonstrated that the N.sativa extract at a dose of 400 mg/kg reduced levels of urea and creatinine compared to the negative control group. Histopathological assessment of the kidney tissues revealed no significant morphological differences between the control and treated groups. Furthermore, the lumen and epithelial lining of the renal convoluted tubules in the extract-treated group appeared similar to those in the negative control group, with no statistically significant changes observed (p 0.05). Based on these findings, further long-term studies are recommended to investigate the potential of N.sativa extract in reducing elevated urea and creatinine levels in various pathological conditions. This extract may serve as an effective agent in managing renal dysfunction associated with different diseases.

Keywords: Plasmodium berghei, malaria, Nigella sativa, renal histology

PrtA-Focused Immunoinformatics Exploration for Next-Generation Novel Multi-Epitope Vaccines against Streptococcus pneumoniae

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BACKGROUND AND OBJECTIVES: To prevent pneumococcal infections and overcome the serotype-dependent limitation of polysaccharide-based vaccines, the development of conserved protein-based vaccines is essential. This study aimed at investigate epitope mapping and immunogenicity profile of Pneumococcal Serine Protease A(PrtA) to design the multi-epitope based vaccines candidates.

MATERIALS AND METHODS: The linear B-cell and MHCII binding epitopes, IL-4, and IFN-γ inducer epitopes of PrtA (UniprotID:Q9S4M8) were predicted using IEDB, IL-4Pred, and IFNepitope databases, respectively. The immunogenicity, allergenicity, toxicity, and conservation score of the predicted epitopes among pneumococcal serotypes were evaluated using VaxiJen, AllerTop, ToxinPred, and IEDB databases, respectively. Physicochemical properties of protein were assessed by Protparam server. Finally, the immune simulation of PrtA administration in mammals and potential regions involved in PrtA-TLRs interactions were analyzed by C-ImmSim site and molecular docking via ClusPro server, respectively.

RESULTS AND DISCUSSION: This protein had five predicted linear B-cell and six helper T-cell epitopes with a vaxijen score of 1.9 and conservation score of 99.80% among pneumococcal serotypes without any toxicity and allergenicity properties. Furthermore, PrtA was considered an IL-4 and IFN-γ inducer protein. The immune simulation demonstrated induction of both humoral and cellular immunity against PrtA. In addition, PrtA had good interaction with TLR2 and TLR4 (binding energy of-1426.4 and-1258.4kcal/mol). Protparam analysis showed this protein with molecular weight of 240726.25Da and pI of 27.47 was considered as a stable vaccine candidate.

Keywords: Streptococcus pneumoniae, PrtA, Multi-epitope vaccine, Immunoinformatics.

Purification, and Characterization of the Polysaccharide Intercellular Adhesin (PIA) Antigen in Staphylococcus epidermidis

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BACKGROUND AND OBJECTIVES: This study aimed to isolate, purify, and characterize the polysaccharide intercellular adhesin (PIA), a key factor in biofilm formation and pathogenicity of Staphylococcus epidermidis.

MATERIALS AND METHODS: Biofilm-forming strains were initially identified using biochemical and molecular methods, followed by in vitro biofilm formation assays. Both PIA-positive (S. epidermidis 1457) and PIA-negative (M-10/transmutant 1457) strains were used for comparative investigation. PIA purification was achieved with high-performance liquid chromatography (HPLC) using a C18 column, where fractions near the void volume were identified as containing PIA.

RESULTS AND DISCUSSION: Recovered fractions were analyzed colorimetrically, confirming significant carbohydrate (hexosamine = 5700 µg/ml) content in the PIA-positive samples. Structural analysis employed Fourier-transform infrared spectroscopy (FTIR) and nuclear magnetic resonance spectroscopy (NMR). FTIR profiles revealed characteristic polysaccharide peaks at 1746 cm^{-1} and a specific NH group peak at 3543 cm^{-1}, supporting the identification of PIA, which exhibited a molecular weight of approximately 100 kDa. NMR spectroscopy showed a distinct signal at 3–4 ppm corresponding to proton environments within the PIA structure. Comparative results with the transmutant strain confirmed the specificity and efficiency of the extraction procedure. Approximately 5 mg of PIA per liter of culture medium (at 40–60 rpm) was produced and successfully isolated by the described method. These results confirm that S. epidermidis is capable of synthesizing and secreting measurable quantities of PIA, which can be effectively purified and structurally characterized using combined chromatographic, colorimetric, FTIR, and NMR techniques.

Keywords: Staphylococcus epidermidis, Purification, PIA

Quantitative Assessment of Biological product Color Using the CIE Lab Color Space

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BACKGROUND AND OBJECTIVES: Color assessment of biological products, particularly vaccines, can provide important insights into their physical and chemical stability. Color variations during storage may signify chemical reactions, degradation, or structural changes in the active components. The CIE Lab color space, introduced by the International Commission on Illumination (CIE), is a widely accepted model for scientific color analysis. The objective of this study is to employ the CIE Lab color space for the quantitative evaluation of vaccine color as a sensitive biological product, to monitor quality and ensure stability across storage conditions.

MATERIALS AND METHODS: Samples of the target vaccine were prepared, sample was photographed five times for consistent analysis. Imaging was conducted under controlled conditions: the camera was placed away from the sample surface, with the lens axis positioned perpendicularly to the sample surface. The light source was angled uniform illumination. Image processing and color analysis were performed using Adobe Photoshop. Chromaticity (Chroma) was calculated to determine the color saturation of each sample.

RESULTS AND DISCUSSION: Data analysis revealed that the values of the color indices (L, a, b) were effective in identifying subtle differences in the color of the biological product and to monitor color changes over time or under different storage conditions. The findings confirm that the CIE Lab method is capable of reporting vaccine color changes in a precise and reproducible manner. Therefore, the CIE Lab method can be regarded as a reliable scientific tool for the quantitative assessment of biological product coloration.

Keywords: biological products color, vaccine, CIE Lab, quantitative

Quantitative real-time PCR analysis of gut microbiota in rheumatoid arthritis patients compared to healthy controls

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BACKGROUND AND OBJECTIVES: Rheumatoid arthritis (RA) is an autoimmune disorder with synovial inflammation of joints and extra articular manifestations. The results of recent researches consider the relationship between microbiota and the immune system as a double-edged sword. Considering that the relationship between the composition of intestinal microbiota and the immunological and clinical status of the body has been confirmed.

MATERIALS AND METHODS: The current study was determined using 16S rRNA gene sequencing to explore the 4 selected gut microbiota from 25 people suffering from rheumatism with a time interval of at least 3 years from the onset of the disease and 25 Healthy people by real time PCR. Gut dysbiosis in patients with rheumatoid arthritis (RA) is identified alongside key serological and clinical markers such as C-reactive protein (CRP), erythrocyte sedimentation rate (ESR), immunofluorescence (IF), anti-cyclic citrullinated peptide (Anti-CCP), white blood cell count (WBC), mean corpuscular volume (MCV), aspartate aminotransferase (AST), alanine aminotransferase (ALT), blood urea nitrogen (BUN), Platelet count (PLT), thyroid-stimulating hormone (TSH), creatinine (Cr), and hemoglobin (Hb).

RESULTS AND DISCUSSION: Bacteroides fragilis, Roseburia faecis and Fusobacterium nucleatum genera showed a much lower median in Rheumatoid arthritis patients in comparison with healthy people (P0.001, p=0.002, P0.001 respectively). While the difference in the median of E. coli genera was not significant in the two studied groups (p=0.31). In such a way that the change in the Gut normal flora homeostasis and the reduction of beneficial bacteria such as Bacteroides fragilis, Roseburia faecis, Fusobacterium nucleatum genera, may stimulate the immune system to initiate autoimmunity.

Keywords: Microbiota, Dysbiosis, Rheumatoid arthritis, Auto-immune

Recalcitrant Endodontic Infections: From Microbial Causes to Treatment Strategies

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BACKGROUND AND OBJECTIVES: Recalcitrant endodontic infections represent a significant clinical challenge due to their resistance to conventional root canal therapies. These persistent infections are often fueled by complex microbial biofilms and resilient bacterial species that evade disinfection. The objective of this review is to elucidate the microbial landscape underlying recalcitrant infections and evaluate emerging therapeutic strategies aimed at enhancing treatment outcomes.

MATERIALS AND METHODS: This narrative review synthesizes findings from peer-reviewed publications, clinical trials, and molecular microbiology studies related to endodontic infections. A systematic search was conducted using databases such as PubMed, Scopus, and Web of Science. Studies were selected based on relevance to microbial causation, diagnostic advancements, and treatment innovations, including antimicrobial techniques, irrigation protocols, and regenerative therapies.

RESULTS AND DISCUSSION: The literature reveals that persistent endodontic infections are dominated by biofilm-forming pathogens such as Enterococcus faecalis, Candida albicans, and unculturable bacterial consortia. Molecular diagnostics have transformed the understanding of these infections, uncovering polymicrobial interactions and previously undetected species. Treatment innovations—including photodynamic therapy, nanomaterials, and probiotic approaches—have shown promising results in disrupting biofilms and improving clinical outcomes, though more randomized controlled trials are needed to confirm efficacy

Keywords: endodontic infections, biofilms, antimicrobial therapy, persistant bacteria

Recent Advances in the Diagnosis and Treatment of Brucellosis

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BACKGROUND AND OBJECTIVES: Brucellosis, caused by Brucella spp, is one of the most widespread zoonosis, with over 500,000 human cases annually . It poses a persistent public health challenge, particularly in endemic regions. Recent years have brought significant advances in both diagnostic and therapeutic strategies

MATERIALS AND METHODS: A literature review of studies published between 2020 and 2024 was conducted, focusing on human brucellosis diagnostics and treatments. Sources included PubMed, Web of Science, and Scopus, emphasizing molecular assays, novel serological tests, and clinical trials assessing antibiotic regimens (BES Journal 2024).

RESULTS AND DISCUSSION: Result Advances in diagnostics include high-sensitivity molecular techniques such as real-time PCR, loop-mediated isothermal amplification (LAMP), recombinase polymerase amplification (RPA), and CRISPR/Cas-based assays, offering rapid detection suitable for low-resource settings. Refined ELISA and lateral flow immunoassays have improved point-of-care capabilities. Therapeutic breakthroughs are supported by a network meta-analysis of 43 randomized clinical trials (n ≈ 4,283), indicating that doxycycline plus gentamicin (6 weeks + 1–2 weeks, respectively) achieves the highest cure and lowest relapse rates, followed by doxycycline-streptomycin and triple therapy (PLOS NTDs 2024). Conclusion While diagnostic and treatment strategies for brucellosis have improved markedly, especially with molecular tools and optimized antibiotic regimens, challenges remain in endemic regions with limited resources. A comprehensive One Health approach—integrating veterinary control, human health interventions, and public awareness—is essential for sustainable disease reduction. Future priorities include shortening treatment duration, improving compliance, and scaling rapid diagnostics in field settings.

Keywords: Brucelosis,Diagnosis,Treatment,PCR

Recognition of Th2 cells epitopes in spike protein of SARS-COV-2 for Iranian common MHC-II alleles by immunoinformatic

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BACKGROUND AND OBJECTIVES: Since WHO declaration of COVID-19 pandemic in 2020, a lot of researches have concentrated on recognizing the SARS-CoV-2 virus molecules responsible in infection procedure to find therapeutic aims. Spike (S) protein of Since WHO declaration of COVID-19 pandemic in 2020, a lot of researches have concentrated on recognizing the SARS-CoV-2 virus molecules responsible in infection procedure to find therapeutic aims. Spike (S) protein of SARS-CoV-2 is fundamental for its capability to attach and transfer into cells, leading to infection. Moreover S protein is greatly immunogenic and so could be a good target for vaccine development. S protein specific T cell responses are mainly of Th2 type mediating humoral immunity. In this study, Th2 cells specific epitopes located on spike protein of SARS-COV-2 virus for common MHC II alleles in Iranian population were detected by immunoinformatic

MATERIALS AND METHODS: The amino acid sequence of spike protein from SARS-COV-2 virus was found by NCBI database. The most abundant MHC II alleles in the Iranian population were determined using allele frequency net database and the specific epitopes of CD4+ T (Th2) lymphocytes were expected by NETMHCPan.

RESULTS AND DISCUSSION: In this study, 16 Th2 cells specific epitopes situated on spike protein of SARS-COV-2 for Iranian common MHC-II alleles were detected by immunoinformatic. In current study, lots of Th2 cells specific epitopes on spike protein of SARS-COV-2 for Iranian common MHCII alleles were recognized. Supplementary studies for revealing of epitopes inducing strong immune response to make more efficient anti- SARS-COV-2 vaccines are required.

Keywords: SARS-COV-2, epitopes, immunoinformatic, Th2 cells

Recurrent MRSA-Infected Wounds in an Immunocompetent Individual: A Case Emphasizing the Need for Routine Antibiotic Susceptibility Testing

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BACKGROUND AND OBJECTIVES: Recurrent wounds are particularly vulnerable to colonization and infection by multidrug-resistant bacteria, most notably Methicillin-Resistant Staphylococcus aureus (MRSA), which poses serious treatment challenges. In this case study, we report a laborer with multiple relapsing wounds on different parts of the body. Despite various antibiotic treatments, the infection persisted. Also, immunological tests ruled out underlying immune deficiencies. This study emphasizes clinicians should conduct antibiotic susceptibility testing prior to initiating empirical antibiotic therapy.

MATERIALS AND METHODS: A clinical isolate was obtained from a chronic wound swab was evaluated microbiological and biochemical methods. Some commonly prescribed antibiotics available in the pharmaceutical market were prepared and antibiotic susceptibility testing (AST) was performed using the well- diffusion method.

RESULTS AND DISCUSSION: Microscopic observations and biochemical tests revealed that isolated bacteria is Methicillin resistant Staphylococcus aureus (MRSA). The findings indicated that the bacterial isolate from the wound exhibited resistance to the commonly prescribed antibiotics Cloxacillin and Ciprofloxacin 500. In contrast, it demonstrated notable susceptibility to Levofloxacin 500, Tetracycline 250, Metronidazole 500, Cefixime 400, Cephalexin 500, Doxycycline 100, and Clindamycin 300 by 25 - 45 mm inhibition zones respectively. Based on the results, Levofloxacin 500 therapy was recommended. Serial assessments demonstrated significant improvement in wounds healing. Empirical use of routine antibiotics, such as Cloxacillin, plays a key role in the persistence and spread of multidrug-resistant bacteria, particularly MRSA. This leads to prolonged infections, increased treatment failures, and public health challenges. Routine AST is essential to guide targeted therapy and reduce the development and transmission of resistance.

Keywords: MRSA, Antibiogram test, Chronic wounds, Antibiotic resistant

Relationship Between Oral Microbiota and Oral Squamous Cell Carcinoma

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BACKGROUND AND OBJECTIVES: Oral squamous cell carcinoma (OSCC) is the most common malignancy of the oral cavity, with a multifactorial etiology. In addition to well-known risk factors like tobacco and alcohol, the role of the oral microbiota has gained increasing attention. Dysbiosis, or imbalance in microbial communities, may contribute to carcinogenesis by promoting chronic inflammation, immune modulation, and production of carcinogenic metabolites. This review aimed to explore the relationship between oral microbiota composition and OSCC development, with emphasis on microbial mechanisms potentially involved in tumor initiation and progression.

MATERIALS AND METHODS: This review included a comprehensive search of relevant studies indexed in scientific databases such as PubMed, Scopus, and Web of Science. Studies were selected based on relevance to oral microbiota, OSCC, bacterial virulence, inflammatory response, and carcinogenic processes. Both observational and experimental research, including in vitro and animal models, were analyzed and synthesized.

RESULTS AND DISCUSSION: Several microbial genera, including Fusobacterium, Porphyromonas, Prevotella, and Capnocytophaga, have been frequently associated with OSCC. These bacteria can promote carcinogenesis via direct genotoxic effects, induction of pro-inflammatory cytokines, inhibition of apoptosis, and disruption of cell cycle control. Moreover, microbial biofilms can support tumor microenvironment changes. The evidence suggests a significant link between microbial dysbiosis and OSCC pathogenesis, indicating the potential of microbiota profiles as biomarkers or therapeutic targets.

Keywords: Oral squamous cell carcinoma, Oral microbiota, Dysbiosis, Inflammation, Carcinogenesis

Removal of Acinetobacter rpoB Gene from Municipal Wastewater Using Chlorination and UV Radiation

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BACKGROUND AND OBJECTIVES: Antibiotic-resistant Acinetobacter spp. is prevalent in municipal wastewater and this bacterium play a role in spreading antibiotic resistance genes. The rpoB gene is a key marker in antibiotic-resistant bacteria. Disinfection methods such as chlorination and UV irradiation target microbial DNAs and proteins, but the effectiveness in removing the rpoB depends on operational conditions. Therefore, assessing the treatments in removing these resistance gene is essential.

MATERIALS AND METHODS: Effluent samples were collected from three critical points: prior to treatment, after chlorination, and following UV disinfection. The genomic DNA was directly extracted from the samples. The presence and quantification of the rpoB gene in Acinetobacter spp. were assessed by PCR amplification. The specific primers, targeting the rpoB gene was used.

RESULTS AND DISCUSSION: The rpoB gene, in prior of treatment was detected in all three sampling points. Using chlorination, this gene was detected in two out of the three at post treatment sampling points. Similarly, after UV radiation, the rpoB gene was detectable in two out of the two at post treatment sampling points. The rpoB gene was found in raw wastewater and persisted after chlorination and UV, showing only partial removal. This indicates that disinfection may stop bacterial growth but genetic material can still spread antibiotic resistance. Some bacteria can enter a Viable but Non-Culturable (VBNC) state, remaining alive but undetectable by culture. This makes molecular methods essential to evaluate their risk in aquatic environments.

Keywords: Antibiotic resistance genes, PCR, Sewage, Wastewater treatment, Water microbiology

Repurposing Sulfadiazine as a potential Inhibitor of Yersinia pestis Dihydrofolate Synthetase: An In silico Study

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BACKGROUND AND OBJECTIVES: Yersinia pestis, the gram-negative bacterium responsible for various plague forms, relies on dihydrofolate synthetase(DHPS) for folate biosynthesis, a critical pathway for bacterial growth and survival. Notably, Y. pestis DHPS share over 74% sequence similarity with Klebsiella pneumoniae DHPS, this study explored repurposing sulfadiazine, a known Klebsiella pneumoniae DHPS inhibitor, as a potential therapeutic candidate against Y. pestis through molecular docking and pharmacokinetic analysis.

MATERIALS AND METHODS: Sequence alignment of two proteins was done using ClustalW web server. The 3D structure of Y. pestis DHPS (PDBID:3TYZ) was obtained from the RCSB PDB database. The structure of K. pneumoniae DHPS-targeting drug, sulfadiazine with PubChemCID5215, was retrieved from the PubChem database in SDF format. After preparing the protein, molecular docking was performed using Molegro Virtual Docker v.6. The interactions and energy binding score were analyzed through Molegro Molecular Viewer. Finally, pharmacokinetic properties were assessed via the SwissADME server.

RESULTS AND DISCUSSION: Molecular docking analysis revealed that sulfadiazine exhibited a binding energy of -72.7227kcal/mol. This ligand created two hydrogen bonds with Asn180 and Lys181, and four steric interactions with Asn180, Lys181, Pro135, and Leu3, without electrostatic interaction. The ADME results demonstrated that this ligand has water solubility score of -1.66, hydrophilic score of 0.79, polarity score of 106.35 and lastly, hydrogen bond donors of 2 and hydrogen bond acceptors of 4. These results indicates that sulfadiazine is a good candidate for inhibiting DHPS of Yersinia pestis. Further in vitro and in vivo studies are required to confirm its potential as a therapeutic agent.

Keywords: Yersinia pestis, Drug repositioning, Molecular docking, ADME.

Reverse Vaccinology approach to design a multi-epitope protein against Brucella melitensis and in vitro immunogenicity assessment

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BACKGROUND AND OBJECTIVES: Brucella melitensis, a facultative intracellular pathogen, drives zoonotic brucellosis with high relapse rates due to antibiotic resistance and suboptimal vaccine safety for human applications (e.g., Rev.1 strain's virulence reversion). Reverse vaccinology offers a paradigm for designing multi-epitope constructs to elicit broad-spectrum CTL/HTL responses without live organisms. This study applies immunoinformatics to design a chimeric vaccine candidate targeting conserved antigens, addressing gaps in human prophylaxis due to the multidrug-resistant strains.

MATERIALS AND METHODS: Six virulence-associated proteins (Omp10, VirB5, VirB8, Omp31, Omp28/Bp26, and DnaK) from B. melitensis 16M were screened via VaxiJen and AllerTOP for antigenicity and non-allergenicity. Epitopes (46 B-cell linear, 26 CTL, 32 HTL) were predicted using IEDB-AR and NetMHC algorithms, prioritizing high MHC-I/II binding affinities (90% conservation). The construct was assembled with AAY/GPGPG linkers, 3D-modeled via I-TASSER for stability, codon-optimized, cloned into pET28a, expressed in E. coli BL21 (DE3), and purified by Ni-NTA affinity with Triton X-114 endotoxin removal. Immunogenicity was quantified by Western blot using sera collected from confirmed brucellosis patients (n=20) and healthy controls (n=10).

RESULTS AND DISCUSSION: The 54 kDa construct showed high solubility (instability index 40), strong antigenicity (0.7), and modeled stability. SDS-PAGE confirmed 95% purity. Western blotting demonstrated 90% specific recognition by patient sera, indicating robust, specific humoral responses without cross-reactivity. The in vitro immunogenicity of this multi-epitope vaccine suggests its promise as a safe candidate for human brucellosis prevention. Preclinical in vivo studies are now needed to confirm efficacy and Th1/Th2 polarization.

Keywords: Brucella melitensis, Epitopes, Reverse Vaccinology, Immunoinformatics

Review of Targeted Drug Delivery Systems Using Positively Charged Fe_3O_4–Chitosan Nanopolymers for the Treatment of Drug-Resistant Infections

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BACKGROUND AND OBJECTIVES: Bacterial drug resistance particularly the formation of resistant biofilms poses a global threat by hindering antibiotic penetration and causing treatment failure.Targeted delivery approaches using superparamagnetic Fe_3O_4 nanoparticles coated with chitosan have emerged as promising platforms: their positive surface charge,magnetic guidance,and ROS generation enhance drug accumulation at infection sites and biofilm eradication.Recent research has tackled challenges in synthesizing and modifying these nanoparticles,loading them with cisplatin,curcumin,or nisin, penetrating biofilms,and achieving controlled drug release.This review aims to synthesize these findings and outline future directions for applying positively charged Fe_3O_4–chitosan nanoparticles in targeted therapies against resistant infections.

MATERIALS AND METHODS: Articles published from 2012 to 2025 were identified via concurrent searches in Google Scholar, PubMed, and Scopus using the keywords "Fe_3O_4–chitosan," "nanoparticles," "biofilm," and "targeted drug delivery," then screened and reviewed.

RESULTS AND DISCUSSION: Fe_3O_4–chitosan nanoparticles (10–70 nm) retain superparamagnetic behavior and strong positive charge, showing robust antibiofilm activity against MRSA, P. aeruginosa, and E. coli. In vitro, they achieve 4-log bacterial kills via enhanced drug uptake, ROS-mediated disruption, and deep biofilm penetration; photodynamic activation under low-intensity light spares mammalian cells. In MRSA-infected wound models, magnet-guided, drug-loaded nanoparticles clear 90 % of bacteria, accelerate reepithelialization, and cause minimal toxicity. Pharmacokinetics reveal an initial lag followed by sustained release, reducing dosing needs. By modularly loading antibiotics, peptides, or photosensitizers, these platforms enable targeted therapies for resistant infections. Future efforts should explore comprehensive safety and biodistribution, scalable GMP synthesis, magnetically guided delivery devices, optimized dosing regimens, and regulatory toxicology to support early clinical trials.

Keywords: Superparamagnetic Fe_3O_4–Chitosan Nanoparticles,drug delivery,drug resistance

Revisiting the Overuse of Probiotics: The Necessity for an Evidence-Based Approach in Clinical Microbiology

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BACKGROUND AND OBJECTIVES: Probiotics have recently been recognized as safe and versatile supplements in public health and medicine, with claims ranging from improving gastrointestinal function to modulating mood. However, do all these applications rest on a solid scientific foundation? The widespread, indiscriminate use of these products without thorough evaluation of their safety and efficacy may lead to unforeseen consequences. Objective: This presentation aims to critically review the extensive and sometimes irrational consumption of probiotics, examining less addressed aspects of the field based on recent scientific evidence—including scenarios where probiotic use is not only ineffective but potentially harmful. Content Overview: Clinical studies indicate that the beneficial effects of probiotics on gut microbiota are typically transient, with the microbiome generally reverting to its baseline state following cessation of supplementation. Furthermore, laboratory investigations have demonstrated that certain adapted probiotic strains can transfer antibiotic resistance genes to human gut bacteria—a concerning phenomenon that may contribute to

MATERIALS AND METHODS: ...

RESULTS AND DISCUSSION: In light of these findings, developing evidence-based clinical strategies for rational probiotic prescription is imperative. This presentation emphasizes the importance of "supplement stewardship" and proposes recommendations for the targeted, safe, and scientific use of probiotics, particularly among vulnerable patient

Keywords: Keywords: probiotics, antibiotic resistance, microbiota, rational supplementation, stewardship

Risk Progress of Listeria monocytogenes

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BACKGROUND AND OBJECTIVES: Listeria monocytogenes (LM) is a major problem for the food industry. LM biofilms are a persistent source of cross-contamination in housing storage and food processing environments.

MATERIALS AND METHODS: In order to investigate the prevalence of LM in meat products in China, a meta-analysis method was used to systematically analyze the contamination information. Focusing on the cross-contamination caused by LM biofilm, systematic research has been conducted in food processing and housing storage.

RESULTS AND DISCUSSION: Firstly, the biofilm formation of LM in simulated meat processing was explored, and the biofilm formation probability boundary model of LM under simulated meat processing conditions was established. Then beef juice and standard medium were used as cultures to observe formation process and microstructure of LM biofilms. Secondly, the biofilm formation model of Pseudomonas aeruginosa and LM in a simulated chicken environment was established, and the formation of LM biofilm and the expression of related genes were studied under nutritional stress conditions. Finally, the transfer and residual of biofilm cells after a single and successive contacts at specific stages was studied. Our findings provide a theoretical reference for the prevention and control of LM biofilms in food processing.

Keywords: Listeria monocytogenes; Risk; Biofilm

Role of Indigenous Probiotic Treatment in Enhancing Memory and Reducing Tau Expression in an Experimental Alzheimer's Model

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BACKGROUND AND OBJECTIVES: Background and Objective: Alzheimer's disease (AD) is a progressive and prevalent neurodegenerative disorder in the elderly, characterized by cognitive impairment, the accumulation of abnormal proteins such as beta-amyloid (Aβ) and Tau, and the activation of inflammatory pathways. Recent evidence suggests that probiotics, owing to their anti-inflammatory and antioxidant properties, may modulate these pathological processes. This study aimed to investigate the effect of an indigenous Iranian probiotic combination on Tau protein expression and learning and memory performance in an animal model of Alzheimer's disease.

MATERIALS AND METHODS: Methods: In this experimental study, 21 male Wistar rats were randomly assigned to three groups: control, Alzheimer's, and treatment. AD was induced in the Alzheimer's and treatment groups by intra-hippocampal injection of Aβ1-42 into the CA1 region of the brain. The treatment group received a daily oral gavage of 1 mL of a probiotic mixture containing Lactobacillus acidophilus, L. paracasei, L. reuteri, and Bifidobacterium longum for three weeks. Cognitive and memory function were assessed using the shuttle box test, and Tau protein expression in hippocampal tissue was evaluated using the western blot technique.

RESULTS AND DISCUSSION: Results: Injection of Aβ significantly increased Tau protein expression and impaired memory performance in the Alzheimer's group compared to the control group (P0.001). Probiotic administration significantly improved cognitive performance and reduced Tau expression in the treatment group (P0.01). Conclusion: The native Iranian probiotic showed neuroprotective effects by enhancing memory and lowering Tau expression, supporting its potential as an adjunct therapy for Alzheimer's disease.

Keywords: Alzheimer's disease, probiotics, Tau protein, western blot, memory

Saffron Stamens and Pollen to Wheat Flour: Effect on Sensory, Nutritional and Microbial Properties of leavened bread

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BACKGROUND AND OBJECTIVES: Today, the use of bread made from high-yielding flours is recommended due to their high nutritional value. Despite the beneficial effects in these flours, the concentration of some undesirable substances such as phytic acid is also high. Malnutrition has been especially Iran. The practical of the recent study is to prepare a high-value bakery product.

MATERIALS AND METHODS: For this purpose, saffron stamens and pollen at 1, 3and 5% (w/w) levels were added to wheat flour and its effects on nutritional, chemical, sensory and microbial characteristics of leavened bread were investigated.

RESULTS AND DISCUSSION: The results showed that the addition of these additives can significantly improve the characteristics of bread and produce higher- yielding breads. The highest amount of phytic acid related to control treatment and 18.28 (mg / kg) and the lowest to the obtained results, the highest amount of iron related to treatment that these additives reduce phytic acid and very little increase in fiber in bread, which improves the absorption of minerals and increases the nutritional value of bread. In sensory evaluations, breads containing

Keywords: Nutritional and Sensory Characteristics, Saffron Stamens

Salivary Detection of Helicobacter pylori in Pediatric Patients: Implications for Gastrointestinal and Oral Health Integration

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BACKGROUND AND OBJECTIVES: Although the oral cavity has long been considered a potential niche for Helicobacter pylori, its exact role—especially in relation to oral health—remains uncertain. This study aimed to assess the simultaneous presence of H. pylori in saliva and gastric tissue of pediatric patients with gastrointestinal symptoms and explore its association with dental caries.

MATERIALS AND METHODS: In a descriptive-analytical cross-sectional study conducted in 2024, unstimulated saliva and gastric biopsy samples were collected from 100 children aged 4–18 years undergoing endoscopy. Parents completed questionnaires and provided informed consent. Prior to endoscopy, an oral examination was performed to assess dental health using the dmft/DMFT index. Saliva samples were analyzed using PCR assays to detect H. pylori DNA. Statistical analysis was conducted to examine correlations between molecular findings and dental caries.

RESULTS AND DISCUSSION: The presence of Helicobacter pylori was evaluated through both gastric biopsy and salivary testing, with a notable degree of agreement between the two diagnostic methods. Interestingly, in some cases, the bacterium was detected in saliva despite negative gastric biopsy results, supporting the hypothesis that the oral cavity may serve as a silent, persistent reservoir. A significant association was also observed between salivary detection of H. pylori and higher levels of dental caries, suggesting a potential link between oral colonization and compromised oral health.The findings highlight the relevance of integrating dental assessments into the clinical management of H. pylori infection. Saliva-based screening may provide a non-invasive supplementary tool for early detection, surveillance, or relapse prediction in pediatric patients.

Keywords: Helicobacter pylori, saliva, PCR, DMFT

Screening of resistant bacteria to zinc and manganese heavy metals from hydrocarbon-contaminated soil

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BACKGROUND AND OBJECTIVES: There are environmental concerns due to heavy metal pollution, particularly the elements such as zinc and manganese. Though necessary in small concentrations, these metals are toxic in high concentrations and alter microbiome and soil ecology. Metal-resistant bacteria are good choice for bioremediation. Accordingly. The aim of this study was to screen and isolate resistant bacteria to heavy metals such as zinc and manganese.

MATERIALS AND METHODS: Sampling of hydrocarbon-contaminated soil was carried out. The sample was added to Bushnell-Haas medium containing 1 mM zinc and manganese, and bacteria were isolated by serial dilution method. Identification at genus level was performed by biochemical tests. To evaluate the tolerance of isolates to heavy metals, an enriched agar culture medium with zinc sulfate and manganese sulfate was used at concentrations of 1 to 5mM.

RESULTS AND DISCUSSION: Among the isolated bacteria, 3 isolates grew with a halo around the colony concentration of up to 4mM zinc, and all 10 isolates showed growth at a concentration of up to 5mM. 3 out of 10 isolate had the maximum tolerance to zinc. Zinc and manganese concentrations were tolerated by the isolated bacterial strains. The bacterial strains grew well intensively even in larger concentrations of used metals. Their ability to survive and potentially mobilize heavy metals is their promise as effective agents for sustainable bioremediation in metal-polluted environments.

Keywords: Bacteria, Zinc, Manganese, Heavy metals, Bioremediation.

Secondary bacterial infections in post-COVID-19 mucormycosis cases: a retrospective study at Imam Khomeini Hospital Complex, March 2020-April 2021

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BACKGROUND AND OBJECTIVES: To explore the prevalence and characteristics of secondary bacterial infections among patients suffering from mucormycosis following COVID-19 infection

MATERIALS AND METHODS: We conducted a cross-sectional, retrospective analysis from March 2020 to April 2022 at Imam Khomeini Hospital Complex in Tehran. The study included patients with histopathologically confirmed mucormycosis and documented secondary bacterial infections. We extracted and analyzed data from hospital records using SPSS software, version 26.

RESULTS AND DISCUSSION: The study comprised 27 patients, with a predominance of females (70.4%) and an average age of 56 years. The majority of these patients (63%) had pre-existing diabetes mellitus. The severity of their COVID-19 infections varied. Treat- ment regimens included immunosuppressive drugs and antibiotics. Rhinocerebral mucormycosis was the most common form observed. The predominant secondary infections involved the urinary tract, respiratory system, bloodstream (bacteremia), and soft tissues, with resistant strains of Acinetobacter baumannii, Escherichia coli, and Klebsiella pneumoniae being the most frequently identified microorganisms. Notably, cases of bacteremia and pneumonia exhibited a higher mortality rate. Ultimately, 55.6% of patients were discharged, while 44.4% succumbed to their infections.

Keywords: Bacterial infection; Mucormycosis; COVID-19; Acinetobacter baumannii; Klebsiella pneumonia; Escherichia coli

Seroprevalence of Brucellosis among Pet animal clinic workers in Mashhad: A cross-sectional analysis of occupational exposure and risk factors

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BACKGROUND AND OBJECTIVES: Brucellosis, a zoonotic bacterial disease caused by Brucella spp., is a significant occupational hazard for veterinary workers due to frequent contact with infected animals. Pet clinic workers, though at lower risk compared to livestock handlers, remain vulnerable through contact with infected pets or consumption of unpasteurized dairy. This study aimed to determine the seroprevalence of brucellosis among pet clinic workers in Mashhad, Iran (2023) and identify associated risk factors.

MATERIALS AND METHODS: A cross-sectional study was conducted in 2023 among 95 pet animal clinic workers in Mashhad. Blood samples were collected, and IgG antibodies against Brucella were detected using enzyme-linked immunosorbent assay (ELISA). Participants completed a questionnaire on demographics, occupational exposure, and risk factors, including raw milk consumption. Statistical analysis (Chi-square test, p 0.05) assessed associations between seropositivity and risk factors.

RESULTS AND DISCUSSION: Of the 95 samples, 4 (4.2%) tested positive for Brucella IgG, indicating prior exposure. Statistical analysis revealed significant associations (p 0.05) between seropositivity and older age, likely due to cumulative exposure, and raw milk consumption, a known transmission route. No significant relationships were found with gender or employment duration. The study highlights a notable seroprevalence of brucellosis among pet clinic workers in Mashhad, emphasizing age and raw milk consumption as key risk factors. Routine serological screening, enhanced occupational safety measures, and public health education on pasteurizing dairy products are essential to mitigate brucellosis transmission in veterinary settings.

Keywords: Brucella, Infectious diseases, Mashhad

Serotyping and molecular evaluation of quinolone resistance in Shigella strains isolated from diarrhea patients and their clonal evaluation using ERIC-PCR

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BACKGROUND AND OBJECTIVES: Shigellosis is an important and highly communicable diarrheal disease which around 70% of cases and 60 % of deaths occur in children under 5 years of age. Quinolones have been utilized globally for an extended period in the treatment of Shigellosis. The aim of this study was to investigate the presence of plasmid-mediated quinolone resistance (PMQR) genes in quinolone-resistant Shigella isolates collected from patients with diarrhea resistant to quinolones.

MATERIALS AND METHODS: Between November 2022 and October 2023, 352 stool samples were collected from children with diarrhea. Shigella species were identified by biochemical and molecular methods. Antibiotic resistance was evaluated using the broth microdilution method. PMQR genes (qnrA, qnrB, qnrC, qnrD, qnrE, qnrS, qepA, oqxA, and aac(6′)-Ib-cr) were detected by PCR. ERIC-PCR was performed to assess clonal relatedness.

RESULTS AND DISCUSSION: A total of 57 Shigella isolates were identified, including S. flexneri (21 isolates, 36.84%), S. sonnei (18 isolates, 31.57%), S. boydii (11 isolates, 19.29%) and S. dysenteriae (7 isolates, 12.28%). All were resistant to at least one quinolone; resistance to nalidixic acid was highest (63.15%). PMQR genes were detected as follows: aac(6′)-Ib-cr (36.84%), qnrB (26.31%), qnrS (17.54%), qnrA (8.77%), and oqxA (5.26%). Other PMQR genes were not found. ERIC-PCR grouped the isolates into 18 genotypes, indicating high genetic diversity. S. flexneri and S. sonnei were the most common species. The presence of aac(6′)-Ib-cr and qnrB suggests a major role in quinolone resistance. Genetic diversity among isolates highlights the need for local surveillance to control resistant Shigella strains.

Keywords: Shigella, quinolone, plasmid-mediated quinolone resistance, ERIC-PCR

Screening and Identification of Streptococcus thermophilus Strains with Antimicrobial and Probiotic Potential from Traditional Meybod Yogurt, Yazd Province

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BACKGROUND AND OBJECTIVES: Streptococcus thermophilus is the only Streptococcus species utilized in the food industry, consumed by humans without causing any disease. In addition to its traditional use in yogurt preparation, it is also employed in the production of various types of cheese. The primary role of S. thermophilus is to increase acidity, which inhibits the growth of undesirable microorganisms. S. thermophilus produces potent bacteriocins, which are used as food additives. Due to important technological properties such as proteolytic activity, urease activity, exopolysaccharide production, antibiotic resistance, etc., S. thermophilus belongs to the group of beneficial microorganisms.

MATERIALS AND METHODS: Streptococcus thermophilus isolates were then separated using standard microbiological methods and selective M17 agar. For genus identification of Streptococcus, Gram staining, catalase test, motility test, H2S production, growth in the presence of 6.5% salt, and growth at 10, 15, and 45°C were performed. For species identification, growth ability at pH 6 and 9, growth in the presence of 2% and 3% salt concentrations, esculin hydrolysis, arginine hydrolysis, MR-VP test, and fermentation of carbohydrates including lactose, mannitol, sorbitol, sucrose, arabinose, fructose, and raffinose were employed. Subsequently, antimicrobial activity, DNA extraction, and sequencing were carried out.

RESULTS AND DISCUSSION: After growth of the isolates and removal of redundant ones, biochemical and molecular tests identified two isolates, MT and MY, showing similarity to Streptococcus thermophilus strains. Isolate MY showed 90% similarity, and isolate MT showed 91% similarity to Streptococcus thermophilus. The tested isolates demonstrated antimicrobial activity against spoilage and pathogenic bacteria, including E. coli and Bacillus cereus.

Keywords: Bacteriocins, Streptococcus thermophilus, Probiotic

Synergistic Antimicrobial Effects of Silver Nanoparticles and Conventional Antibiotics against Multidrug-Resistant Acinetobacter baumannii Isolates from ICU Patients

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BACKGROUND AND OBJECTIVES: The emergence of multidrug-resistant (MDR) Acinetobacter baumannii strains, particularly in intensive care units (ICUs), poses a significant therapeutic challenge. This study aimed to investigate the antimicrobial efficacy of silver nanoparticles (AgNPs) against MDR A. baumannii isolates from ICU patients and evaluate their potential synergistic effects when combined with conventional antibiotics.

MATERIALS AND METHODS: Thirty MDR A. baumannii isolates were collected from ICU patients at a hospital in Tehran, Iran. AgNPs were synthesized using a chemical reduction method and characterized by UV-Vis spectroscopy, X-ray diffraction (XRD), and transmission electron microscopy (TEM). Antibacterial activities of AgNPs, ciprofloxacin, and ceftazidime were evaluated individually and in combination using broth microdilution and disk diffusion assays. The minimum inhibitory concentration (MIC) of AgNPs was 0.5 mg/mL. The combination of subinhibitory concentrations of AgNPs (0.25 mg/mL) with ciprofloxacin (8 µg/mL) or ceftazidime (32 µg/mL) demonstrated synergistic effects, enhancing growth inhibition by 51.2% and 39.8%, respectively, compared to individual agents. Disk diffusion assays confirmed the synergistic activity with significant inhibition zones for the antibiotic-AgNP combinations. DNA fragmentation analysis revealed no detectable DNA damage.

RESULTS AND DISCUSSION: This study demonstrates the synergistic antimicrobial effects of combining AgNPs with conventional antibiotics against MDR A. baumannii isolates from ICU patients. The findings suggest that AgNPs could serve as a promising adjunctive therapy to overcome antibiotic resistance in these infections.

Keywords: Acinetobacter baumannii, Drug Resistance, Silver Nanoparticles, Intensive Care Units

Silibinin-Functionalized Fe_3O_4@SiO_2 Nanocomposites as Potent Antibacterial Agents

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BACKGROUND AND OBJECTIVES: Antibiotic resistance is a critical global health issue, especially in multidrug-resistant (MDR) bacteria with biofilm formation and active efflux pumps. Ciprofloxacin efficacy is often compromised by mechanisms like mexX overexpression and limited penetration. Nanotechnology-based drug delivery offers improved antibiotic performance through targeted delivery, enhanced solubility, and resistance modulation. Magnetic nanocarriers are biocompatible, stable, and capable of controlled release. Silibinin, a natural flavonolignan with antimicrobial and antibiofilm activity, has poor water solubility. This study aimed to develop biodegradable, water-soluble Fe_3O_4@SPN@Silibinin nanocomposites to potentiate ciprofloxacin activity against MDR Pseudomonas aeruginosa by suppressing mexX expression.

MATERIALS AND METHODS: Fe_3O_4@SPN@Silibinin nanocomposites were synthesized and characterized using FT-IR, XRD, FE-SEM, TEM, and TGA. Particle sizes ranged from 34–58 nm with high thermal stability. Magnetic properties were evaluated for biomedical suitability. Antimicrobial activity was tested by MIC determination of ciprofloxacin alone and in combination with nanocomposites against clinical isolates. Biofilm inhibition was quantified, and mexX gene expression was analyzed via RT-qPCR to assess efflux pump suppression.

RESULTS AND DISCUSSION: Nanocomposite–ciprofloxacin combinations reduced MIC by 4–16-fold, showing strong synergy against MDR strains. mexX downregulation increased intracellular ciprofloxacin accumulation, enhancing bactericidal activity. Biofilm formation was significantly inhibited, addressing chronic infection risk. Structural stability, biocompatibility, and improved solubility support clinical applicability. Silibinin provided additional antimicrobial and antibiofilm effects, creating a dual-function system for antibiotic potentiation and resistance suppression.

Keywords: Fe_3O_4 nanocomposite; Silibinin delivery; Magnetic nanoparticles; Ciprofloxacin synergy; Biofilm inhibition;

Silver nanoparticles synthesized with Kelussia elburzenisis plant extract reduce mecA gene expression in Meticilin-Resistant Staphylococcus aureus MRSA and inhibit MSSA growth: A microbial and molecular study

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BACKGROUND AND OBJECTIVES: Staphylococcus aureus is a leading cause of treatment-resistant hospital-acquired infection. To date, for the first time, we compared antibacterial activity of Kelussia elburzenisis plant extract, silver nanoparticles biosynthesized from this extract, and their synergistic combination against this pathogen. The mecA gene, which is responsible for antibiotic resistance in methicillin-resistant Staphylococcus aureus (MRSA), was also checked as a marker for resistance.

MATERIALS AND METHODS: The silver nanoparticles were prepared through a green synthesis procedure using Kelussia elburzenisis extract and were characterized using UV-Vis spectroscopy, FTIR, and SEM. The antimicrobial activities of these nanoparticles against S. aureus were studied through MIC, MBC, well diffusion assay, and antibiogram tests. Expression of the mecA gene in MRSA was determined through Real-Time PCR

RESULTS AND DISCUSSION: Silver nanoparticles were successfully synthesized, confirmed by a 400–450 nm UV-Vis peak and FTIR-detected bioactive compounds aiding in their formation. SEM showed an average particle size of 225 nm. Antibacterial tests revealed that the combination of nanoparticles and extract was more effective than either alone, with larger inhibition zones (1.0 cm vs. 0.5 cm) in both well diffusion and antibiogram assays. The combination also significantly reduced mecA gene expression, indicating enhanced antibacterial activity.The findings revealed that AgNP- Kelussia elburzenisis extract exhibit high antibacterial efficacy and are capable of suppressing the synthesis of the mecA resistance gene in MRSA. A synergistic effect between the nanoparticles and extract was seen and recorded.

Keywords: Silver nanoparticles, Kelussia elburzenisis, mecA gene, methicillin-resistant Staphylococcus areus

Simulating Microbial Risks in Pharmaceutical Water Systems: Activated Carbon and Pseudomonas Analysis

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BACKGROUND AND OBJECTIVES: High-quality water is critical for non-sterile pharmaceutical production, directly impacting product safety and GMP compliance. Activated carbon filters, used for water purification, can become microbial hotspots, such as for Pseudomonas aeruginosa, when organic matter accumulates. These bacteria form resistant biofilms, jeopardizing water quality. This study evaluates contamination risks in activated carbon filters, identifies vulnerabilities, and proposes control measures to ensure safe pharmaceutical manufacturing.

MATERIALS AND METHODS: Contamination scenarios in activated carbon filter zones were simulated using dynamic modeling to assess risk factors. Key parameters included water properties (pH, temperature, TOC), filter characteristics (pore size, age), and operational conditions (pressure, flow rate). Qualitative Risk Assessment (QRA) identified critical control points, contamination likelihood, and consequences. Microbiological cultures and biochemical tests confirmed Pseudomonas aeruginosa, while biofilm analysis evaluated bacterial resistance, providing insights into contamination dynamics

RESULTS AND DISCUSSION: Water temperatures of 20–30°C, TOC levels above 0.5 mg/L, and filters older than six months significantly increased microbial contamination risks. Biofilms enhance bacterial resistance, complicating eradication. Inadequate sampling allowed contaminants to persist into later purification stages, such as pre-reverse osmosis (RO), threatening product quality and GMP complianceConclusion: To mitigate risks, we recommend regular filter sampling, timely replacement, backwashing to reduce organic buildup, and staff training on monitoring protocols. These measures prevent microbial proliferation, ensuring water quality and pharmaceutical integrity. By addressing these vulnerabilities, manufacturers can uphold GMP standards and safeguard patient safety.

Keywords: Microbial contamination, activated carbon, water purification system, Pseudomonas aeruginosa,

Smart Microfluidics and AI-Based Systems for Rapid Detection of Pathogens and Antimicrobial Resistance: Toward Next-Generation Diagnostics

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BACKGROUND AND OBJECTIVES: Timely detection of pathogens and their antimicrobial resistance is essential for controlling infectious diseases and ensuring food safety. Conventional methods such as culture, PCR, and ELISA are time-consuming, costly, and not suited for on-site testing. There is a growing need for fast, accurate, and low-cost alternatives.

MATERIALS AND METHODS: Microfluidic technologies like micro total analysis systems (μTAS) and paper-based analytical devices (μPADs) offer miniaturized, portable platforms for phenotypic and genotypic testing using minimal samples. These systems integrate biosensors (e.g., aptamers, antibodies) and nucleic acid amplification techniques (e.g., LAMP, PCR) to detect live pathogens and resistance genes. Artificial intelligence (AI), particularly convolutional neural networks (CNNs), has been used to analyze complex biosignatures such as Raman spectra with enhanced precision.

RESULTS AND DISCUSSION: Integrated microfluidic-AI platforms have demonstrated diagnostic accuracies above 98%, significantly reducing processing time and labor. These systems can detect pathogens and resistance markers across diverse samples and conditions. The synergy of AI with microfluidics improves sensitivity and specificity, enabling reliable diagnostics in clinical and environmental settings. The combination of advanced microfluidic systems and AI-driven analytics represents a major advancement in microbiological diagnostics. These integrated platforms hold great promise for replacing or complementing traditional methods, especially in point-of-care and low-resource environments. Their rapid, affordable, and high-accuracy performance can significantly improve disease monitoring, antibiotic stewardship, and public health interventions worldwide.

Keywords: Microfluidics, Pathogen Detection, Antimicrobial Resistance (AMR), Point-of-Care Diagnostics, Artificial Intelligence

Status of Zoonotic Diseases in Iran

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BACKGROUND AND OBJECTIVES: Zoonotic diseases remain a significant public health concern in Iran due to their endemicity, widespread distribution, and potential for severe morbidity and mortality. This study reviews the recent epidemiological trends of major zoonoses, including rabies, brucellosis, cutaneous leishmaniasis, Crimean–Congo hemorrhagic fever (CCHF), and anthrax, based on national surveillance data for 2024 (1403).

MATERIALS AND METHODS: This descriptive review was conducted using official National Department of Zoonotic Disease Control from the Ministry of Health and Medical Education for the year 1403 (2024).

RESULTS AND DISCUSSION: In 1403, 24 human rabies cases were reported in Mazandaran, Razavi Khorasan, Kerman, Gilan, and Alborz, mostly in males, with 30% under 18; dogs (80%) and cats (15%) were the main sources, and 5% involved other animals. Brucellosis remained highly prevalent with 19,972 cases (23/100,000), particularly in Razavi Khorasan, Lorestan, West and East Azerbaijan, Hamadan, and Ardabil. Cutaneous leishmaniasis, endemic in 19 provinces, accounted for 8,267 cases (10/100,000), mostly in Isfahan, Razavi Khorasan, Fars, Golestan, and Khuzestan. Crimean–Congo hemorrhagic fever (CCHF) had 79 confirmed cases, mainly in Sistan and Baluchestan, Kerman, Yazd, and Hormozgan, with historical predominance in Sistan and Baluchestan. Anthrax persisted with 142 cases, most in Isfahan, West Azerbaijan, Chaharmahal and Bakhtiari, Razavi Khorasan, and Kermanshah, reflecting the continued burden of major zoonotic diseases across multiple regions of Iran. Priorities include public awareness campaigns, vaccination of animals, improved diagnostic capacity, and cross-border collaboration to prevent reintroduction and spread.

Keywords: Rabies, Brucellosis, Cutaneous Leishmaniasis, Crimean–Congo Hemorrhagic Fever, Anthrax, Zoonoses

Structural insights into Smf1-mediated iron transport in Saccharomyces boulardii: A MIB2-guided In Silico exploration

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BACKGROUND AND OBJECTIVES: Saccharomyces boulardii, a probiotic yeast, expresses Smf1, a transporter involved in iron uptake. Smf1 belongs to the low affinity pathway which directly transports Fe2+ into the cytosol. However, its potential for iron binding has not been systematically explored. In this study, we utilized the MIB2 (Metal Ion Binding 2) server to predict iron-binding sites in S. boulardii Smf1 based solely on its amino acid sequence. MIB2 analysis identified six high-confidence Fe^{2+}-binding sites (score above 3). This work provides the first MIB2-based evidence of iron-binding potential in S. boulardii Smf1, supporting its potential repurposing in microbial biofortification strategies. The use of MIB2 may ensure reproducibility and accessibility for future functional annotation of metalloproteins.

MATERIALS AND METHODS: Sequence Retrieval The amino acid sequence of Smf1 Iron Transport of Saccharomyces boulardii was retrieved from the UniProt database (UniProt ID: A0A0L8VHY6). Iron-Binding Site Prediction The MIB2 server was used to predict Fe^{2+}-binding sites.

RESULTS AND DISCUSSION: The MIB2 server identified six binding sites with scores above 3.0, distributed across various protein templates within S. boulardii Smf1transporter. Each site comprises a specific set of residues mapped to its corresponding structural model, indicating regions of potential molecular interaction. The combination 295D, 298H, 300N, and 332A shows the high-scoring predictions across six unique templates, suggesting it may represent a structurally conserved and functionally important binding pocket.

Keywords: Saccharomyces boulardii, Smf1, iron binding, biofortification, in silico, metal transporter

Study and Investigation of Drinking Water Contamination in the Irandegan Region, Balochestan, Regarding the Presence of Pathogenic Coliforms

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BACKGROUND AND OBJECTIVES: This study aimed to investigate the presence of pathogenic coliforms in the drinking water of the Irandegan qanat region in Baluchestan. Since the presence of bacteria in surface waters is common, this research focused on identifying pathogenic bacteria of potential soil, animal, or human origin—particularly coliforms, which serve as indicators of fecal contamination and potential enteric pathogens.

MATERIALS AND METHODS: Water samples were collected using pre-sterilized, screw-cap glass bottles submerged 10 cm below the water surface, avoiding surface collection and direct hand contact. Microbial analysis was performed in three stages: presumptive, confirmed, and completed tests. The Most Probable Number (MPN) method was used with lactose broth in Durham tubes. Tubes showing gas production were recorded and compared with MPN standard tables. For confirmation, Brilliant Green Lactose Bile Broth (BGLB) was used to suppress non-coliform growth. Positive tubes were further tested in the completed stage using nutrient agar and EMB media. The presence of dark colonies with a metallic green sheen on EMB, confirmed by Gram staining, indicated Escherichia coli.

RESULTS AND DISCUSSION: The presence of E. coli confirms that the water is contaminated with fecal coliforms and may pose health hazards. It is recommended that local residents disinfect drinking water and storage sources using methods such as chlorination to reduce the risk of waterborne diseases.

Keywords: Pathogenic coliforms, Escherichia coli, Fecal contamination, MPN method

Study of fosfomycin and Fennel oil effects on resistant Staphylococcus aureus.

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BACKGROUND AND OBJECTIVES: Staphylococcus aureus causes many infections, and methicillin-resistant Staphylococcus aureus (MRSA) is hard to treat due to antibiotic resistance. A study on 23 MRSA isolates tested their response to fosfomycin and Fennel essential oil. Results showed some susceptibility to fosfomycin and resistance in others. A significant percentage of isolates showed improved treatment effects when combining essential oils with fosfomycin

MATERIALS AND METHODS: microbiological methods. It assessed antibiotic susceptibility with the disk diffusion method and aimed to find the minimum inhibitory concentration (MIC) and minimum lethal concentration (MLC) of fosfomycin. The study also evaluated the MLC of Fennel essential oil at various concentrations and investigated potential synergistic effects by adding the essential oil to the liquid culture medium. After incubation, the minimum bactericidal concentration (MBC) of fosfomycin was determined.

RESULTS AND DISCUSSION: In a study of 23 oxacillin-resistant isolates, 13% were susceptible to fosfomycin, while 8.7% were resistant. The average minimum inhibitory concentration (MIC) for other MRSA isolates was 56 µg/ml, and the mean minimum lethal concentration (MLC) was 11.76 µg/ml. The essential oil showed an average MLC of 4% and had synergistic effects with the drug in 77% of isolates.The study shows that the examined isolates are highly resistant, stressing the need for careful assessment of antibiotic susceptibility. It suggests caution with fosfomycin used alone and encourages further research on combining it with essential oils for better treatment

Keywords: Staphylococcus aureus,Fosfomycin,MIC,MLC,Fennel Essential Oil

Study of resistance to carbapenems and carbapenemase enzyme production in clinical isolates of Pseudomonas aeruginosa in Guilan

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BACKGROUND AND OBJECTIVES: This study investigated carbapenem resistance and the prevalence of metallo-beta-lactamase production in clinical isolates of Pseudomonas aeruginosa, an important Gram-negative opportunistic nosocomial infection pathogen with a tendency to acquire multidrug resistance.The frequency of the metallo-beta-lactamase genes blaIMP and blaVIM in resistant strains was also assessed.

MATERIALS AND METHODS: A total of 107 Pseudomonas aeruginosa isolates were collected from different laboratories in Rasht and identified using biochemical methods. The antibiotic resistance of the strains was evaluated using the disk diffusion method.The combined disk method was used to identify the strains producing extended-spectrum beta-lactamase and metallo-beta-lactamases.The presence of blaIMP and blaVIM genes in the resistant strains was investigated in the PCR reaction.

RESULTS AND DISCUSSION: Among 107 isolates of Pseudomonas aeruginosa, 50 isolates (46.7%) were resistant to imipenem.Also, in the phenotypic test,29 isolates (27.1%) were carbapenemase producers and 33 isolates (30.8%)were ceftazidime and extended-spectrum beta-lactamase producers were identified. Of the 50 imipenem-resistant isolates, 21 isolates (42%) produced a fragment of approximately 382 base pairs in the PCR reaction and were identified as having the VIM gene. Also, 5 isolates (10%) were identified as positive for the presence of the IMP gene by producing a fragment of approximately 587base pairs. Of these,3 isolates (6%) simultaneously possessed both genes. All isolates that carried the IMP and/or VIM genes were also carbapenemase producers in the phenotypic test.Given the importance of metallo-beta-lactamase-producing strains in hospitals,rapid identification and tracking of these strains can be an important and fundamental step in the treatment and control of infections caused by these strains.

Keywords: Metallobetallactamase,Pseudomonasaeruginosa,Antibiotic‹resistance, blaIMP, blaVIM

Study of the effect of Aloe vera barbadensis Miller juice on cell proliferation and survival (MTT assay)

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BACKGROUND AND OBJECTIVES: Healing of all types of wounds is one of the most serious problems of society. The study of cell proliferation and survival is considered to be essential. Methods for calculating cell survival are essential for optimizing cell culture conditions, evaluating cell growth factors, etc., evaluating the toxic effects of environmental pollutants, and studying apoptosis.

MATERIALS AND METHODS: Five mg of Thiazolyl blue tetrazolium bromide powder was dissolved in one ml of PBS solution. After counting the cells, an appropriate number of cells were cultured in a 96-well plate in serum-containing medium. We pour the appropriate amount of the drug into each well. After 24 h, the medium of the wells was completely emptied and 180 µl of culture medium and 20 µl of MTT solution were added to each well. It was placed in an incubator at 37°C for four h. The medium was removed from the wells and 200 µl of DMSO was added to each well. After 10 min, the light absorption of the samples was read at a wavelength of nm.

RESULTS AND DISCUSSION: It was observed that the substance under study acted in a concentration-dependent manner, such that with increasing concentration of this compound for treatment, the growth and survival of fibroblast cells decreased. In a 48-hour study, a concentration of about 20 µg was obtained, 50% of the cells in its vicinity were viable and survived (IC50). This new compound can be considered as a repair compound due to its induction of proliferation in cells.

Keywords: Wound healing ،cell proliferation and survival

Study on presence of Entamoeba spp. from watershed of Maharlo-Bakhtegan using 7067 protocol of ISIRI

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BACKGROUND AND OBJECTIVES: Amoebiasis is a parasitic infection in human that is caused by Entamoeba histolytica an extra cellular protozoon. Amoebiasis is a third main reason of disease after Malaria and Schistosomiasis. The organism it could be transfer by swallowing cyst type using contaminated water, vegetables and human using contaminated hands.

MATERIALS AND METHODS: In this project 25 water samples were collected from water washed basin of Maharlo-Bakhtegan. the samples were checked for the organisms using ISIRI protocol (7067). then the isolates were identified using molecular techniques and the results were recorded. in addition, physical and chemical parameters of the water were checked and recorded.

RESULTS AND DISCUSSION: The results obtained from this study indicated that out of 25 samples, 4 were positive for the organism, which is one of them belong to Maharloo and the 3 isolates were detected from Bakhtegan parts. furthermore, the results were confirmed using molecular techniques. Although this organism is very important for human health and detection of the isolates is one of the important points in water, we suggest isolation of this kind of organism from water basin due to their importance on gastro-intestinal tract specially in children.

Keywords: Entamoeba histolytica, Water basin, ISIRI protocol 7067, Molecular technique

Study the effect of Oscillatoria extract on increasing the sensitivity of cisplatin resistant ovarian cancer cells

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BACKGROUND AND OBJECTIVES: Introduction: Resistance to chemotherapy is one of the challenges in cancer treatment. Recent findings show that Oscillatoria cyanobacterium extract has an positive effect on cancer treatment. The aim of this study was to examine the activity and possible mechanism of the effect of Oscillatoria extract in increasing the sensitivity of ovarian cancer cell line A2780/CP to cisplatin.

MATERIALS AND METHODS: Methods: In the current study, ovarian cancer cells resistant to cisplatin (A2780/CP) and sensitive ovarian cancer cells (A2780) were treated with various concentrations of Oscillatoria extract ranging 0, 50, 100, 200 microgram/mL for 24 hours. The effect of Oscillatoria extract on cisplatin cytotoxicity was evaluated using MTT method. The gene expression of survivin and XIAP were measured using Real time-PCR. The effect of Oscillatoria extract on apoptosis was evaluated using flow cytometry. Data analysis was performed using GraphPad Prism 6.01.

RESULTS AND DISCUSSION: Results: The MTT results showed that the Oscillatoria extract increased the cytotoxic effects of cisplatin in cisplatin-resistant A2780/CP ovarian cancer cells in dose dependent mode compared to A2780 cells. The Oscillatoria extract had no effect on survivin gene expression. Moreover, the mRNA levels of XIAP in A2780/CP cells were significantly decreased. In addition, Oscillatoria extract increased the apoptotic effects of cisplatin in A2780/CP cells.Conclusion: The data suggest that Oscillatoria extract can increases the sensitivity of A2780/CP cells to the cytotoxic effects of cisplatin. Therefore, Oscillatoria extract may be an effective compound for combination therapy in resistant ovarian cancer cells.

Keywords: Keywords: Oscillatoria extract, Drug Resistance, Ovarian Cancer

Studying the antifungal effects of Nanocinnamon compared to amphotericin B against Rhizopus oryzae isolates

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BACKGROUND AND OBJECTIVES: Introduction: Mucormycosis is a rare invasive fungal infection that often affects immunocompromised individuals. In general, Diabetes mellitus, COVID-19 along with comorbidities, immunosuppressive drugs, ICU patients, and undergoing invasive mechanical ventilation are main risk factors for Mucormycosis. Mortality is high with mucormycosis, so finding drugs that cause less resistance is a useful approach. Purpose: The purpose of this study was to determine the antifungal effect of Nanocinnamon compared to amphotericin B against Rhizopus oryzae isolates Conclusion: According to the findings of this article, compared to amphotericin, nanocinnamon inhibited the growth of Rhizopus oryzae. The findings of the present research also indicate the possibility of increasing resistance to amphotericin B in Rhizopus oryzae isolates.

MATERIALS AND METHODS: : To determine the antifungal properties of nanocinnamon, two disc diffusion and microdilution tests were used based on CLSI standard on five isolates of Rhizopus oryzae. It was done with two methods of microdilution according to CLSI M27-A2 standard and disk agar diffusion according to CLSI M44-S2 standard.

RESULTS AND DISCUSSION: : The results of the present research showed that the maximum diameter of the inhibition zone in the dilution of 6% by volume of nanocinnamon was 13 mm. In comparison with amphotericin B, nanocinnamon was chosen to create a bigger halo diameter. The smallest halo diameter was also in 750 ppm dilution and about 9 mm. The results of microdilution showed that it was weak from the growth of nanocinnamon on Rhizopus oryzae isolates, it was 375 ppm and amphotericin B was 1 ppm.

Keywords: mucormycosis, nanocinnamon, Rhizopus oryza, amphotericin B

Studying the effect of magnesium oxide nanoparticles on the expression of toxin-antitoxin genes in the drug-resistant bacterium Stenotrophomonas maltophilia

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BACKGROUND AND OBJECTIVES: Stenotrophomonas maltophilia is an opportunistic,multidrug-resistant (MDR) pathogen increasingly implicated in nosocomial infections.The persistence of this bacterium and its resistance to conventional antibiotics necessitate novel diagnostic and therapeutic approaches.This study aimed to assess the prevalence of type II toxin-antitoxin systems, evaluate the antimicrobial, gene expression-modulating effects of biosynthesized magnesium oxide nanoparticles.

MATERIALS AND METHODS: Thirty clinical isolates of S. maltophilia were subjected to standard biochemical and microbiological tests, followed by molecular confirmation using PCR targeting the 23S rRNA gene. Antibiotic susceptibility was determined via disk diffusion for levofloxacin, trimethoprim-sulfamethoxazole, and minocycline. TA systems were identified through bioinformatic analysis of reference strains and detection S. maltophilia by PCR. MgO-NPs were synthesized and characterized using FESEM, XRD, DLS, UV-Vis spectroscopy, and BET surface analysis. The MIC of MgO-NPs was determined against TA-positive strains.

RESULTS AND DISCUSSION: Phenotypic assays confirmed that all isolates were Gram-negative, oxidase-negative, catalase-positive, and exhibited characteristic biochemical patterns. Genotypic confirmation via 23S rRNA PCR validated all isolates as S. maltophilia. Resistance rates were highest for levofloxacin (33.8%), followed by trimethoprim-sulfamethoxazole (16.4%) and minocycline (8.1%). PCR screening revealed the prevalence of TA systems as follows: pmenTA (30%), pumAB (80%), hipAB (50%), higAB (17%), rlegTA (6.66%), and pp4152 (0%). Synthesized MgO-NPs had an average particle size of \~21 nm with a band gap of 2.64 eV. The MIC against TA-positive isolates was 512 µg/mL.RT-qPCR results demonstrated significant modulation in TA gene expression under sub-MIC nanoparticle exposure. with all changes being statistically significant (p 0.05).

Keywords: Stenotrophomonas maltophilia Multidrug resistance (MDR) Toxin-antitoxin systems Nanoparticle synthesis RT-qPCR

Studying the frequency of Porphyromonas gingivalis bacteria in infected deep gingival pocket samples to determine antibiotic sensitivity in vitro

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BACKGROUND AND OBJECTIVES: Periodontal diseases are inflammatory and destructive diseases of the tooth-gingival complex caused by specific pathogens residing in the periodontal pocket. The specific habitat of this bacterium is pockets deeper than 5 mm, and it does not show a satisfactory long-term response to non-surgical and pharmacological treatments to eliminate the bacteria. In addition to causing tooth loss, Porphyromonas gingivalis is associated with other systemic diseases. The aim of this study was to investigate the frequency of Porphyromonas gingivalis in infected samples of chronic periodontitis patients in children and adults

MATERIALS AND METHODS: In an experimental laboratory study conducted from 1402-1403, 62 patients (23 females and 39 males) aged 7-55 were examined in the periodontology department of a dental clinic in Karaj. Patients with advanced chronic periodontitis were selected, and their periodontal diseases were confirmed by at least two dentists after clinical examinations and reviewing dental radiographs. Sterile thioglycollate transport medium was used for sample transfer, with samples taken from the first molar, first premolar, and central teeth in each jaw

RESULTS AND DISCUSSION: This study indicates an increase in the destructive power of key microorganisms causing chronic periodontitis in adult teeth.he results showed that bacteria isolated from samples were highly sensitive to metronidazole and resistant to amikacin.The identification of isolated bacteria was confirmed through biochemical tests.Anaerobic bacteria play a significant role in the development of periodontal infections, with Porphyromonas gingivalis being a primary factor.

Keywords: Porphyromonas gingivalis,Periodontal pathogens,Microbial diagnosis of periodontitis

Studying the possible connection between some virulence genes and antibiotic susceptibility in Enterobacter cloacae complex

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BACKGROUND AND OBJECTIVES: Enterobacter cloacae complex (ECC) including different species are isolated from different human clinical samples. ECC is armed by many different virulence genes (VGs) and they were also classified among ESKAPE group by WHO recently. The present study was designed to find probable association between VGs and antibiotic susceptibility in different ECC species.

MATERIALS AND METHODS: Forty-five Enterobacter isolates that were harvested from different clinical samples were classified in four different species. Seven VGs were screened by PCR technique and antibiotic susceptibility assessment was performed by disk-diffusion assay.

RESULTS AND DISCUSSION: Four Enterobacter species; Enterobacter cloacae (33.3%), Enterobacter hormaechei (55.6%), Enterobacter kobei (6.7%) and Enterobacter roggenkampii (4.4%) were detected. Minimum antibiotic resistance was against carbapenem agents and amikacin even in MDR isolates. 33.3% and 13.3% of isolates were MDR and XDR respectively. The rpoS (97.8%) and csgD (11.1%) showed maximum and minimum frequency respectively. Blood sample isolated were highly virulent but less resistant in comparison to the other sample isolates. The csgA, csgD and iutA genes were associated with cefepime sensitivity. The fepA showed a predictory role for differentiating of E. hormaechei from other species. More evolved iron acquisition system in E. hormaechei was hypothesized. The fepA gene introduced as a suitable target for designing novel anti-virulence/antibiotic agents against E. hormaechei. Complementary studies on other VGs and ARGs and with bigger study population is recommended.

Keywords: Enterobacter cloacae complex, Virulence gene, Antibiotic resistance, MDR, Antivirulence

Surveillance of Candida auris and Antifungal Resistance in ICU Patients in Iran

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BACKGROUND AND OBJECTIVES: The emergence of Candida auris, a multidrug-resistant fungal pathogen, poses a significant global health threat alongside the COVID-19 pandemic. This study aimed to assess C. auris colonization among immunocompromised patients in an Iranian ICU and evaluate antifungal resistance patterns among Candida spp. isolates.

MATERIALS AND METHODS: Sixty-six clinical swabs were collected from 32 ICU patients upon admission and after 7–14 days. Samples were cultured on Sabouraud dextrose agar (SDA) supplemented with 10% NaCl and incubated at 40°C to enhance C. auris recovery, with confirmation by species-specific PCR. Antifungal susceptibility testing was performed using broth microdilution (CLSI M27-A3) against seven antifungals.

RESULTS AND DISCUSSION: No C. auris was detected. The predominant colonizer was Candida albicans (78.9%, 15/19), followed by C. glabrata (36.8%, 7/19), C. parapsilosis (10.5%, 2/19), and C. tropicalis (5.2%, 1/19). C. glabrata exhibited unique growth on salt SDA with D-mannitol. Resistance rates among isolates were 31.5% to fluconazole, 21.05% to amphotericin B, 15.7% to itraconazole, and 5.2% to voriconazole. While C. auris was absent in this cohort, the presence of other resistant Candida species underscores the need for ongoing surveillance. Routine ICU screening for C. auris remains critical for early outbreak detection and infection control. Given the observed antifungal resistance, continuous monitoring of species distribution and susceptibility profiles is essential to guide therapeutic strategies and prevent the spread of resistant strains in healthcare settings.

Keywords: Candida auris, Colonization, ICU, Culture, C. auris-specific PCR

Surveying the prevalence of common bacterial diseases in commercial poultry

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BACKGROUND AND OBJECTIVES: Bacterial diseases of poultry are one of the main limitations in the development of the poultry industry, which cause significant economic losses to the poultry industry in the world. Therefore, the aim of this study was to investigate the incidence of bacterial infections in commercial poultry.

MATERIALS AND METHODS: Samples were taken from heart blood and liver's visceral surface of 125 carcasses obtained from 30 flocks (including 27 broiler flocks, 1 laying flocks and 2 breeder flocks) located in different parts of Ardabil province. The isolates of bacteria were determined based on microbiological standard methods. The antibiotic susceptibility test was performed using the Kirby-Bauer disk diffusion method .

RESULTS AND DISCUSSION: Among the 125 samples tested, 91 (72.8%) different bacteria were isolated with 98 isolates, and 34 (27.2%) no bacterial was isolated. Of the 98 isolates, 64 (65.31%) were E. coli, 13 (13.26%) Salmonella spp, 8 (8.16%) Staphylococcus aureus, 7 (7.14%) Proteus mirabilis, and 6 (6.13%) Streptococcus spp. The highest antibiotic resistance was against antibiotics commonly used in the Iranian poultry industry such as doxycycline, sulfamethoxazole + trimethoprim, enrofloxacin, neomycin, soltrim and tetracycline. The results of the present study showed that although the highest bacterial contamination of heart and liver lesions was related to E. coli, other bacterial agents should also be considered. The drug resistance pattern of the isolates were also relatively high and diverse, which requires the careful implementation of health and disease control programs as well as the systematic use of antibiotics in poultry farms.

Keywords: E. coli, Salmonella spp, Antibiotic resistance, Liver, Heart

Synergistic Therapeutic Potential of Antimicrobial Peptides, Phages, and Antibiotics Against Multidrug-Resistant Pathogens

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BACKGROUND AND OBJECTIVES: Antimicrobial resistance (AMR), particularly multidrug resistance (MDR), poses a serious global health threat, Innovative therapeutic strategies are urgently needed to address this obstacle. This study explores the promising potential of antimicrobial peptides (AMPs) derived from phages, phage therapy, and combination therapies against MDR pathogens, particularly Acinetobacter baumannii.

MATERIALS AND METHODS: Phage-derived AMPs and phages were assessed for their effectiveness against MDR A. baumannii using in vitro and in vivo approaches. Minimum inhibitory concentration (MIC), biofilm eradication assays, cytotoxicity evaluation, and survival analyses in murine models were performed. Synergistic interactions between phages, AMPs, and antibiotics such as colistin, tigecycline, and rifampicin were studied.

RESULTS AND DISCUSSION: AMPs (e.g., PE04-2) and phages demonstrated significant antimicrobial activity against MDR pathogens, biofilm inhibition, and low cytotoxicity. In combination with antibiotics like colistin, rifampicin, and tigecycline, they exhibited pronounced synergistic effects, enhancing membrane permeability and improving survival rates in infection models. Specifically, the combination of phage vB_AbaSi_W9 with rifampicin achieved 100% survival in murine models infected with carbapenem-resistant A. baumannii, outperforming antibiotic- or phage-only treatments. These findings highlight the robust synergistic potential of AMPs, phages, and antibiotics for overcoming AMR. Their ability to disrupt biofilms, inhibit resistance development, and improve survival rates underscores their significance as innovative tools in combating MDR infections. Further clinical evaluation is necessary to optimize their application and establish them as effective therapeutic strategies in global healthcare.

Keywords: Antimicrobial Peptides (AMP), Antimicrobial resistance (AMR), Multidrug resistance (MDR), Synergistic

Synergizing CRISPR-Cas and AI to Combat Antimicrobial Resistance and Innovate Drug Discovery

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BACKGROUND AND OBJECTIVES: Antimicrobial resistance (AMR) is a serious global problem caused by antibiotic overuse and spreading resistance genes. This reduces antibiotic effectiveness and makes infections harder to treat. Researchers are using CRISPR-Cas to target resistance genes and AI to find new drugs faster. Together, these tools help fight resistant bacteria and develop new treatments.

MATERIALS AND METHODS: Targeted Gene Disruption CRISPR-Cas9 disables resistance genes such as mecA, blaKPC, and mcr-1 in bacteria like E. coli and MRSA, restoring antibiotic sensitivity and offering a precise alternative to broad-spectrum drugs. CRISPR-Enhanced Phage Therapy Phages engineered with CRISPR-Cas3, like those from Locus Biosciences, target resistant E. coli, reducing bacterial load and removing resistance genes. Anti-Biofilm Strategies CRISPR-Cas9 and CRISPRi silence biofilm-related genes (luxS, fimH, bolA) in drug-resistant E. coli and Salmonella, weakening their defenses. AI-Driven Antibiotic Discovery AI accelerates the discovery of antimicrobial peptides and new antibiotics (e.g., halicin, abaucin) by analyzing large datasets and exploring novel chemical structures. Microbial Cell Factories CRISPR activates silent gene clusters in microbes like Streptomyces. With AI-guided DBTL cycles, this enables efficient production of new antimicrobial compounds.

RESULTS AND DISCUSSION: While CRISPR shows great promise, delivering it effectively—via phages, plasmids, or nanoparticles—still needs improvement to ensure precision and avoid off-target effects. Meanwhile, regulatory guidelines are being developed to ensure the safe and ethical use of CRISPR and AI in medicine. By combining CRISPR's precision with AI's discovery power, researchers are creating new tools to fight AMR, develop novel drugs, and build scalable microbial platforms—ushering in a new era in antimicrobial therapy.

Keywords: AMR, CRISPR, AI

Synthesis and Antibacterial Evaluation of a novel Cu(II) Complex with 2-Aminopyrimidine-Based Sulfonate Ligand

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BACKGROUND AND OBJECTIVES: Sulfonamides, a class of organosulfur compounds, exhibit a wide range of pharmacological properties, including antimicrobial, antiviral, and antitumor activities. The present study aimed to synthesize, structurally characterize, and evaluate the biological activity of a sulfonamide derivative of 2-aminopyrimidine and its copper(II) complex.

MATERIALS AND METHODS: The proton transfer ligand, 2-aminopyrimidin-1-imino-4-methylbenzenesulfonate (L), was synthesized via the reaction of 2-aminopyrimidine with p-toluenesulfonyl chloride under reflux conditions for 8 hours. The copper(II) complex (C) was obtained by reacting copper(II) chloride with L at room temperature for 24 hours. The precipitate was characterized by FTIR, ^{1}H NMR, and X-ray crystallography. The Cu(II) complex crystallized in the monoclinic $P2_1/m$ space group as a 1D polymer $[Cu(amp)Cl_2]_n$, formed via coordination with the amino group of L. Antibacterial activity was assessed against four bacterial strains (Bacillus subtilis, Escherichia coli, Pseudomonas aeruginosa, and Staphylococcus aureus) using the agar well diffusion method and the minimum inhibitory concentration (MIC).

RESULTS AND DISCUSSION: The agar well diffusion assay indicated moderate to significant antibacterial activity for L (14.8–21.3 mm) and for C (22–28 mm) against the tested bacterial strains. MIC values ranged from 0.312 to 10 µg/mL for the ligand and from 0.078 to 5 µg/mL for the copper complex. The results demonstrated that the copper(II) complex exhibited significantly enhanced antibacterial activity compared to the free ligand. These findings suggest that such coordination complexes hold promise as potential candidates for structural optimization and further development of novel antibacterial agents.

Keywords: Sulfonamide, metal complex, X-ray crystallography, antibacterial properties

Synthesis of bioactive compounds from strains of genus Enterococcus for human health

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BACKGROUND AND OBJECTIVES: It is known that lactic acid bacteria synthesis several bioactive compounds (bacteriocins and exopolysaccharides). Bacteriocins have antimicrobial and anti-inflammatory effect, exopolysaccharides plays an important role in fermented dairy products and can also be beneficial to human health.

MATERIALS AND METHODS: The antimicrobial activity of bacteriocins and exopolysaccharides (in vitro) investigated against conditionally pathogen bacteria. Purification of bioactive compaunds were carried out by gel filtration method on Sephadex G-50 (exopolysaccharides) and G-25(bacteriocins) and with FPLC method. Determination of the immunostimulating property (lymphocytes) was carried out using the ELISA method.

RESULTS AND DISCUSSION: In recent years we investigated LAB strains (n=21) of Enterococcus genus. It was shown that the selected strains have antimicrobial, antioxidant, resistance to pepsin, trypsin, aggregation, hydrophobicity properties and adhesion to the cell surface. Selected different strains (n=6) are able to synthesize at the same time bacteriocins (0.6-1.5KDa) and exopolysaccharides (17-40KDa) with the different molecular weight. Were carried out the study of immunostimulating properties of some exopolysaccharides and bacteriocins with interleukin IL-6. It was shown that exopolysaccharide Enterococcus faecium KE 5 decrease in biotic activity in the blood of patients with pneumonia, which is close to the blood samples of the control group. Conclusion: Bioactive compounds from strains of genus Enterococcus can be used for the development of a novel biopreparations (probiotic) for human health. Acknowledgements: The work was supported in the frames of the research projects ANSEF microbio 32-71

Keywords: bacteriocin, exopolysaccharide, antimicrobial properties

Systematic review and meta-analysis of the effect of probiotics in reducing the progression of MS.

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BACKGROUND AND OBJECTIVES: Multiple Sclerosis (MS) is an autoimmune disease, it seems that inflammation is important cause of MS. Recently, several studies have shown intestinal microbiota dysbiosis is involved in some immune-mediated diseases, such as MS and Rheumatoid arthritis. Probiotics can alter the gut microbiota and thus affect health status. Administration of probiotics such as lactobacilli and bifidobacteria, can reduce the severity of EAE(Experimental Autoimmune Encephalomyelitis). There is little information regarding the effects of probiotic bacteria on the central nervous system; therefore, the aim of this systematic review and meta-analysis was to evaluate the potential effectiveness of probiotics on MS.

MATERIALS AND METHODS: PubMed, Scopus, Cochrane, and Google Scholar databases were searched using multiple relevant keywords, and screening was carried out based on the inclusion/exclusion criteria from January 2004 to August 16, 2024.

RESULTS AND DISCUSSION: In 17 animal studies, it was concluded probiotics such as Prevotella and Lactobacillus can decrease the T helper 1 (Th1) /Th17 ratio while inducing interferon gamma (IFN-γ) and interleukin (IL)-17 levels. In all cases, probiotics can modulate immune cells and cytokines and consequently decrease EAE signs and symptoms. In all human studies (6 studies), probiotics decreased the severity of disease and changed the gut microbiota population. These findings systematically indicate that probiotic consumption may have potentially beneficial effects in reducing the incidence and severity of MS and in delaying disease progression. Since probiotic therapy may be considered a promising opportunity for the treatment of MS, physicians and nutritionists should consider approved probiotic supplements to manage health concerns in MS.

Keywords: Probiotic, Multiple sclerosis,EAE

Targeting gp120 Glycoprotein in HIV-1: In Silico Discovery of Novel Inhibitors to Block Viral Attachment

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BACKGROUND AND OBJECTIVES: The HIV-1 pandemic remains a critical global health challenge, affecting 40.8 million people in 2024. Despite advances and reduced mortality, prevention methods and therapies are essential. This study targets the glycoprotein gp120, essential for viral entry, by employing in silico molecular docking to identify potent inhibitors.

MATERIALS AND METHODS: The 3D structure of HIV-1 gp120 (PDB ID: 3TIH) was retrieved from RCSB PDB database. Structures of BMS-378806 (PubChemCID:5495818), a potent and well-characterized inhibitor, and its 93 analogs were selected based on Lipinski's Rule of Five from PubChem database in SDF 3D format. After preparing the protein and ligands, molecular docking was conducted using Molegro Virtual Docker v.6. Only the top pose for each ligand was selected in Molegro Virtual Viewer v.7, and the ligand with the lowest binding energy was further evaluated. Finally, the pharmacokinetic properties of the lead ligand were predicted using the SwissADME database.

RESULTS AND DISCUSSION: The most efficacious ligand targeting HIV-1 gp120 is 1-(4-benzoylpiperazin-1-yl)-2-[4-methoxy-7-(4-methylimidazol-1-yl)-1H-pyrrolo[2,3-c]pyridin-3-yl]ethane-1,2-dione (PubChemCID:15958844), with a calculated binding energy of –138.472kcal/mol and a molecular weight of 472.5g/mol. It forms one specific hydrogen bond with residue Tyr330 within gp120 and establishes six steric contacts with Asp325, Tyr330, Pro299, Lys328, Arg298, and Asn301. SwissADME analysis revealed a water solubility of –3.80, lipophilicity of 2.91, and a topological polar surface area of 113.42 Å^2, along with one hydrogen bond donor and six acceptors. Our findings showed promise in accelerating anti-HIV agent development, offering new therapeutic insights to reduce HIV-1 virulence; further in vitro and in vivo validation is necessary.

Keywords: Molecular Docking, gp120, HIV-1, BMS-378806.

Targeting Klebsiella aerogenes Urease Enzyme: A Computational Drug Discovery Approach

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BACKGROUND AND OBJECTIVES: Klebsiella aerogenes is a pathogen responsible for severe hospital-acquired urinary tract infections and surgical site infections, increasingly complicated by its ability to develop antibiotic resistance, making treatment challenging. This study targets the bacterial urease enzyme, critical for the pathogen's physiology and similar in sequence to that of Enterococcus aerogenes, to explore therapeutic inhibition via repurposing acetohydroxamic acid, a known urease inhibitor the of Enterococcus aerogenes.

MATERIALS AND METHODS: Using bioinformatics, the urease protein sequences from both bacteria were aligned using ClustalW to confirm similarity. The 3D structure of Klebsiella aerogenes urease (PDBID:1FWJ) was obtained from RCSB PDB. The structures of acetohydroxamic acid (PubChemCID:1990) and its analogs were selected according to Lipinski's rules of five from PubChem. Molecular docking was conducted using the MVD program and analyzed by the MVV program. Finally, pharmacological properties were evaluated through SWISSADME .

RESULTS AND DISCUSSION: The docking results showed that compound with PubChemCID 173416439 has the best interaction with the lowest binding energy (-46.0107 kcal/mol) with urease protein. This ligand forms two hydrogen bonds with amino acids Tyr473 and Lys443, and five steric interactions with Ala445, Ser436, Lys443, Tyr473, and Pro444. The results from Swiss ADME demonstrated that this ligand has a logP:0.63, logS:0.7, molecular weight of 75.07g/mol, and TPSA:49.34 Å, with 2 H-bond acceptors and 2 H-bond donors. These results indicated that acetyl(sulfanyloxy)azanium (PubChemCID: 173416439) is a good candidate for inhibiting urease from Klebsiella aerogenes, and further studies should be conducted under laboratory conditions to investigate the potential therapeutic agent.

Keywords: Molecular Docking, Urease, Klebsiella aerogenes, Enterococcus aerogenes, Acetohydroxamic Acid.

Tetracycline detection kit using real-time PCR with structural switching aptamer

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BACKGROUND AND OBJECTIVES: We have developed a novel method that utilizes conformational aptamers for the real-time PCR analysis of tetracycline. These aptamers are designed to adopt one secondary structure in the absence of tetracycline and a different structure in its presence. The aptamer structure that binds to the antibiotic tetracycline creates a specific binding site for the addition of a real-time PCR primer. This method allows for the detection of tetracycline concentraIt offers advantages over traditional proximity binding assays (including microbiological assays, physicochemical methods like chromatography and spectroscopy, and immunological assays like ELISA) . tions in the picomolar range, even in the presence of cell lysates.

MATERIALS AND METHODS: Pre-ligation mixtures (45 µL) contained: designed conformation-switching anti-tetracycline aptamer ligation mixtures (50 µL) contained: The final concentration of ATP in the 50 µL ligation mixture was 0.75 mM, Detection of tetracycline by ligation followed by real-time PCR:

RESULTS AND DISCUSSION: Designing a PCR template that amplifies exclusively in one conformational state would be challenging. This is because conformational equilibration can occur even in the absence of the analyte, resulting in some template being available at all times, particularly during thermal cycling and in the presence of DNA polymerase capable of reading through restrictive conformations. Consequently, using a single conformation-switching aptamer as a PCR template would inevitably lead to a high background signal. To address this issue, we decided to incorporate a ligation step to produce competent templates for PCR amplification. This approach allows for the optimization of the ligation reaction separately, minimizing background interference. Moreover, this configuration prevents

Keywords: Tetracycline,aptamer,real-time PCR

Tetracycline resistance in Diarrheagenic Escherichia coli in South of Iran

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BACKGROUND AND OBJECTIVES: Diarrhea is a predominant contributor to childhood mortality in nations, those age of five. Among bacterial pathogens, diarrhea genie Escherichia coli is one of the main endemic and epidemic worldwide. The objective of this research was to assess antibiotic resistance and the occurrence of tetracycline genes in diarrheagenic E. coli strains from children younger than 5 years old.

MATERIALS AND METHODS: In this observational study, from April 2018 to December 2019 a total of 550 stool samples were collected from population. The bacteria isolated and identified. Antimicrobial susceptibility testing was performed using the disk diffusion according to CLSI 2019 guidelines. Molecular of the tetracycline resistance genes (tetA and tetB) performed using Multiplex PCR.

RESULTS AND DISCUSSION: Based on the number of specimens examined, 112 diarrhea genie E. coli strains isolated. Antibiogram analysis that the highest and lowest rates of resistance against tetracycline (57.1%), amikacin, and nitrofurantoin (3.3%). Eighty-five (75.9%) isolates showed a multidrug-resistant (MDR) pattern. Of the 64 tetracycline-resistant isolates, 56 (87.50%) contained tetracycline resistance genes. The frequencies of tetracycline resistance , including tetA and tetB, in the tetracycline-resistant were 58.9% and 44.6%, respectively.

Keywords: Diarrheagenic Escherichia coli, Enteropathogenic E. coli, E. coli Infections, Antimicrobial

The antibacterial effect of a new designed recombinant protein against antibiotic resistant A. baumannii PTCC 1985

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BACKGROUND AND OBJECTIVES: The growing threat of antibiotic resistance in Acinetobacter baumannii, a critical member of the ESKAPE pathogens, presents a significant global health concern. According to a 2024 World Health Organization (WHO) report, A. baumannii has developed resistance to carbapenems, with increasing cases of treatment failure worldwide. This highlights the urgent need for novel therapeutic alternatives. Recombinant peptides have attracted interest due to their anti-biofilm effects, specificity for bacterial membranes, and minimal risk of resistance development. In this study, a new recombinant protein was designed using two peptides with known anti-biofilm activity and ability to target Gram-negative bacterial cell walls, aiming to assess its effect on A. baumannii.

MATERIALS AND METHODS: The recombinant protein was expressed in Escherichia coli and extracted by lysis of the cells using sonicating process followed by centrifugation. For functional evaluation, 108 cells of fresh A. baumannii PTCC1985 strain (log- phase in TSB) were spread in TSA medium. Spot test was performed by applying 5, 10, and 20 µL of the cell lysate and lysis buffer as a control onto the bacterial plate culture. The plates were incubated at 37°C for 24 hours.

RESULTS AND DISCUSSION: The inhibition zones were observed on the plates in all amounts of lysates. The size of the zone was significant in 20 µL, suggesting its potential antibacterial activity against antibiotic resistant A. baumannii strain PTCC 1985. this protein was showed effective inhibition against clinical isolate of antibiotic-resistant A. baumannii, supporting its potential as a new therapeutic candidate for combating antibiotic-resistant infections.

Keywords: Recombinant protein, peptides, A. baumannii, Spot Test

the Antimicrobial Activity of Ethanol and Acetone Extracts of Mustard Seeds Against Staphylococcus aureus

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BACKGROUND AND OBJECTIVES: The increasing resistance of bacteria to various antibiotics and the ineffectiveness of these drugs in treating certain infections have prompted researchers to seek alternative strategies to combat microbial pathogens. In addition to contributing to antimicrobial resistance, antibiotics can disrupt the natural microbiota of the human body. Given the historical use of medicinal plants and their extracts for treating diseases for centuries, there is growing scientific interest in plant-based antimicrobials. This study aimed to evaluate the antimicrobial activity of ethanolic and acetonic extracts of sinapis albaagainst Staphylococcus aureus.

MATERIALS AND METHODS: : sinapis albaagainst were collected, ground, and subjected to extraction using the maceration method. The antimicrobial activity was assessed using 24-well microplates, a 0.5 McFarland microbial suspension, and a stock solution with a concentration of 0.5 mg/mL. Mueller-Hinton agar/broth was used as the culture medium. The bacterial susceptibility was determined using the macrodilution method and serial dilution to evaluate the minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC).

RESULTS AND DISCUSSION: Following extraction and microbiological testing, both ethanolic and acetonic sinapis alba against extracts exhibited significant antimicrobial activity against Staphylococcus aureus. Based on the results of serial dilution assays, the MIC values for ethanolic and acetonic extracts were respectively15.6 and 3.9 mg/mL, while the MBC values were 31.2 and 7.8 mg/mL. The findings of this study indicate that the ethanolic extract of sinapis alba against possesses superior antimicrobial properties and is effective at lower concentrations, whereas the acetonic extract exhibits antimicrobial effects at higher concentrations.

Keywords: Sinapis alba , Staphylococcus aureus , Plant extract

The Effect of Curcumin on Biofilm-Related Genes in Pseudomonas aeruginosa Isolates

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BACKGROUND AND OBJECTIVES: Pseudomonas aeruginosa is known for its ability to form biofilms, which contribute to its persistence and resistance in infections. Curcumin, a natural compound with antimicrobial properties, has been studied for its potential to inhibit biofilm formation. This study aimed to evaluate the impact of curcumin nanoparticles on the expression of biofilm-associated genes in P. aeruginosa clinical isolates under laboratory conditions.

MATERIALS AND METHODS: In an experimental setup, clinical isolates of P. aeruginosa were treated with curcumin nanoparticles. The effect on biofilm formation was assessed using standard biofilm quantification assays. Additionally, changes in the expression levels of key biofilm-related genes, including algD, were measured using molecular techniques such as PCR and gene expression analysis.

RESULTS AND DISCUSSION: The results demonstrated that treatment with curcumin nanoparticles significantly reduced biofilm formation in P. aeruginosa isolates. Correspondingly, the expression of biofilm-related genes, particularly algD, showed a marked decrease after curcumin exposure. These findings suggest that curcumin disrupts the biofilm formation process at the genetic level, potentially weakening the bacteria's defense mechanisms and reducing its pathogenicity. Curcumin nanoparticles exhibit promising anti-biofilm activity against Pseudomonas aeruginosa by downregulating genes essential for biofilm production. This natural compound could serve as a valuable adjunct in managing biofilm-associated infections, especially those caused by antibiotic-resistant strains. Further studies are recommended to explore curcumin's clinical applications and mechanisms in detail.

Keywords: Pseudomonas aeruginosa, curcumin, biofilm, algD gene, antimicrobial resistance

The effect of pseudomonas aeruginosa bacteria on the spread of hospital infection in the intensive care unit

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BACKGROUND AND OBJECTIVES: The purpose of this article is to identify the causes of nosocomial infections caused by the Pseudomonas aeruginosa in the intensive care unit,as well as to provide ways of prevention,control,treatment.it's oneofthemostcommon opportunistic pathogens causing nosocomial infections,especially in the ICU.Hospital-acquired infection is an infection that a patient acquires in a hospital and is one of the main causes of mortality and increased recovery time and hospitalization.According to research conducted by the World Health Organization,the microbes that cause hospital-acquired infections are usually resistant to treatment and antibiotics.It can cause infection in people with immune system abnormalities and is a predominant pathogen in people with cystic fibrosis and burn wounds.

MATERIALS AND METHODS: We studied more than 100 research review articles pubmed,ISI,google scholarand examined the types of hospital infections,the causes of infection,prevention and treatment methods,the types of bacteria that cause hospital infections,and the comparison and ranking of Pseudomonas aeruginosa with other bacteria.

RESULTS AND DISCUSSION: Consequently,given the harmful effects of Pseudomonas aeruginosa in the spread of hospital infections and its impact on the intensive care unit,it's necessary to consider measures to control infections.Among the methods of infection control is increasing the awareness of medical and health center staff,doctors,nurses in hospitals and intensive care units.Ways to prevent hospital infections caused by Pseudomonas aeruginosa in the ICU include wearing latex gloves by medical staff,avoiding contact with droplets from infected patients,not leaving wet and contaminated waste in the hospital environment,and washing hands.Hand washing alone has reduced the transmission of contamination and infection by staff by 30%.

Keywords: Hospital infection,intensive care unit ,Pseudomonas aeruginosa.

The prevalence of carbapenem-resistant Klebsiella pneumoniae isolates and the effect of risk factors on hospital stay duration and mortality rates

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BACKGROUND AND OBJECTIVES: The emergence of carbapenem-resistant Klebsiella pneumoniae (CRKP) infections has been identified as a serious threat. This study aimed to investigate the prevalence of K. pneumoniae infections, antibiotic resistance patterns, and risk factors involved in increased mortality among patients with CRKP infection.

MATERIALS AND METHODS: 200 infectious samples were collected from ICU patients. After identifying Klebsiella pneumoniae isolates and examining their antibiotic resistance patterns, the effect of several possible risk factors on hospitalization duration and mortality was investigated using linear regression and a multivariate logistic regression model.

RESULTS AND DISCUSSION: One hundred and twenty-four samples (62%) contained K. pneumoniae isolates. The resistance to carbapenems (54.8%), cephalosporins (72%), fluoroquinolones (87.7%), aminoglycosides (87%), and colistin (75%) was significantly higher among CRKP patients than those susceptible to carbapenem. The proportions of multidrug-resistant (MDR) and extended-spectrum beta-lactamase (ESBL)-producing isolates were 67.7% and 29%, respectively. Underlying diseases (P= 0.03) and resistance to carbapenem (P=0.001) were two independent risk factors associated with the duration of hospitalization. Additionally, there was a significant association between older age (P=0.04) and resistance to carbapenem (P=0.03) with mortality. Given the high rate of CRKP, its association to length of hospital stays and patient mortality, and the increase in multidrug-resistant isolates, the need for monitoring of microbial resistance patterns and the prescription of new combination antibiotic regimens could be effective in improving the recovery process and reducing the duration of hospital stays of patients.

Keywords: CRKP, Hospitalization duration, Intensive care unit, Mortality, Antibiotics, Risk factors

"The Effect of Extracellular Vesicles Derived from Helicobacter pylori on Glucose Metabolism and Induction of Insulin Resistance in HepG2 Cells"

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BACKGROUND AND OBJECTIVES: Helicobacter pylori is a gram-negative microorganism that primarily resides in the stomach lining and has been linked to several gastric disorders. Recent insights have revealed that its influence may not be confined to the stomach alone, as it can secrete extracellular vesicles (EVs). These nano-sized structures are capable of transporting bacterial molecules—such as proteins, lipids, and nucleic acids—to other parts of the body, including the liver, where they might disrupt normal cellular mechanisms. The purpose of this research is to evaluate how extracellular vesicles produced by H. pylori influence glucose regulation and potentially contribute to insulin resistance in HepG2 hepatic cells.

MATERIALS AND METHODS: Extracellular vesicles (EVs) were isolated from Helicobacter pylori cultures using differential and ultracentrifugation. Their size and morphology were confirmed via dynamic light scattering (DLS) and transmission electron microscopy (TEM). Different amounts of EVs obtained from H. pylori were applied to cultured HepG2 cells for treatment over 24 and 48 hours. The amount of glucose internalized by HepG2 cells was determined via an enzymatic detection method. Insulin-related gene expression was analyzed by qRT-PCR, and cell viability was assessed through the MTT assay.

RESULTS AND DISCUSSION: The experimental findings showed that HepG2 cells exposed to extracellular vesicles derived from Helicobacter pylori exhibited noticeable alterations in glucose handling. Specifically, these cells responded less effectively to insulin, indicating impaired insulin sensitivity. Such changes suggest that bacterial EVs might play a role in disturbing cellular metabolic balance, potentially contributing to the early stages of insulin resistance.

Keywords: Helicobacter pylori, extracellular vesicles, insulin resistance, glucose metabolism, HepG2 cells

The effect of curcumin on the expression of abaI/R quorum-sensing genes and some related phenotypes in Acinetobacter baumannii clinical isolates

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BACKGROUND AND OBJECTIVES: Acinetobacter baumannii is an opportunistic pathogen commonly associated with hospital-acquired infections and high antibiotic resistance. Quorum sensing (QS), particularly regulated by the abaI and abaR genes, plays a critical role in its virulence and survival. Given the rise of multidrug-resistant strains, alternative strategies are needed. Curcumin, a natural compound from Curcuma longa, has shown antimicrobial and QS-inhibitory effects. This study aimed to assess the impact of curcumin on abaI and abaR gene expression and virulence-related traits in clinical isolates of A. baumannii.

MATERIALS AND METHODS: Sixty clinical isolates were identified using biochemical tests and PCR targeting 16S rRNA and blaOXA-51 genes. MIC and MBC values for curcumin were determined using broth microdilution. The expression of abaI and abaR genes was assessed via qRT-PCR after treatment with ½ MIC of curcumin. Phenotypic assays evaluated curcumin's impact on surface motility, protease and phospholipase C activity, oxidative stress sensitivity, and virulence in the Galleria mellonella infection model. Statistical analyses included t-tests and one-way ANOVA.

RESULTS AND DISCUSSION: Curcumin showed MIC values of 0.625–2.5 mg/mL and significantly reduced abaI and abaR expression by 42% and 58%, respectively. It also decreased surface motility (up to 61%), protease activity (up to 25%), phospholipase C production, and resistance to hydrogen peroxide. In vivo, curcumin increased G. mellonella survival from 23% to 36%, indicating reduced virulence. These findings support curcumin as a potential QS-targeting agent for controlling A. baumannii infections.

Keywords: Acinetobacter baumannii, Curcumin, Quorum sensing, Virulence

The effect of essential oil of simple species of Pelargonium leaves on the toxin production of Aspergillus flavus fungus isolated from walnut (Juglans regia)

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BACKGROUND AND OBJECTIVES: Although Aspergillus is an important fungus in food industries, therefore this study investigated the effect of essential oils of one simple species of Pelargonium leave on the toxin production of Aspergillus flavus fungus isolated from walnuts and investigated the expression of the toxin-producing gene (afl R) under the influence of extracted essential oils.

MATERIALS AND METHODS: Molded walnuts were collected from Shiraz in the fall and winter of 2010. Then the fungal isolates were identified using specific culture media and lactophenol cotton blue staining. Afterward, the simple type of Pelargonium plants, were obtained from reputable flower shops and the essential oils of the plants were taken using Clevenger device. The growth rate of the fungal isolate was examined by mixing and microdilution methods, and finally the expression level of the aflR gene was examined by real-time PCR technique.

RESULTS AND DISCUSSION: The present study showed that simple geranium at a concentration of 2000 mg/ml were significantly able to produce less growth halo than the negative control group. The results were confirmed using disk method as well as MIC. On the other hand, the results indicated that essential oil have the ability to reduce the expression of the aflR gene. Conclusion: The findings of this study indicated that the high potential of plant essential oil of geranium plant has ability for managing fungal contamination and it could affect food safety. These results require further studies to identify the exact mechanisms of action of these essential oils and evaluate their effects in different conditions.

Keywords: aflatoxin, Aspergillus flavus, Pelargonium

The effect of methyl vanillyl nonenamide on the growth and pathogenic factors in A. fumigatus

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BACKGROUND AND OBJECTIVES: A. fumigatus can cause various diseases. Despite the development of new antifungal drugs and treatments, the increase of pathogenic fungi that are resistant to drugs requires a new treatment approach. Biofilm is a special feature of fungi that protects fungal cells. Ergostrol is an essential lipid component that controls fungal permeability and phospholipase is associated with the membrane, which can make treatment challenging. Here we studied the effects of methyl vanillyl nonenamide on the growth of A. fumigatus, biosynthesis of ergosterol, biofilm formation and on the expression of phospholipase genes.

MATERIALS AND METHODS: A. fumigatus cells were treated with methyl vanillyl nonenamide at a concentration of 100 µg/ml – 0/024 µg/ml for 72 h at 37˚c. Fungal cells were estimated as an indication of fungal growth. Biofilm formation and ergosterol biosynthesis were evaluated by the effect of methyl vanillyl nonenamid. Investigating the expression of phospholipase B & D genes was done by real time PCR.

RESULTS AND DISCUSSION: Result: Methyl vanillyl nonenamide inhibited the growth of A. fumigatus. The ergosterol content was decreased at the highest concentration. Biofilm formation was also inhibited at the highest concentration. The expression of phospholipase B and D genes was suppressed in different concentration. Discussion: This study was to find an effective substance from the source of microorganisms that can inhibit the growth and inhibit the pathogenic factors of A. fumigatus. This evidence shows that methyl vanillyl nonenamide can have an inhibitory effect on the growth of A. fumigatus as an antifungal agent.

Keywords: A. fumigatus, methyl vanillyl nonenamide, Ergostrol, Biofilm, Phospholipase

The effect of phage therapy on the treatment of antibiotic-resistant bacteria in wastewater: a systematic review

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BACKGROUND AND OBJECTIVES: The increase in antibiotic-resistant microbes, resulting from the overuse of antimicrobials in human and animal health, has reduced the effectiveness of existing antimicrobial drugs and increase resistant strains in recent years. wastewater acts as a rich reservoir for bacterial accumulation for gene exchange. Lytic bacteriophages are considered a potential solution to combat AMR due to their specificity. The aim of this study was assessment the effect of different phages in wastewater treatment.

MATERIALS AND METHODS: We searched in PubMed/Medline, OvidEmbase, Scopus, Google Scholar, SID, MagIran to 12 February, 2024 with "phage therapy," "wastewater," "antibiotic resistance," keyword and their equivalent compounds.

RESULTS AND DISCUSSION: From an initial pool of 1,615 records,18 studies were selected after reviewing titles, abstracts, and complete texts ،including hospital (n = 6), municipal (n = 6), livestock (n = 2), and synthetic (n = 2).The bacteria that were most frequently included Escherichia coli, Salmonella, Pseudomonas aeruginosa, and Klebsiella. The concentration range of phages utilized varied from 104 PFU/mL to 1013 PFU/mL and the highest frequency of phages in inactivating were related to the Siphovirideae family. In all studies, a reduction of at least 90% in the number of bacterial strains was observed after at least 24 hours, except for two cases of Pseudomonas aeruginosa. Studies on a real wastewater sample showed a 100% reduction in bacterial strains after 6 months. The findings show that the appropriate selection of phage cocktails and providing optimal conditions can have a significant impact on reducing resistant bacteria, mortality and economic costs.

Keywords: antibiotic resistance ،bacteriophage ،phage therapy wastewater.

The Effect of Probiotics on Serum Endotoxin, CRP, and TNF-α Levels in a Mice Model of Polycystic Ovary Syndrome (PCOS)

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BACKGROUND AND OBJECTIVES: Background and Objective: Polycystic ovary syndrome (PCOS) is a prevalent endocrine disorder in women, characterized by anovulation and disrupted folliculogenesis. It is associated with weight gain and overgrowth of Gram-negative gut bacteria. Given the anti-inflammatory properties of probiotics, this study aimed to assess their impact on serum endotoxin levels and inflammatory factors, particularly CRP and TNF-α, in a mouse model of PCOS.

MATERIALS AND METHODS: Materials and Methods: Twelve female mice were randomly assigned to three groups: control, PCOS, and treatment. PCOS was induced in the PCOS and treatment groups via subcutaneous injection of dehydroepiandrosterone (DHEA) for 21 days. The treatment group then received a 21 day oral gavage of Lactobacillus acidophilus and Bifidobacterium bifidum. Serum hormone and cytokine levels (CRP, TNF-α) were measured using ELISA, endotoxin levels by LAL assay, gene expression via RT-PCR, and tissue changes assessed histologically

RESULTS AND DISCUSSION: Results: Probiotic supplementation significantly decreased (P0.001) serum levels of estrogen, LH, CRP, and TNF-α, and downregulated their gene expression. Progesterone and FSH levels significantly increased in the treatment group compared to the PCOS group. Histological analysis revealed a notable reduction in adipocyte diameter and improved folliculogenesis (P0.01). Furthermore, serum endotoxin levels were significantly lower in the treatment group (P0.01). Conclusion: Probiotic administration in PCOS mice positively influenced inflammatory status and hormonal balance. These effects may occur through modulation of the gut–ovary axis, indicating the potential therapeutic value of probiotics in managing PCOS-related inflammation and metabolic disruptions.

Keywords: PCOS, probiotics, CRP, TNF-α, endotoxin, inflammation, female mice.

The Effect of Punica granatum Extract on Enhancing the Antibiotic Sensitivity of Escherichia coli (ATCC 25922)

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BACKGROUND AND OBJECTIVES: Due to the increasing prevalence of antibiotic resistance, interest in natural compounds with antibacterial effects has grown as a complementary strategy. Punica granatum (pomegranate) is a widely used medicinal plant in traditional medicine, known for its phenolic compounds, flavonoids, and antibacterial tannins. This study aimed to investigate the effect of pomegranate peel extract on the antibiotic susceptibility of the standard strain Escherichia coli (ATCC 25922).

MATERIALS AND METHODS: A hydroalcoholic extract of pomegranate peel was prepared and tested using the disk diffusion method on Mueller-Hinton agar. Four experimental groups were designed: (1) antibiotic disc alone (ampicillin, tetracycline, ciprofloxacin), (2) extract alone, (3) antibiotic + extract combination, and (4) negative control (blank disc). Antibacterial effects were evaluated by measuring the diameter of the inhibition zones.

RESULTS AND DISCUSSION: The results showed that the pomegranate extract alone exhibited mild inhibitory activity against E. coli, while the combination of extract with antibiotics significantly increased the inhibition zone diameter (p 0.05), indicating a synergistic effect. These findings suggest that combining pomegranate extract with conventional antibiotics may serve as a promising strategy to enhance antibiotic efficacy, reduce drug dosage, and combat antimicrobial resistance.

Keywords: Pomegranate, Escherichia coli ,Antibiotic resistance

The effect of selenium nanoparticles diet on snail physiology

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BACKGROUND AND OBJECTIVES: Among the trace elements, selenium has great demand as a health supplement. Selenium plays an important role in various physiological process: it is necessary for normal immune system functioning, participates in redox process regulation and iodine metabolism, and also performs anti-inflammatory and antiviral functions.Compared to its other forms, selenium nanoparticles have minor toxicity, superior reactivity, and excellent bioavailability.In this study we try biosynthesis of selenium nanoparticles by probiotics then we investigate the influence of this diet on snail physiology.

MATERIALS AND METHODS: MRS culture medium was inoculated with lactobacillus bacteria and enough amount of sodium selenite in order to promote SeNPs synthesis. The reaction was allowed to start until the characteristic red color of the elemental nano-selenium was achieved.Then we added enough amount of selenium nanoparticles to the diet of snail.

RESULTS AND DISCUSSION: The nanoparticle treated group was observed to have increased shell size and weight compared to the control group. Conclusion: In this research we find out that SeNPs can significantly influence on physological parameters in snail.This study highlight the positive potential of SeNPs in biocompatibility and less toxic side effect at the right dosage usage.

Keywords: selenium nanoparticles, biosynthesis, probiotics, minor toxicity ,diet,snail

The effect of Urtica dioica and ZnO Nanoparticles Against the Growth and the Expression of Two Virulence Genes (kpsMT and ompT) of Multiple Drug Resistant (MDR) Escherichia coli strains Isolated from Burn Ulcers

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[1] Educational Assistant

BACKGROUND AND OBJECTIVES: Background: Burn wound infection is a common disease in society, and Multidrug-resistant E. coli bacteria often cause infections and burn ulcers in people. Nanoparticles, due to their ability to enhance healing, fight infection, and reduce inflammation.

MATERIALS AND METHODS: This study was conducted on samples containing E. coli bacteria, which were collected from burned wounds of people for eight months. After antibiogram test, colloidal ZnO and U dioica nanoparticles were prepared in 100 nm sizes in spherical and spindle shapes at 0.032 to 0.256 mg/ml for these NPs. Minimum Inhibitory Concentration and Minimum Bacterial Concentration of nanoparticles were studied. The expression rate of the kpsMT and ompT genes was assessed by Real-Time PCR. Data were analyzed by SPSS Software Version 20.

RESULTS AND DISCUSSION: Twenty-one of 100 (21%) Burn ulcer samples were infected with E. coli. The highest resistance of E. coli to antibiotics belonged to Polymyxin B, Amoxicillin. The results showed that U. dioica and ZnO NPs (100 nm), as well as after 24 h at 37°C, can be used to treat burn ulcer infections caused by E. coli. The best antibacterial property was achieved by Urtica dioica nanoparticles at 0.256 mg/ml. Discussion: The results show a decrease 70 % in ompT and 80% kpsMT gene expression among MDR Escherichia coli isolates, with a significant difference compared to the control sample in the presence of nanoparticles. According to the results, this study confirmed the high prevalence of MDR E. coli strains in burn ulcer infections.

Keywords: Urtica dioica, E. coli spp, Nanoparticles, burn ulcer, Green-synthesized

The effect of UVA and UVB radiation on the production of mycosporin-like amino acids in Chlorella sp.

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BACKGROUND AND OBJECTIVES: UVA and UVB radiation cause both direct and indirect damage to microorganisms, aquatic organisms, and human skin cells, leading to issues like skin cancer. Microalgae protect themselves from harmful UV radiation by producing UV-absorbing compounds known as mycosporine-like amino acids (MAAs). These compounds are colorless, water-soluble, bioactive secondary metabolites, mainly found in the cytoplasm, which absorb and convert harmful UV light into heat. MAA accumulation is influenced by several factors, with UV radiation being the primary inducer of their production.

MATERIALS AND METHODS: Chlorella sp. cultures at the end of the logarithmic growth phase were exposed to UVA and UVB light at doses of 12.43 J/cm². MAA content was analyzed spectrophotometrically across 250–600 nm after methanol extraction and compared to controls.

RESULTS AND DISCUSSION: MAA content of Chlorella sp. increase from 0.116 to 0.39 mg g DW-1 under UV stress, indicating enhanced production in response to UV exposure. Due to microalgae MAA production, they have significant potential for use in the pharmaceutical industries, particularly as natural sunscreens. Further research should focus on optimizing environmental conditions to maximize MAA yields.

Keywords: Microalgae, Mycosporine-like amino acids (MMAs), UV-protective compounds

The first simultaneous assessment of antibiotic resistance, phylogenetics, and the abundance of resistance genes and super antigens in human, animal, and food-borne Staphylococcus aureus isolates in East Azerbaijan Province in the country

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BACKGROUND AND OBJECTIVES: Staphylococcus aureus is a key pathogen causing hospital and community infections, with antibiotic resistance and potent toxins like TSST-1 and PVL. This study examines resistance, phylogeny, and virulence genes in human and animal isolates from East Azerbaijan, informing local control strategies.

MATERIALS AND METHODS: Between 2018 and 2019, sterile nasal swabs from 400 healthy students, 122 mastitic sheep milk samples, and 30 traditional cheese samples were collected and stored at 4°C. Staphylococcus aureus isolates were identified by biochemical tests and molecular PCR targeting 16S rRNA and nuc genes, with confirmation via Sanger sequencing. Antibiotic susceptibility was assessed using Kirby-Bauer disk diffusion per CLSI 2025 guidelines, with E-test confirming methicillin resistance. Multiplex PCR screened for resistance (mecA) and superantigen genes (TSST-1, PVL, ACME-arcA, hla, hlb). Phylogenetic analysis using MEGA 11 and the Kimura 2-parameter model generated maximum likelihood trees compared with GenBank sequences.

RESULTS AND DISCUSSION: From 400 student nasal swabs, 60 Staphylococcus aureus isolates were found, with 18.34% methicillin-resistant (MRSA). MRSA showed higher resistance to erythromycin (45%), ciprofloxacin (30%), cloxacillin (25%), and cefotaxime (20%), but full susceptibility to vancomycin. Among 30 traditional cheese samples, 4 isolates (13.3%) resisted oxacillin and vancomycin but were susceptible to cefoxitin. From 122 mastitic milk samples, 28 isolates (23%) were detected. Enrofloxacin and trimethoprim were effective, with no resistance to chloramphenicol, vancomycin, or ciprofloxacin. High prevalence of mecA, hla, PVL, and TSST-1 highlights significant pathogenicity and need for better antibiotic management.

Keywords: Staphylococcus aureus, antibiotic resistance, super antigen, phylogeny, East Azerbaijan

The impact of chlorination and UV treatment of municipal wastewater on removing Enterococcus antibiotic resistance genes

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BACKGROUND AND OBJECTIVES: Anti-microbial resistance (AMR) is a rising and complex global health concern. Water sources are reservoirs of Antibiotic resistance genes (ARGs) and Antibiotic-resistance bacteria (ARBs). Enterococci are opportunistic Gram-positive bacteria that have become its resistance to macrolides, tetracyclines, and vancomycin. Although Chlorine disinfectants in removing them are effective, but low doses can increase resistance gene transfer. On the other hand, high doses remove more resistance genes, but produce harmful by-products that they can increase horizontal gene transfer. In this study, we aim to investigate the impact of water sources, chlorine disinfection, and UV treatment on the dissemination of ARGs in Enterococcus strains.

MATERIALS AND METHODS: Sampling was conducted across different seasons. At the pre-treatment stage, the presence of ARGs, including tet(M), ermB, and vanA was analyzed in Enterococcus strains using PCR. These genes were also examined in wastewater samples collected during various months following chlorination and UV treatment.

RESULTS AND DISCUSSION: The ermB was the most common ARG in Enterococcus strains, followed by tet(M) and vanA, indicating higher macrolide and tetracycline resistance than vancomycin resistance. Chlorination effectively removed Enterococcus spp. and tet(M), but not vanA or ermB. While UV treatment reduced vanA, but left tet(M) and ermB detectable, highlighting their persistence after treatment. Conventional wastewater treatment methods such as chlorination and UV are not effective in completely eliminating ARGs; therefore, simultaneously using chemical disinfectants with UV is suggested for noticeable reducing the dissemination of ARGs in the environment.

Keywords: Antibiotic resistance genes, Disinfection, Environmental microbiology, PCR, Sewage, Water pollution

The impact of irrational use of antibiotics on drug resistance

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BACKGROUND AND OBJECTIVES: Antibiotics are drugs used to treat bacterial infections and have significantly reduced mortality from these infections. However, the inappropriate and irrational use of these drugs, especially when prescribed for viral infections or when the course of treatment is not completed, has led to the emergence and spread of drug resistance in bacteria.

MATERIALS AND METHODS: This article examines the effects of irrational use of antibiotics on drug resistance, analyzes the factors affecting this and presents solutions to reduce this problem.

RESULTS AND DISCUSSION: If antibiotics are taken arbitrarily and without a doctor's prescription, some microbes and bacteria become resistant to these drugs, and the antibiotic may no longer have any effect on improving the disease and antibiotic resistance may arise. In this case, the bacteria are not destroyed and their growth does not stop, but they continue to grow and spread Drug resistance is one of the serious health challenges in today's world that can have serious consequences for public health and health systems. Given the increase in treatment-resistant bacterial infections, it is essential to take effective measures to combat this problem. By educating and raising awareness among doctors and the general public, rational prescribing of antibiotics, controlling and monitoring their use, and developing new drugs, we can help reduce drug resistance. Also, improving hygiene and infection control in health centers and international cooperation can help better manage this crisis. Ultimately, to combat

Keywords: Keywords:, irrational use, antibiotics, drug resistance

The Impact of Nutraceuticals on Oral Microbiota: A Therapeutic Approach to Prevent and Treatment of Oral and Systemic Diseases

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BACKGROUND AND OBJECTIVES: The oral microbiota plays a critical role in human health by helping to prevent periodontal disease, dental caries, and oral carcinoma. It also affects systemic diseases through its impact on inflammatory responses, modulation of immune system activities, and reduction of pathogen colonization. Nutraceuticals, such as probiotics and plant-based components, have gained increasing attention for their ability to enhance microbial diversity, discourage dysbiosis, and modulate the oral-gut axis microbiota. This review aims to assess the impact of nutraceuticals on oral microbiota, as key players in overall health.

MATERIALS AND METHODS: The search was conducted, using search engines such as google scholar, PubMed, Scopus, articles that met our criteria were included in our study.

RESULTS AND DISCUSSION: Available evidences have shown that nutraceuticals, particularly those containing probiotics and herbal components, can influence the oral microbiota. They do so by reducing pathogenic bacteria and promoting beneficial microbial populations. Probiotics, such as Lactobacillus strains, significantly reduce cariogenic bacteria like Streptococcus mutans. Additionally, polyphenol-rich nutraceuticals, such as oolong tea and cranberry extract, can inhibit the growth and adhesion of oral pathogens. These findings suggest that targeted nutraceutical strategies have the potential to reduce the risk of dental caries, gingivitis, and oral carcinoma during their period of consumption. Due to key role of oral microbiome and the detrimental impact of harmful habits, enhancing oral hygiene has become more challenging. However, the direct influence of dietary choices on the overall health can contribute to an increased demand for nutraceuticals in daily routines to establishment of favorable health states.

Keywords: Oral Microbiota, Nutraceuticals, Oral Health

The influence of oral microbiota on stem cell differentiation

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BACKGROUND AND OBJECTIVES: The oral microbiome is a diverse and complex ecosystem of microorganisms that not only contribute to oral health but also influence digestion, immunity, and overall systemic health. Recent studies have demonstrated that the oral microbiome interacts with stem cells and affects tissue repair and regeneration. In particular, pathogenic species such as Porphyromonas gingivalis have been shown to inhibit the functions of mesenchymal stem cells (MSCs), whereas probiotics enhance MSC activity and mobility.

MATERIALS AND METHODS: This review explores the bidirectional interactions between the oral microbiota and MSC functions, emphasizing mechanisms such as bacterial byproducts and inflammatory signaling pathways. It also examines the impact of factors that influence oral microbiota composition, including hygiene practices, diet, and antibiotic use, in shaping MSC behavior.

RESULTS AND DISCUSSION: Findings suggest that both pathogenic and beneficial microbes interact with MSCs. Pathogens induce inflammation, influencing MSC migration and differentiation, while probiotics promote anti-inflammatory responses and enhance MSC activity. Microbial dysbiosis exacerbates both oral and systemic diseases, underscoring the importance of maintaining microbial balance. This review highlights the therapeutic potential of microbiota-targeted strategies—including probiotics, prebiotics, and postbiotics—to optimize MSC function. Moreover, novel personalized approaches that integrate microbiome profiling and state-of-the-art technologies, such as gene editing, hold great promise for advancing regenerative medicine.

Keywords: Oral microbiota, Stem cell differentiation, Mesenchymal stem cells, Regenerative medicine

The inhibitory impacts of akkermansia muciniphila derived extracellular vesicles on the growth of colorectal cancer cells

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BACKGROUND AND OBJECTIVES: Colorectal cancer the third most common type of cancer.the key role that extracellular vesicles derived from probiotics play on this point is being unveiled. EVs are lipid bilayer enclosed particles that carry a wide range of cargo compounds and act in different signalling pathways. Akkermansia muciniphila is a gram negative anaerobic bacterium, which represents a part of the commensal human microbiota.Due to its mucin reducing and immunomodulatory properties, the use of probiotics containing Akkermansia sp.

MATERIALS AND METHODS: Akkermansia muciniphila was grown in Brain heart infusion and cultured in an anaerobic chamber at 37 °C. Evs were isolated from the media by using Exocib isolation kit. Evs preparations were studied using DLS to determine the approximate size of the vesicles. standard Bradford assay was used to determine the total protein concentration of each EVs sampling. The MTT assay was performed using concentrations of 40, 60, 80, 100,120 µg/mL over 48 hours.

RESULTS AND DISCUSSION: Results: we accurately assess the size distribution of EVs by using a high throughput non perturbative technique DLS .The particle size was 485.2 nm and polydispersity index was 0/047.Evs Average concentrations according to standard curved was 8748 µg/mL at 595 nm. significant IC50 was observed at the 100 µg/mL concentration. Discussion: This study demonstrated that Exocib isolation kit was an easy to operate method for isolating.Extraction using this method enabled us to obtain nanoparticles with appropriate size and concentration. Its potential to reduce tumor growth and improve treatment outcomes warrants further investigation in clinical studies.

Keywords: 1.colorectal cancer(CRC) 2.(Akkermansia muciniphila(A.muciniphila 3.Extracellular vesicles (EVs)

The Inquiry of Possible New Candidates of YopH Inhibitors (T3SS Secreted Effector) of Yersinia Enterocolitica: A Computational Analysis

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BACKGROUND AND OBJECTIVES: Yersinia enterocolitica infection causes a range of health complications, particularly yersiniosis, a widely occurring form of gastroenteritis across the globe. A key virulence factor, YopH, plays a crucial role by disrupting actin cytoskeleton, blocking phagocytosis,and weakening adaptive immune responses. The rise of multidrug-resistant Yersinia strains highlights the need for alternative treatments targeting this virulence factor. This approach shows promise in preventing related illnesses. This study aims to find the best inhibitory ligands for YopH through molecular docking analysis.

MATERIALS AND METHODS: The 3D structure of YopH (PDB ID:4ZN5) was retrieved from the RCSB PDB database. Sulfonamide (PubChemCID 5333) and 855 related analogs were obtained from PubChem in SDF format. After preparing the protein by removing water and existing ligands and performing energy minimization, molecular docking was performed using Molegro Virtual Docker v.6. The best binding interaction with the lowest energy was analyzed through Molegro Molecular Viewer. Pharmacokinetic properties were assessed via the SwissADME server.

RESULTS AND DISCUSSION: The top ligand was identified as 4-amino-N-nona-1,3,5,7-tetraynylsulfonylbenzenesulfonamide (MW 346.36g/mol) with a binding energy of -116.607kcal/mol. It formed five hydrogen bonds with YopH's residues Ala390, Asp393, Arg380, Arg423, Arg255, and seven steric interactions with Lys396, Leu397, Arg380, Arg423, Asn253, Arg255,and Asp374 residues. ADME analysis demonstrated a LogS of -3.15, a LogP of 1.87, TPSA of 123.09, with 2 hydrogen bond donors and 5 acceptors. Among all 856 ligands, the ligand with PubChemCID:118605287 exhibited excellent binding and favorable drug-like properties, making it a promising YopH inhibitor candidate, pending further in vitro and in vivo validation.

Keywords: Molecular Docking, Yersinia Enterocolitica, YopH, ADME.

The Link Between Gut Microbiome and Parkinson's Disease: Mechanisms and Novel Therapeutic Strategies

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BACKGROUND AND OBJECTIVES: Parkinson's disease (PD) is a neurodegenerative disorder affecting over 10 million people globally, characterized by motor symptoms like tremors and stiffness, along with non-motor symptoms such as constipation and depression. Studies show that PD patients have altered gut microbiome profiles compared to healthy individuals, with over 30% of microbial species and genes showing altered abundances. These microbiome imbalances may contribute to PD via the gut-brain axis. This study explores how gut microbiome alterations affect PD and evaluates therapeutic strategies like fecal microbiota transplantation (FMT) and dietary interventions, such as probiotics, to restore balance and alleviate PD symptoms.

MATERIALS AND METHODS: The study involved Parkinson's patients and healthy controls. Stool samples were collected from participants and analyzed using 16S rRNA gene sequencing. Clinical data on PD symptoms were recorded, and dietary information was gathered via a food frequency questionnaire (FFQ). The study focused on analyzing microbial species richness, diversity, and abundances of bacterial taxa between the groups. FMT and dietary interventions, such as probiotics, were explored to assess their effects on gut microbiome balance and PD symptoms.

RESULTS AND DISCUSSION: Results indicated significant differences in the gut microbiome between PD patients and controls, with lower species richness and altered bacterial abundances. Higher levels of Firmicutes and Proteobacteria were linked to inflammation and motor dysfunction. FMT and dietary interventions showed promising results in restoring microbial balance and alleviating PD symptoms. These findings suggest that targeting the gut microbiome may be a novel strategy for PD, though further research is needed to confirm long-term benefits.

Keywords: Gut, Microbiome, Parkinson's Disease

The most prevalent parasitic diseases of children and adults in Ardabil, Iran

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BACKGROUND AND OBJECTIVES: Parasitic diseases are considered one of the most important public health problems in Iran. Ardabil province, due to its specific climatic and geographical conditions, shows a specific epidemiological pattern of these diseases. The aim of this systematic review is to identify the most common parasitic diseases in children and adults in Ardabil and compare them with other provinces of the country.

MATERIALS AND METHODS: A search was conducted in PubMed, Scopus, SID, Magiran, and IranMedex databases using the keywords "Ardabil", "Parasitic diseases", "Epidemiology", "Visceral leishmaniasis", and "Intestinal parasites" for articles published between 1985 and 2025.

RESULTS AND DISCUSSION: Visceral leishmaniasis (Kala-azar) was the most common parasitic disease in the province, with a seroprevalence of 4.1% (1985–2018) in the general population. More than 78% of cases were observed in children under 5 years of age. The highest incidence was reported in Meshginshahr (59%) and Germi (22%). The causative species is Leishmania infantum and the main vector is Phlebotomus kandelakii. This rate is higher than the national average (~3.2% in endemic areas). Overall prevalence of intestinal parasitic infections was 15.7% in Meshginshahr. Most common species were Blastocystis spp. (8.1%), Entamoeba coli (5.7%), Giardia lamblia (1.5%), Dicrocoelium dendriticum (2.2%), Fasciola spp. (0.2%), and Hymenolepis nana (0.2%). This is lower than the national average (19.3%) and significantly lower than the southeastern provinces (up to 34%). Visceral leishmaniasis is the most important parasitic problem in Ardabil province, especially in young children, and requires targeted and continuous preventive measures. Intestinal infections, despite a relative

Keywords: Intestinal parasites, Epidemiology, Ardabil Province, Iran, Parasitic infections

The Mouth as a Mirror of the Body: The Oral Microbiome's Emerging Role in the Pathogenesis of Systemic Diseases

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BACKGROUND AND OBJECTIVES: The oral microbiome, as one of the densest and most diverse microbial ecosystems in the human body, is increasingly recognized not merely as a local determinant of oral health, but as a pivotal player in the oral-systemic health axis. A growing body of evidence highlights the role of oral dysbiosis as a potential initiator or amplifier of systemic pathologies, including cardiovascular diseases, type 2 diabetes, rheumatoid arthritis, neurodegenerative disorders, and certain malignancies.

MATERIALS AND METHODS: This is a review of the latest evidence about the oral microbiome and systemic diseases.

RESULTS AND DISCUSSION: This presentation delves into the taxonomic and functional complexity of the oral microbiome, elucidating key molecular and immunological pathways through which microbial components—such as lipopolysaccharides (LPS), virulence factors, and bacterial-derived microRNAs—translocate beyond the oral cavity, triggering systemic inflammatory cascades. Additionally, the emerging utility of oral microbiota-derived biomarkers in early disease detection, and the therapeutic potential of oral microbiome modulation strategies, will be discussed. By decoding the intricate interplay between oral microbes and systemic health, we move toward a more integrated, predictive, and personalized paradigm in medicine.

Keywords: Oral Medicine. Microbiota, systemic disease, dysbiosis.

The new multidisciplinary approaches to developing effective food bio-preservatives

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BACKGROUND AND OBJECTIVES: The development of biological food preservatives is an exciting area of research that combines various disciplines, including microbiology, food science, biochemistry, and chemical engineering. Microbial fermentation is one of the oldest methods of producing biological materials that is still widely used. In this method, research is being conducted on new bacteriocin producers such as LAB to produce natural biological preservatives (such as nisin) that inhibit spoilage and pathogenic bacteria, and also isolation of yeast and fungal safe strains (GRAS strains) that can produce antibacterial and antifungal compounds or metabolites that increase food shelf life. Searching for new plant extracts compounds, biopolymer coatings, nanostructure molecules, new designed enzymes and biocatalysts, and the use of synthetic biology, such as genetic engineering and metabolic pathway engineering, are some of the new approaches to designing new bio-preservatives. Food matrix engineering such as microencapsulation, smart packaging, and biotechnology, bioinformatics and omics approaches are other innovative

MATERIALS AND METHODS: In this lecture, I will talk about my activities in the Food Biotechnology Laboratory of IROST. I will also discuss about new technologies such as nanotechnology, enzyme technology, natural enzymes, synthetic biology and genetic engineering. I will then discuss about effect of natural antioxidants, biopolymer coatings and edible films that can incorporate antimicrobial agents to create a barrier against microbial contamination.

RESULTS AND DISCUSSION: The integration of these interdisciplinary approaches can lead to innovative solutions for food preservation that are effective, sustainable, and acceptable to consumers.

Keywords: Biopreservative, safety, Innovative researches, multidisciplinary approaches

The Pathway of Antibiotic-Resistant Bacteria from Food to Humans

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BACKGROUND AND OBJECTIVES: many papers have described the appearance and transmission of new bacterial pathogens including through food to humans.regrettably in some developing countries, the misuse of antibiotics has caused a great increase in resistance for these microorganisms. This increasing AMR constitutes a major global public health threat for the years to come. Our research group targeted S.pseudintermedius, a bacterium predominantly associated with cats and dogs and previously considered as having lower significance. For the first time, we reported this isolate from poultry, more precisely broiler chickens

MATERIALS AND METHODS: Sample Collection and Identificatio: 50 nasal swabs were collected from broiler chickens in tabriz city. Identification of S. pseudintermedius was achieved through PCR amplification of the nuc gene Antibiotic Susceptibility Testing: Susceptibility testing was performed using the Kirby Bauer disk diffusion method, with a specific focus on beta-lactam antibiotics, such as penicillin. Genomic Analysis: The presence of the blaZ gene was determined through PCR assays

RESULTS AND DISCUSSION: Staphylococcus pseudintermedius is a bacterium whose resistance to beta-lactam antibiotics is typically measured by the production of beta-lactamase enzymes. This study investigates the presence of S. pseudintermedius. Fifty nasal swabs from broilers were sampled for analysis. The identification of S. pseudintermedius was performed using PCR amplification of the nuc gene. Antibiotic susceptibility testing was conducted via the Kirby Bauer technique, and the presence of the blaZ gene was confirmed. Results showed that 33 samples (66%) contained the nuc gene, with 21 samples harboring the blaZ gene, indicating a 63% resistance to penicillin.

Keywords: Antibiotic-Resistant,Staphylococcus pseudintermedius, Nuc gene, blaZ, food

The relation of psychiatric disorders and gut-brain axis (GBA) microbiota

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BACKGROUND AND OBJECTIVES: The study of its effect on mental problems has become the main topic of this study. As a matter of fact, every change in the gut microbiota composition can influence on mood and anxiety and vice versa.

MATERIALS AND METHODS: In this narrative review, the most recent reproduced information on GBA roles in neuropsychiatric disorders, and clinical significance have been considered. The gut microbial population is formed from birth and transforms from an immature state to the postnatal period into a more intricate and diverse adult ecosystem.

RESULTS AND DISCUSSION: In this review, we had some findings that GBA implicated in some psychiatric problems which can be a dysregulation consequence. In addition, some bacteria have been implicated in causing mental disorders in humans such as depression, obsessive-compulsive disorder, psychiatric disorders, stress disorders, schizophrenia and, autism.The absence of balance in GBAnatural state can cause several negative consequences on host health which leads to neurological problems. Possibly, findings were delineating an interesting new etiological pathway for future exploration

Keywords: Gut-brain axis (GBA); Microbiota; Obsessive-compulsive disorder; Psychiatric disorders; Stress-related disorders;

The Relationship Between Gut Microbiota and Neurotransmitter Systems: The Role of Psychobiotics in Depression and Anxiety

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BACKGROUND AND OBJECTIVES: Emerging evidence highlights the critical role of the gut–brain axis in mental health, particularly the bidirectional communication between gut microbiota and the central nervous system. This review explores how psychobiotics—live microorganisms with neuroactive properties—modulate gut microbiota composition and influence neurotransmitter systems such as serotonin, GABA, and dopamine. By integrating findings from preclinical and clinical studies, we examine underlying mechanisms and therapeutic potential in mood disorders.

MATERIALS AND METHODS: A systematic review was conducted on preclinical and clinical studies published between 2019 and 2024. Focus was placed on randomized controlled trials (RCTs) investigating psychobiotic interventions—mainly Lactobacillus and Bifidobacterium strains—in individuals with depression or anxiety. Mechanistic studies assessing microbial metabolites like short-chain fatty acids (SCFAs), GABA, and serotonin were also reviewed to clarify microbiota–neurotransmitter interactions.

RESULTS AND DISCUSSION: Psychobiotic interventions reduced depressive and anxiety symptoms in approximately 68% of RCTs. These effects were linked to increased BDNF levels, enhanced 5-HT synthesis, and GABA receptor modulation. Greater microbial diversity was observed, including elevated levels of Faecalibacterium and Bifidobacterium. Mechanistically, microbial metabolites influenced the HPA axis, decreased inflammatory markers (IL-6, TNF-α), and enhanced vagal signaling.Psychobiotics demonstrate antidepressant and anxiolytic potential by restoring gut microbial balance and modulating neuroimmune pathways. Although further research is needed to define optimal strains and protocols, current evidence supports their use as adjunctive treatments for mood disorders.

Keywords: Gut-brain axis, Psychobiotics, Gut microbiota, Depression, Anxiety, Neurotransmitters, Microbiome, Probiotics,

The Relationship Between the Microbiome and Microbiota in Parkinson's Disease

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BACKGROUND AND OBJECTIVES: Introduction: Parkinson's disease (PD) is one of the most prevalent neurodegenerative disorders, characterized by the progressive loss of dopaminergic neurons. Emerging evidence suggests that the gut–brain axis and alterations in gut microbiota may significantly contribute to the onset and progression of PD.

MATERIALS AND METHODS: This study was conducted as a narrative review. Scientific articles published between 2013 and 2024 were collected using keywords such as "Parkinson's disease," "gut microbiota," "microbiome," "gut-brain axis," and "alpha-synuclein." Databases including PubMed, Scopus, and Google Scholar were searched. After initial screening, relevant studies exploring the relationship between gut microbiota and PD were selected and qualitatively analyzed.

RESULTS AND DISCUSSION: Significant changes in gut microbiota composition have been reported in PD patients, including a decrease in anti-inflammatory bacteria and an increase in pro-inflammatory species. These alterations may contribute to increased intestinal permeability, systemic inflammation, and the pathological transmission of alpha-synuclein from the gut to the brain. Some studies also support the therapeutic potential of interventions such as probiotics, specific diets, and fecal microbiota transplantation (FMT) in alleviating PD symptoms.

Keywords: Parkinson's disease, microbiota, microbiome, gut–brain axis, neuroinflammation, alpha- synuclein

The Relationship Between Urinary Tract Infection Symptoms and the Rate of Positive Suprapubic Aspiration in Children Under Five Suspected of UTI in Imam Sajad Hospital

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BACKGROUND AND OBJECTIVES: Urinary tract infections (UTIs) are among the most common infectious diseases in children, presenting with or without symptoms. Bacteria are the primary cause of UTIs, with higher prevalence in uncircumcised boys during the first year of life. This study aimed to investigate the association between UTI symptoms and positive suprapubic aspiration results in children under five years suspected of UTI, referred to Imam Sajad Hospital, Yasuj.

MATERIALS AND METHODS: In this descriptive cross-sectional study, 105 children with UTI symptoms were evaluated using suprapubic aspiration. A positive culture was defined as the growth of even a single colony. Statistical analysis was conducted with a significance threshold of p0.05.

RESULTS AND DISCUSSION: Of 105 urine culture samples, 68 (64.8%) were positive, and 37 (35.2%) were negative. A statistically significant association was found between certain symptoms (nausea, vomiting, abdominal pain) and risk factors (labial adhesion in girls, neonatal jaundice, prior UTI) with positive culture results (p0.05). Escherichia coli was the most common UTI pathogen in both sexes, while other microorganisms were identified only in girls. No significant difference was observed in the mean age of children with positive versus negative cultures (p0.05). This study indicates a higher UTI prevalence at older ages. A significant association was observed between risk factors, including labial adhesion, neonatal jaundice (10.5%), and prior UTI (10.5%), and UTI occurrence (p0.05). Given increasing antibiotic resistance, periodic cultures and antibiotic susceptibility testing are essential for timely diagnosis and effective UTI treatment.

Keywords: Urinary Tract Infections, Pediatrics, Suprapubic Aspiration, Antibiogram

The remarkable antibacterial effect of a recombinant endolysin against Acinetobacter variabilis PTCC 1986

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BACKGROUND AND OBJECTIVES: Acinetobacter variabilis, is a species of the Acinetobacter genus identified as an antibiotic-resistant pathogen that increasingly isolated from the under-hospitalization patients. This issue similar to the global problem of the A. baumannii, the other member of Acinetobacter genus, should be considered for alternative therapeutics. In this study a new recombinant endolysin was used against a clinical isolate of A. variabilis PTCC1986 and its antibacterial effect was examined.

MATERIALS AND METHODS: 108 fresh bacterial cells were treated by 200 µg/ml of the purified recombinant protein with and without 0.5 mM EDTA for 2 h at 37°C. 1/100 dilution of treated cells were spread on the TSA plates and incubated at 37°C for 24 h. The colonies became apparent after incubation were counted for computing of the antibacterial effect of the endolysin

RESULTS AND DISCUSSION: Results: a significant decrease in number of the colonies was observed on the plates treated with the recombinant endolysin in both the presence and absence of EDTA. conclusion considering the obtained results, the recombinant endolysin can be addressed as effective antibacterial candidate against gram negative pathogens as A. variabilis

Keywords: Recombinant endolysin, A. variabilis, antibiotic resistant

the role of AI in the diagnostic and treatment of the most common cancers with epigenetic roots :surveying its effectiveness in Iranian patients

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BACKGROUND AND OBJECTIVES: Epigenetic studies have shown that reversible changes in gene expression occur without any changes in DNA sequence, this phenomenon plays a key role in the formation of some diseases such as cancers. This study has strong evidence indicating the importance of pattern recognition of epigenetic factors involved in triggering the cells to become cancerous in vivo and the possibility of using AI to foresee the fate of these cells. As previously established, epigenetic changes such as abnormal DNA methylation, improper regulation of gene expression, etc., play a key role in the occurrence and reoccurrence of some well-known malignancies in patients.Although the process of diagnosis and the initiation of treatment in Iran is still according to traditional methods but AI and its immense medical achievements will be extremely welcomed by experts and the government. Reducing additional costs of the health organizations, lower health care staff, and patient satisfaction due .

MATERIALS AND METHODS: Articles from 2000 to 2025 on epigenetic effects in cancer formation and progression were thoroughly reviewed. The data is categorized based on artificial intelligence

RESULTS AND DISCUSSION: The results indicate that with the help of artificial intelligence (AI), in identifying abnormal patterns of cell proliferation, drastic epigenetic changes in the cells, biomarker-related diagnosis approaches, and proposing new strategies for targeted therapy in cancer studies, there is a bright future for cancer prevention in the first place and effective treatments due to early diagnosis after all

Keywords: artificial intelligence, cancer, epigenetics, treatment, diagnosis

The Role of Gut Microbiota in the Spread of Antibiotic Resistance

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BACKGROUND AND OBJECTIVES: The human gut microbiota is one of the largest reservoirs of antibiotic resistance genes (ARGs) and plays a critical role in the horizontal transfer of these genes between commensal and pathogenic bacteria. The accumulation of ARGs in the gut environment represents a major public health concern, as it may lead to the emergence of multidrug-resistant pathogens.

MATERIALS AND METHODS: In this review study, articles published between 2021 and 2024 were examined using keywords such as "gut microbiota," "antibiotic resistance," and "horizontal gene transfer" in databases like PubMed and Scopus. Selected studies included data on resistance profiles within microbiota, mechanisms of ARG transfer, and microbiome-based intervention strategies.

RESULTS AND DISCUSSION: The findings indicate that commensal gut bacteria such as Escherichia coli and Enterococcus spp. play a significant role in carrying and transmitting resistance elements like extended-spectrum beta-lactamases (ESBLs) and carbapenemases. Studies also showed that strategies such as phage therapy, fecal microbiota transplantation, and dietary modulation could help reduce ARGs in the gut. The gut microbiota plays a key role in the dissemination of antibiotic resistance genes through horizontal transfer. Continuous monitoring of gut resistome and employing targeted therapeutic strategies may help prevent the spread of multidrug-resistant pathogens.

Keywords: Gut microbiota; Antibiotic resistance; Horizontal gene transfer; Resistome

The Role of Helicobacter pylori in Gastric MALT Lymphoma

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BACKGROUND AND OBJECTIVES: Helicobacter pylori is a gram-negative, spiral-shaped bacterium that colonizes the human gastric mucosa and is recognized as one of the most prevalent chronic infections worldwide. While its association with peptic ulcer disease and gastric adenocarcinoma is well established, growing evidence has highlighted its critical role in the pathogenesis of gastric mucosa-associated lymphoid tissue (MALT) lymphoma—a rare type of extranodal marginal zone B-cell lymphoma. Chronic infection with H. pylori induces a persistent inflammatory response in the gastric mucosa, promoting lymphoid tissue formation and B-cell proliferation. In early stages, gastric MALT lymphoma is often dependent on the continued presence of H. pylori, making eradication therapy a potentially curative approach. Understanding the biological mechanisms linking H. pylori to MALT lymphomagenesis is essential for accurate diagnosis, risk assessment, and therapeutic decision-making.

MATERIALS AND METHODS: This review was conducted by systematically searching the scientific literature to identify relevant studies examining the role of Helicobacter pylori in gastric mucosa-associated lymphoid tissue (MALT) lymphoma. Electronic databases including PubMed, Scopus, and Web of Science were searched for articles published from [e.g., 2013 to 2025] Inclusion criteria consisted of: Peer-reviewed original research, clinical trials, meta-analyses, and review articles Studies written in English Publications specifically focused on gastric MALT lymphoma in relation to H. pylori infection

RESULTS AND DISCUSSION: Helicobacter pylori infection is strongly linked to gastric MALT lymphoma. Chronic inflammation drives B-cell proliferation and lymphoid tissue formation. Eradication therapy often induces remission in early-stage cases, though genetic alterations may reduce responsiveness, requiring alternative oncologic treatments.

Keywords: Helicobacter pylori, MALT lymphoma,Gastric lymphoma ,B-cell lymphoma, Chronic gastritis ,Lymphomagenesis,

The Role of Helicobacter pylori Infection in Gene Expression Alterations and Cancer Development: Focus on p53 and p16 Expression

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BACKGROUND AND OBJECTIVES: Helicobacter pylori is a gram negative bacterium strongly associated with gastric cancer. Its chronic colonization of the gastric epithelium leads to inflammation and genetic disruptions. This study aims to investigate how H. pylori infection alters the expression of key oncogenes and tumor suppressor genes, particularly c-Myc, p53, and p16, to better understand its role in gastric carcinogenesis.

MATERIALS AND METHODS: AGS and MKN-45 gastric cancer cell lines were infected with a CagA-positive H. pylori strain. Cells were harvested at 24, 48, and 72 hours. Gene expression was analyzed by qPCR, and protein levels were confirmed via Western blot. Inflammatory cytokines and tissue morphology were also assessed. Results and Discussion H. pylori infection led to a time-dependent increase in c-Myc expression, with the highest levels observed at 72 hours. In contrast, p53 and p16 were significantly downregulated at 48 and 72 hours. IL-6 and TNF-α levels were also elevated, indicating an inflammatory environment. These results suggest that H. pylori contributes to gastric cancer development by promoting oncogene activation, suppressing tumor suppressors, and inducing chronic inflammation.

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Keywords: Helicobacter pylori, gastric cancer, c-Myc, p53, p16, gene expression,

The Role of Probiotics in Cancer Prevention

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BACKGROUND AND OBJECTIVES: The human gastrointestinal tract is a reservoir of a population of microorganisms (the gut microbiota) which apply a significant influence on the host during homeostasis and disease. potential application of probiotics in prevention of cancer was reviewed here.

MATERIALS AND METHODS: In recent years, there has been growing interest in the possible application of probiotics as a part of combination therapy with conventional treatment of cancer. As a result of imbalance of the digestive system may be proinflammatory immune responses and initiate disease processes, including cancer.

RESULTS AND DISCUSSION: There is a lot of evidence that the use of probiotics can play an important role in cancer prevention and support anti-cancer therapies.The anticarcinogenic activity of probiotics is based on: (1) modification of the intestinal microbiota composition, (2) metabolic activity of the intestinal microbiota, (3) production of compounds with anticarcinogenic activity, such as short-chain fatty acids and, (4) inhibition of cell proliferation and induction apoptosis in cancer cells, (5) influence on other mutagenic and carcinogenic factors, (6) immunomodulation and (7) improvement of the intestinal barrier. The results of many clinical studies indicate the effectiveness of probiotics in preventing, treating and reducing the progression of several types of cancer including colorectal, liver, breast, colon, and cervical in cancer patients.

Keywords: probiotics, cancer prevention, gut microbiota

The Role of Probiotics in Preventing the Harmful Effects of Environmental Pollutants

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BACKGROUND AND OBJECTIVES: Environmental pollutants such as heavy metals and microplastics are harmful to health and cause multiple risks through oxidative stress, disruption of intestinal barrier function, and alteration of host microbiota. Our recent studies investigate the ability of indigenous Lactobacillus strains to mitigate the detrimental effects of these pollutants.

MATERIALS AND METHODS: In these studies, several human-derived Lactobacillus strains were evaluated for their capability to biologically remove heavy metals (nickel, arsenic, mercury, and cadmium) and nanoplastics in in vitro and animal models. The effects of these strains on inflammatory and oxidative pathways were also analyzed.

RESULTS AND DISCUSSION: Our results showed that selected probiotic strains were able to reduce the concentration of heavy metals and nanoplastics in the intestinal model, enhance epithelial barrier integrity, and decrease markers of inflammatory and oxidative stress. Protective effects were especially noted in the gut-kidney and gut-brain axes. Indigenous Lactobacillus strains with detoxifying properties and modulatory effects on inflammatory pathways can be considered as biological supplements to reduce the harmful effects of environmental pollutants and provide a foundation for developing novel functional therapies.

Keywords: Probiotic, Lactobacillus, heavy metals, nanoplastics, oxidative stress

The Role of Resistant Biofilms in ICU Treatment Failure and Development of Smart Nanocarriers for Targeted Disruption

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BACKGROUND AND OBJECTIVES: Background: Hospital-acquired infections caused by biofilm-forming bacteria present a major challenge in intensive care units (ICUs), leading to increased antibiotic resistance and treatment failures. Biofilms create a protective environment that shields bacteria from antimicrobial agents, resulting in persistent and recurrent infections. Objective: This study aims to investigate the impact of resistant biofilms on therapeutic failure in ICU patients and to develop innovative nanocarrier-based strategies for targeted disruption of biofilms, enhancing antibiotic efficacy.

MATERIALS AND METHODS: Clinical samples from ICU patients with persistent infections were collected to identify predominant biofilm-forming bacteria. Smart nanocarriers sensitive to biofilm-specific microenvironmental cues—such as pH and enzymatic activity—were synthesized and characterized. These nanocarriers were loaded with anti-biofilm agents and tested in vitro against established biofilms. Additionally, CRISPR-Cas technology was employed to target key biofilm-associated genes, aiming to genetically disrupt biofilm formation and maintenance. The combined efficacy of nanocarrier-mediated drug delivery and gene editing was assessed through quantitative biofilm reduction assays and bacterial viability tests.

RESULTS AND DISCUSSION: Preliminary results demonstrate that smart nanocarriers significantly enhance the penetration and eradication of biofilms, while CRISPR-Cas mediated gene targeting reduces biofilm-forming capacity of pathogens. This dual approach shows promise in overcoming antibiotic resistance mechanisms in ICU pathogens. The findings pave the way for novel, targeted therapeutic modalities that could improve clinical outcomes and reduce the burden of chronic biofilm-associated infections in critical care settings.

Keywords: Antimicrobial Resistance (AMR), Biofilms, ICU Infections, Smart Nanocarriers, CRISPR-Cas

The Role of the Female Reproductive Tract Microbiome in Infertility and Assisted Reproductive Technology (IVF) Outcomes

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[1] Shahid Beheshti Medical School, Department of Microbiology

BACKGROUND AND OBJECTIVES: Recent advances in microbiome research have revealed its critical role in various aspects of human health. Among the emerging areas of interest is the influence of the female reproductive tract microbiome—particularly that of the vagina and endometrium—on natural fertility and the success of assisted reproductive technologies (ART), including in vitro fertilization (IVF). Accumulating evidence suggests that infertility, especially in cases labeled as idiopathic, may be associated with alterations in the composition and diversity of the genital tract microbiome. Concurrently, the growing prevalence of recurrent IVF failure, despite the use of advanced laboratory techniques, has led researchers to explore previously overlooked biological factors such as the microbiome. There is increasing recognition that specific microbial patterns may influence the likelihood of ART success, though the exact nature of this relationship remains incompletely understood. Nevertheless, its potential importance in shaping diagnostic and therapeutic strategies is becoming increasingly evident. This presentation will review

MATERIALS AND METHODS: .

RESULTS AND DISCUSSION: .

Keywords: .

The Role of the Human Microbiome in the Development of Personalized Medicine: From Theory to Clinical Applications

SEYEDHOSSEIN KAMALI [1] © ℗

[1] **Student**

BACKGROUND AND OBJECTIVES: The human microbiome, consisting of trillions of microorganisms, plays a pivotal role in modulating host metabolic and immune responses. In recent years, personalized medicine has emerged as a promising approach that integrates individual microbiome profiles for tailored therapeutic interventions. This study aims to systematically explore the clinical relevance of the microbiome in personalized treatments and to identify microbial signatures predictive of therapeutic responses.

MATERIALS AND METHODS: A randomized, double-blind, placebo-controlled longitudinal study was designed, involving 500 participants from 3 continents. Microbiome profiling was conducted using shotgun metagenomics and metabolomics. Participants were divided into four groups: personalized probiotics, autologous fecal microbiota transplant, placebo, and healthy controls. Clinical markers such as HbA1c, weight, and CRP were evaluated over 12 weeks. Data analysis included PCA, XGBoost models, and microbial-host network mapping.

RESULTS AND DISCUSSION: Significant improvements were observed in microbial diversity and metabolic markers in the intervention groups. HbA1c reduction correlated with increased abundance of A. muciniphila and F. prausnitzii. The "microbial life triangle" (A. muciniphila, F. prausnitzii, B. longum) emerged as a key synergistic cluster. These findings suggest that microbiome-targeted interventions can enhance therapeutic outcomes, supporting a paradigm shift toward microbiome-guided precision medicine.

Keywords: Human Microbiome; Personalized Medicine; Probiotics; Fecal Microbiota Transplantation; Metagenomics; A.

The Role of Zoonotic Bacterial Infections in Cytokine Release Syndrome: Pathogenesis and Clinical Relevance

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BACKGROUND AND OBJECTIVES: Introduction: Cytokine release syndrome is a life-threatening hyperinflammatory condition resulting from uncontrolled immune activation. While it may arise from hemophagocytic lymphohistiocytosis, autoimmune diseases, malignancies, or drug reactions, zoonotic bacterial infections are increasingly recognized as major infectious triggers. Identifying their role in the pathogenesis of cytokine storms is critical for early clinical detection, effective management, and controlling zoonotic transmission from animals to humans.

MATERIALS AND METHODS: Methods: This review assessed original research published in the last ten years addressing the contribution of zoonotic bacteria to cytokine release syndrome. Systematic searches were conducted in PubMed, Scopus, and Web of Science using relevant keywords. Studies were included if they offered mechanistic insights or clinical data on bacterial-driven cytokine storms. Information on study design, pathogen type, immune pathways, and clinical outcomes was extracted and analyzed.

RESULTS AND DISCUSSION: Results: A total of 47 studies met the inclusion criteria. Pathogens such as Salmonella enterica, Brucella species, Francisella tularensis, Pasteurella multocida, Campylobacter jejuni, and Leptospira interrogans were found to induce cytokine storms through innate immune receptors including Toll-like and NOD-like receptors. These interactions led to inflammasome activation, macrophage dysfunction, and overproduction of cytokines such as interleukin-6, interleukin-1 beta, and tumor necrosis factor alpha. In genetically susceptible hosts, this contributed to systemic inflammation, immunopathology, and sepsis-like or hemophagocytic syndromes. Discussion: Zoonotic bacteria are key yet underappreciated drivers of cytokine storm syndromes. A deeper understanding of their immune evasion and activation pathways can inform improved diagnostic, therapeutic, and preventive strategies in infectious disease management.

Keywords: Keywords: Zoonotic bacteria, cytokine storm, inflammation, pathogenesis

The statistics on fungal invasive infections and the administration of systemic antifungals in Iran in comparison to global guidelines

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BACKGROUND AND OBJECTIVES: Invasive fungal infections carry significant mortality rates, and antibiotic resistance increases this risk. To enhance the efficacy of antifungal treatments, it is crucial to understand current prescribing patterns, align them with global clinical guidelines, and consider local factors and endemic pathogens. This study examines the prescription of systemic antifungal drugs in hospitals to increase awareness about their use.

MATERIALS AND METHODS: The total number of systemic antifungal drugs prescribed over one year was collected using the pharmacy systems of Tehran's main private and educational hospitals in Microsoft Excel. Prescribed daily doses (PDDs) were calculated based on the patient's medical records and then compared with Defined Daily Dose (DDD) values derived from WHO sources. In addition, each prescription was analyzed to assess its appropriateness according to IDSA (Infectious Diseases Society of America) and CDC (Centers for Disease Control and Prevention) protocols in various aspects not covered by the DDD/PDD method, such as indication and dosing. Then, saliva samples were collected from immunocompromised patients, cultured on Sabouraud Dextrose Agar and CHROMagar™ Candida, and biochemical and molecular tests were used to identify the species.

RESULTS AND DISCUSSION: Detailed evaluations revealed that 41.41% of prescriptions failed to comply with guidelines regarding dosing, duration, route of administration, or drug selection. Furthermore, 97% of prescriptions were for fluconazole, which may lead to an increase in non-albicans Candida species known to be more difficult to treat and associated with higher mortality rates. Systemic antifungal drug prescriptions frequently conflict with global guidelines and epidemiological studies.

Keywords: Invasive Candidiasis, Clinical guidelines, Candida spp., Fluconazole, Caspofungin, Ketoconazole

The survey of Virulence Gene Profiles in Staphylococcus areuos Isolates in Covid-19 Patients Admitted in ICU at Sina Educational Hospital of Hamadan

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BACKGROUND AND OBJECTIVES: COVID-19 was first reported in December 2019 in worldwide. In severe cases, patients expose of the hospital-acquired infections or secondary infections, and subsequently causes high mortality. S. aureus causes various infectious diseases including pneumonia and bacteremia. The genotype virulence of S. aureus has been reported to influence the complications, severity, and mortality of infection

MATERIALS 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 AND DISCUSSION: 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. Conclusions: 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: Key words: Staphylococcus aureus, Virulence gene, COVID-19

The synergistic antimicrobial effect of tetrasodium EDTA and chlorhexidine against Enterobacterales isolates from hospital carriers

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BACKGROUND AND OBJECTIVES: Hospital-acquired infections are a major concern in healthcare settings, often involving Gram-negative bacilli that affect both patients and healthcare personnel. This study aimed to assess the antimicrobial effects of chlorhexidine and EDTA, alone and in combination, on Gram-negative bacilli isolated from carriers, along with their antibiotic resistance profiles and biofilm-forming abilities.

MATERIALS AND METHODS: This cross-sectional study collected 390 samples from hospital personnel, patients and environmental surfaces to investigate Gram-negative bacilli. Antibiotic susceptibility, biofilm formation, and the minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) of chlorhexidine, with and without EDTA, were also determined. PCR was used to detect biocide resistance genes (qacE, qacEΔ1, CepA).

RESULTS AND DISCUSSION: A total of 120 Gram-negative bacilli were isolated and subsequently confirmed through biochemical tests. Klebsiella pneumoniae was the predominant bacterial species, accounting for 70% (n=84). Based on the present findings, 29 (24.1%) isolates were multidrug-resistant (MDR). ESBL and AmpC production were detected in 12.5% and 21% of isolates, respectively. Strong biofilm formation was observed in 58.3% of the samples. Chlorhexidine alone inhibited bacterial growth at a MIC‰ of 0.009%, with a bactericidal effect at 0.019%. When combined with EDTA, a synergistic effect was observed, reducing the MIC to 0.002% and the MBC to 0.004%, indicating enhanced antimicrobial activity. These findings highlight the high prevalence of resistant and biofilm-producing Gram-negative bacilli among carriers. The enhanced activity of chlorhexidine in combination with EDTA suggests its potential as an effective strategy for decontamination and infection control in healthcare environments.

Keywords: Healthcare-associated infections, Enterobacterales isolates , Chlorhexidine, EDTA, hospital carriers

The synergistic interactions of antimicrobial agent against KPC producing Klebsiella pneumoniae

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BACKGROUND AND OBJECTIVES: Carbapenems as another beta-lactam structure have suggested for the first-line therapy of Enterobacteriaceae infections. Unfortunately, carbapenemases have increased among gram-negative bacteria notably in Klebsiella pneumoniae. The most frequent class of carbapenemases is KPC. KPC-producing Klebsiella pneumoniae has displayed the broad spectrum of resistance and hydrolyzed most of the antibiotics.

MATERIALS AND METHODS: The study designed to evaluated MICs of antibiotic against five clinical isolates of KPC-producing Klebsiella pneumoniae by microbroth dilution. Furthermore, determined and compared the synergistic activities of two carbapenems, colistin and ceftazidime antibiotics and clavulanic acid inhibitor by checkerboard method. Synergistic studies divided into two interactions, two antibiotics and one carbapenem with the clavulanic acid inhibitor.

RESULTS AND DISCUSSION: Among isolates, imipenem was more susceptible than other antibiotics. The combination of meropenem-colistin and meropenem-clavulanic acid demonstrated the synergistic effect on KPC-producing Klebsiella pneumoniae. Our study recommended in vitro synergistic interactions of meropenem between clavulanic acid can be more effecient than meropenem with colistin antibiotic.

Keywords: KPC; checkerboard method; antimicrobial susceptibility; antimicrobial combination; synergistic activity

The Significance of Pepper Mild Mottle Virus (PMMoV) Monitoring in Aquatic Environments

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BACKGROUND AND OBJECTIVES: Pepper mild mottle virus (PMMoV) is an RNA virus within the genus Tobamovirus, recognized as a potential water quality indicator. This virus, which affects pepper crops, is predominantly discharged in human stool after consuming contaminated processed foods. Its presence in environmental waters raises public health concerns due to fecal contamination. Various water sources, including recreational pool water, should be monitored for microbial pathogens to reduce the rate of enteric infections in society. This study aims to investigate the presence of PMMoV in recreational water samples from different Tehran city pools.

MATERIALS AND METHODS: In this study, we collected water samples from 10 different swimming pools located in various geographical locations within Tehran. The samples were concentrated, the RNA genome was extracted from each sample, and cDNA was synthesized. Finally, PMMoV genome was detected and the viral load was quantified among collected samples using real-time RT-PCR method.

RESULTS AND DISCUSSION: The results indicated that all of the samples were positive and exhibited varying levels of PMMoV contamination (100% samples, mean concentration=7.8249 log10, genomic copies per litter). Based on the data from this study, PMMoV detection in all samples showed extensive contamination in these water sources. As PMMoV is an indicator of fecal contamination in water, it is essential to carry out continuous monitoring of water safety in pools, along with the implementation of effective treatment methods to reduce contamination and perform effective inactivation.

Keywords: Quantitative Microbial Risk Assessment, Pepper Mild Mottle virus, Tobamovirus, Pool

Therapeutic and Prophylactic Effects of a Lytic Bacteriophage Against Multidrug-Resistant Shigella flexneri in a Mouse Model

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BACKGROUND AND OBJECTIVES: Shigella flexneri is a significant cause of bacillary dysentery, particularly affecting children in developing countries. The increasing prevalence of multidrug-resistant strains has limited the effectiveness of antibiotic treatments, creating an urgent need for alternative strategies. Bacteriophage therapy offers a targeted, safe, and efficient solution without disrupting the host microbiota. This study aimed to isolate, characterize, and evaluate the therapeutic and prophylactic potential of a specific lytic phage against S. flexneri in vitro and in vivo using a murine model.

MATERIALS AND METHODS: A lytic phage was isolated from hospital wastewater and tested against S. flexneri ATCC 12022. Transmission electron microscopy (TEM) was used for morphological analysis. Stability tests were conducted under varying pH, temperatures, and bile salt concentrations. In vivo efficacy was evaluated using five groups of C57 mice, with phage administration occurring before and/or after bacterial challenge. Stool samples were collected for colony counts, and one-step growth curves and adsorption assays were performed.

RESULTS AND DISCUSSION: The isolated phage belonged to the Myoviridae family and demonstrated heat and acid stability. It showed significant bacteriolytic activity in vitro and a burst size of 377 pfu/cell. In vivo, phage administration significantly reduced S. flexneri counts in stool, with prophylactic treatment being most effective. These findings support the potential of lytic phages as viable alternatives to antibiotics for managing resistant Shigella infections.

Keywords: Shigella flexneri, lytic bacteriophage, dysentery, phage therapy, multidrug resistance

Therapeutic effects of IgY on Helicobacter pylori eradication and patients' clinical symptoms: a randomized double-blind clinical trial

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BACKGROUND AND OBJECTIVES: Helicobacter pylori infection is a global health concern linked to gastritis, ulcers, and gastric cancer. With rising antibiotic resistance, egg yolk immunoglobulin (IgY) has emerged as a promising candidate due to its stability and pathogen-neutralizing effects. This clinical trial evaluated the efficacy of anti-H. pylori IgY in improving eradication and reducing clinical symptoms.

MATERIALS AND METHODS: In a randomized double-blind trial, 60 patients with confirmed H. pylori infection received either 14-day standard triple therapy (omeprazole, amoxicillin, clarithromycin) plus IgY enriched egg yolk powder (intervention) or placebo (plain egg yolk powder). The primary outcome was bacterial eradication measured by urea breath test (UBT) at 1.5 months. Secondary outcomes included symptom improvement (abdominal pain, nausea, bloating, anorexia) using the Gastrointestinal Symptom Rating Scale (GSRS) that were examined by phone twice a week for 3 weeks. Data were analyzed using SPSS v24.

RESULTS AND DISCUSSION: Baseline demographics were homogeneous. The intervention group showed a marked reduction in UBT scores, with median values dropping from 77 to 11, compared to no change in the placebo group (median=55). 66.7%of IgY recipients achieved clinical improvement versus only 40% in the placebo group a 26.7% difference. Notably, clinical symptoms resolved more quickly in the IgY group than in the placebo group, and no adverse events were reported with IgY. IgY enhances symptom relief and demonstrates promising anti-H. pylori effects, particularly in reducing bacterial load and accelerating recovery. These findings support IgY as a safe and effective adjunct to standard treatment for H. pylori infection.

Keywords: Helicobacter pylori, Immunoglobulin Y, Clinical trial, Symptom Assessment

Therapeutic Role of Akkermansia muciniphila in Genitourinary Cancers: A Narrative Review

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BACKGROUND AND OBJECTIVES: Urogenital neoplasms, like kidney cancer, prostate cancer, and bladder cancer, are still significant medical challenges because they respond very differently to immunotherapy. Recent advances have highlighted the critical role of the gut and urogenital microbiota in modulating cancer progression and therapeutic efficacy. Among these, Akkermansia muciniphila has become an important gut bacterium that significantly affects how the immune system works, which can improve the success of different cancer treatments.

MATERIALS AND METHODS: This review brings together all the current information about how A. muciniphila affects genitourinary cancers, especially its impact on the results of immunotherapy. Relevant studies, such as clinical trials, lab experiments, and microbiome analyses, were carefully reviewed to understand how changing the levels of A. muciniphila could help in treatment and reveal the reasons behind its effects.

RESULTS AND DISCUSSION: Research indicates that patients with genitourinary cancer who have more A. muciniphila respond better to immune checkpoint inhibitors, particularly PD-1/PD-L1 blockade. Mechanistically, this bacterium promotes antitumor immunity by activating T cells and preserving the mucosal barrier. Ways to increase A. muciniphila, like taking probiotics or receiving fecal microbiota transplants, could help improve the results of immunotherapy. On the other hand, having low levels of A. muciniphila in the gut is linked to cancer growth and making treatments less effective. Despite these promising findings, further well-designed clinical studies are needed to understand the underlying mechanisms fully and to develop standardized microbiome-based strategies as complementary treatments alongside cancer immunotherapy.

Keywords: Akkermansia, Urogenital Neoplasms, Immunotherapy, Gastrointestinal Microbiome

Therapeutic Synergy Between Leech Saliva and Gentamicin in Experimental Salmonella Typhimurium Infection in Poultry

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BACKGROUND AND OBJECTIVES: The ongoing threat of Salmonella enterica serovar Typhimurium emerging as a pathogen to the broiler chicken industry, along with the added emergence of antimicrobial resistance, creates a growing concern associated with this pathogen in the food industry. Leech saliva (Hirudo medicinalis) offers potential promise as an adjunct to treat infections due to its bioactive properties. We aimed to determine whether leech saliva applied on its own or in combination with gentamicin would reduce the severity of infection in chickens that were experimentally infected with Salmonella Typhimurium.

MATERIALS AND METHODS: Sixty Ross 308 chicks were experimentally infected with S. Typhimurium in this study, and were divided into four groups: the control, gentamicin, leech saliva, and combined leech saliva–gentamicin therapy. The bacterial load, gross pathology, and histopathology of the spleen, liver, and intestine were assessed over five days.

RESULTS AND DISCUSSION: Leech saliva monotherapy moderately reduced the microbial load and tissue damage caused by S. Typhimurium infection. Gentamicin showed a higher degree of antimicrobial activity than leech saliva alone. However, combination therapy had the best results, enhancing bacterial clearance and decreasing pathological changes (p 0.05) compared to either monotherapy. Likewise, the histopathology scores suggest that combination therapy was more effective in reducing enteritis and necrosis in hepatic and splenic tissues than either monotherapy group. We demonstrated that leech saliva has a beneficial antimicrobial adjunctive effect. This natural compound can be utilized as an adjunct in treatments and challenges the multidrug resistance of Salmonella Typhimurium in poultry.

Keywords: Hirudo medicinalis, Leeches, Salmonella, Salmonella enterica, Poultry, Gentamicins

Title:Gut Microbial Metabolites in Cancer: Dual Roles in Tumorigenesis and Immune Modulation

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BACKGROUND AND OBJECTIVES: Cancer is the second-leading cause of death worldwide. Emerging evidence highlights the crucial role of gut microbiota and their metabolites in carcinogenesis. Around 20% of cancers are linked to microbial factors, warranting deeper mechanistic insights.

MATERIALS AND METHODS: A systematic review was conducted using PubMed, Scopus, and Web of Science, covering studies from 2015 to 2025. Included were original and review articles examining gut microbiota and microbial metabolites in cancer development and immune regulation. Non-English papers, case reports, conference abstracts, and studies lacking mechanistic data were excluded.

RESULTS AND DISCUSSION: Specific microbes are closely tied to certain cancers. Helicobacter pylori is involved in gastric cancer via HKDC1 and CagA-driven SQLE activation. Fusobacterium nucleatum contributes to colorectal cancer by binding E-cadherin and activating NF-κB through TLR4. Clostridium perfringens, Streptococcus, and Veillonella promote tumorigenesis via PI3K-AKT and COX-2 signaling. Listeria monocytogenes and Salmonella enterica support immune activation and antigen presentation. Microbial metabolites have dual effects. Secondary bile acids (DCA, LCA) promote cancer by polarizing macrophages toward a tumor-supporting M2 phenotype, downregulating IL-6, IFN-γ, and TNF-α, and triggering TGR5-mediated DNA damage. Lipopolysaccharides disrupt the intestinal barrier, increasing exposure to carcinogens. In contrast, IsoalloLCA supports immune tolerance by inducing Foxp3 expression in T cells via ROS generation. Gut microbes and their metabolites can both drive and suppress tumor development. Targeting microbial pathways and metabolites offers promising strategies for cancer prevention and microbiota-based immunotherapies. Further research is needed to support clinical applications.

Keywords: Gut microbiota , Carcinogenesis , Immune modulation , Cancer immunotherapy

Tolerance of isolated biosurfactant-producing bacteria from petrol contaminated soil to Copper and Iron

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BACKGROUND AND OBJECTIVES: The growing level of heavy metals like copper and iron in the environment is exceptionally threatening to the ecology and the health of the human populations. Traditional means of metal removing are usually expensive and inefficient. Biosurfactant-producing bacteria can play a important role in bioremediation. The aim of this research was to isolate the tolerant bacteria to metal concentrations that secrete surface-acting substances with metal mobilizing potential.

MATERIALS AND METHODS: Samples were obtained from diesel-contaminated soil for isolation of biosurfactant-producing bacteria by serial dilution method. They were identified by biochemical tests. Biosurfactant production was evaluated by droplet destruction, oil spreading, and emulsifying activity tests. Finally, their tolerance to heavy metals was investigated using enriched agar medium with iron (II) sulfate and copper sulfate at concentrations of 100 to 1800 mg/L.

RESULTS AND DISCUSSION: Ten isolates were isolated and all had the ability to produce biosurfactants. Two isolates were tolerant to copper up to the concentration of 1300 mg/L, and all isolates grew up to a concentration of 834 mg/L of iron. Tolerance of isolate to cupper was observed higher than iron. All isolates showed emulsifying activities more than 30%. This study highlights the potential of biosurfactant-producing bacteria for the bioremediation of heavy metals. The behavior of isolates revealed that isolated bacteria with production of biosurfactant accompanying with notable tolerance to high concentrations of copper and iron, make them as the good candidates for development of eco-friendly bioremediation.

Keywords: Biosurfactant, Copper, Iron, Heavy metals, Bioremediation.

Toxicity determination of immunogenic CD8+ T cells epitopes of SARS-COV-2 for Iranian common MHC-I alleles by computational immunology

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BACKGROUND AND OBJECTIVES: CD8+ T lymphocytes play a very important role in control of COVID-19. Since WHO announcement of COVID-19 pandemic on January 2020, a lot of studies have focused on identifying the SARS-CoV-2 fragments responsible in infection to find therapeutic targets. The most immunogenic-nontoxic epitopes are the best targets for development of innovative vaccines. In this study, the toxicity of immunogenic CD8+ T cells specific epitopes of SARS-COV-2 for Iranian common MHC-I alleles were detected by computational immunology.

MATERIALS AND METHODS: Six proteins of SARS-CoV-2 including S, M, E, N, ORF1ab and ORF3a, with an essential role in virus immunogenicity, were selected. The amino acid sequences of these proteins were determined in NCBI database at www.ncbi.nlm.nih.gov in FASTA format. Next, CD8+ T cells specific epitopes on SARS-COV-2 for Iranian common MHCI alleles were predicted by immunoinformatic. Then the most immunogenic epitopes of them were selected. Finally toxicity of the selected epitopes was assessed by immunoinformatic.

RESULTS AND DISCUSSION: According to results of this study, 2180 CD8+ T cells specific epitopes on SARS-COV-2 for Iranian common MHCI alleles were predicted by immunoinformatic. 144 of these epitopes were the most immunogenic. Among them 7 epitopes were toxic. Each of S, N, and M proteins had two toxic epitopes. E protein had one toxic epitope. In current study, only 7 of 144 most immunogenic CD8+ T cells specific epitopes of SARS-COV-2 proteins for Iranian common MHCI alleles were toxic. These toxic epitopes must be ruled out for development of highly safe efficient vaccines.

Keywords: SARS-COV-2, epitopes, computational immunology, CD8+ T cells, toxicity

Unveiling the Superbugs of Eastern Iran: High Prevalence of ESBLs Producing Klebsiella pneumoniae Isolates Harboring Resistance Genes

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BACKGROUND AND OBJECTIVES: Introduction: The increasing number of cases of extended-spectrum β-lactamase (ESBL)-producing Klebsiella pneumoniae (ESBL-KP) has led to a serious healthcare crisis in clinical settings in recent years. This research aimed to assess not only the prevalence of ESBL-KP but also to investigate the coexistence of Cefoxitamase-Munich (blaCTX M) with aminoglycoside-modifying enzyme (AME) genes, such as aac(3)IIa and aac(6′)Ib, in CTX-M-producing K. pneumoniae isolates from patients in Birjand province, Iran.

MATERIALS AND METHODS: 121 Methods: K. pneumoniae isolates were gathered from various clinical samples between August 2021 and August 2022. These isolates were identified through conventional microbiological techniques and PCR targeting the mdh gene. Antimicrobial susceptibility testing was performed using the Kirby-Bauer disk diffusion method according to CLSI guidelines. ESBL production was detected via the double disk synergy test. The presence of CTX-M groups and AME genes (aac(3)-IIa and aac(6′)-Ib) was determined by PCR.

RESULTS AND DISCUSSION: Results: Out of 120 isolates, 70 (58.3%) were ESBL producers. PCR analysis revealed that 40% of ESBL-producing isolates harbored blaCTX-M genes, with CTX-M-1 (100%) and CTX-M-9 (10%) being the most prevalent. A significant portion (83.3%) of isolates carried aminoglycoside resistance genes, with aac(3)-IIa present in 46.2% and aac(6′)-Ib in 72.9% of isolates. Aminoglycoside resistance genes and blaCTX-M co-existence were detected in 50% of ESBL-KP isolates (p 0.001). Conclusion: Our findings imply a concerning coexistence of AME genes alongside CTX-M-type β-lactamase genes in K. pneumoniae, possibly rendering initial broad-spectrum aminoglycoside-based empiric therapy for ESBL-KP ineffective in these settings.

Keywords: Klebsiella pneumoniae, Extended-spectrum beta-lactamases, Aminoglycosides, Cefotaximase, Iran

Unraveling Chancroid in Iran: Clinical Manifestations, Regional Variability, and Advancements in Therapeutic and Preventive Strategies

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BACKGROUND AND OBJECTIVES: Chancroid is a severe sexually transmitted infection caused by the Gram-negative, facultatively anaerobic bacterium Haemophilus ducreyi. It can cause painful genital ulcers characterized by soft, undermined edges and is frequently accompanied by tender inguinal lymphadenopathy. The clinical picture of chancroid closely resembles other ulcerative infections, including syphilis and genital herpes, making accurate diagnosis difficult. In Iran, chancroid remains one of the most prevalent sexually transmitted diseases, and its management is further complicated by frequent co-infection with syphilis. Due to the fastidious growth requirements of H. ducreyi, traditional culture methods are often inadequate, and polymerase chain reaction (PCR) has emerged as the diagnostic gold standard, though its accessibility remains limited in many settings. Consequently, a syndromic approach based on clinical findings is commonly employed in resource-restricted areas.

MATERIALS AND METHODS: By reviewing published papers in Iran, we have carefully developed this article to provide an accurate and relevant analysis. Additionally, we have examined recent advancements in treatment strategies, evaluating their efficacy and potential impact on clinical management. Through this research, we aim to contribute valuable insights to the field.

RESULTS AND DISCUSSION: improvements in molecular diagnostics and point-of-care testing are expected to enhance early detection and individualized treatment approaches. Moreover, ongoing vaccine research targeting conserved surface antigens such as OmpA and PilA holds promise for more effective preventive strategies. Strengthened surveillance and refined antibiotic protocols could significantly reduce disease prevalence and curb HIV transmission, ultimately improving public health outcomes nationwide.

Keywords: STI cutaneous infections chancroid Haemophilus ducreyi HIV

Unveiling Plaque Morphology: Insights into Phage Behavior Across Diverse Media

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BACKGROUND AND OBJECTIVES: Phage therapy is gaining renewed attention as a promising alternative for treating multi-drug-resistant bacterial infections. Phage isolation typically employs the enrichment method, enabling multiplication even from a single infectious phage, followed by quantification using the double agar overlay assay. This technique allows enumeration and plaque morphology analysis, which can help distinguish lytic phages (clear plaques) from lysogenic ones (turbid or bull's-eye plaques). However, plaque appearance can vary with different bacteriological media, a factor that remains poorly understood. This study investigates the morphological differences of plaques produced by bacteriophages on various media compositions.

MATERIALS AND METHODS: phage

RESULTS AND DISCUSSION: phage

Keywords: phage, plaque, culture media

Ureaplasma parvum, Mycoplasma genitalium and Chlamydia trachomatis, in Infertile Couples and the Effect on Semen Parameters

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BACKGROUND AND OBJECTIVES: Chlamydia trachomatis, Ureaplasma parvum, andMycoplasma genitaliumare sexually microorganisms. Our study aimed to determine the prevalence ofC. trachomatis, U. parvum, andM. genitaliumin infertile and fertile couples and the effect of microorganismson semen parameters.

MATERIALS AND METHODS: In this case-control study, samples were collected from 50 infertile couples and 50 fertile couples and were subjected to the routine semen analysis and Polymerase chain reaction (PCR).

RESULTS AND DISCUSSION: C. trachomatis and U. parvum were detected in 5 (10%) and 6 (12%) of men. Also, out of 50 swabs from the women, C. trachomatis and M. genitalium detected in 7(14%) and 4 (8%) of s swabs were negative. Also, in the group of infertile infected C. trachomatis and U. parvum, sperm motility was lower than uninfected infertile men.

Keywords: Mycoplasma genitalium, Ureaplasma parvum, Chlamydia trachomatis, Infertility, Semen Analysis, PCR.

Validation of Beta-Lactamase Use for Effective Hydrolysis of Beta-Lactam Rings in Cefazolin Powder for Injection Sterility Testing

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BACKGROUND AND OBJECTIVES: Interference in Sterility Testing: The β-lactam ring's antibacterial activity suppresses microbial growth in samples containing residual antibiotics, creating false-negative sterility test results. For example: • Penicillin and cephalosporins inhibit contaminant bacteria, masking true contamination. • Degradation of β-lactams in growth media (e.g., mecillinam with a half-life of 2–6 hours) can cause "regrowth" of bacteria, complicating test interpretation. Neutralization Strategies: To mitigate interference, β-lactamase enzymes are used to hydrolyze the β-lactam ring: • β-lactamase plates: Contain enzymes that break down antibiotics like penicillin, ensuring uninhibited microbial growth. • Validation: Studies confirm penicillinase effectively inactivates β-lactams in sterility tests for drugs like amoxicillin and cefazolin.

MATERIALS AND METHODS: • Test culture TBS (Tryptic soy broth) • Test culture FTM (Fluid Thioglycolate medium) • Test culture PEW (Buffered Peptone water) • LactamatorTM , product code: #LCT-LQS10 (Sterile Liquid), Batch: 019.LQS.00123, stability of Cephalosporinase and Penicillinase as 93% and 82% ,respectively. It also shows the Cephalosporinase and Penicillinase activity of 19 and 254 (IU/ml), each. • Sterility set • Incubator • HPLC Knauer Platin Blue

RESULTS AND DISCUSSION: Findings demonstrate that incorporating 100 microliters of β-lactamase per gram of sample is sufficient to achieve complete β-lactam ring Hydrolyzation under the specified conditions. This approach not only validates the enzyme's functional performance but also highlights the efficiency gains achieved by direct enzyme addition to the sample matrix rather than the culture medium.

Keywords: Beta-lactamase, Sterility test, Cefazolin, Penicillin, Antibiotics

Virulence genotyping of Mammary Pathogenic Escherichia coli strains, isolated from milk of bovine mastitis in the industrial farms of Hamedan county

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BACKGROUND AND OBJECTIVES: Bovine mastitis is the most widespread and economically important disease worldwide. In particular, Escherichia coli is reported as one of the most frequently isolated causative agents of mastitis. Mammary Pathogenic E. coli (MPEC) has been proposed as a new pathotype of E. coli and responsible for causing mastitis in dairy animals. The pathogenicity of MPEC associated with virulence factors encoded by virulence associated genes (VAG). The aim of the present study was to investigate the presence of four VAGs in MPEC's including fimC (fimbriae mannose-binding type1), cvaA/B (Colicin V A/B), iutA (aerobactin siderophore receptor) and hlyA (encodes a toxin called alpha-hemolysin) in MPEC strains isolated from milk of cows with clinical mastitis in industrial dairies of Hamedan county, west of Iran.

MATERIALS AND METHODS: The present study was carried out on MPEC strains (n=67) isolated from milk of cows with clinical mastitis in Hamedan county. First, genomic DNA was extracted from bacterial strains using rapid boiling method. Extracted DNA were evaluated for the presence of four VAGs including fimC, iutA, hlyA and cvaA/B genes using multiplex PCR technique.

RESULTS AND DISCUSSION: The multiplex PCR results revealed that the 67 isolates (100%) possessed fimC gene, 16 isolates (23.8%) harboured hlyA gene, 11 isolates (16.42%) containrd cvaA/B gene and 11 isolates (16.42%) were positive for iutA gene. Out of 67 isolates tested, 40 isolates (59.7%) had only one fimC gene, 18 isolates (26.8%) contained two VAGs, seven isolates (10.4%) had three VAGs and two isolates (2.9%) had four genes.

Keywords: Mastitis, Dairy cattle, Mammary Pathogenic Escherichia coli, Virulence factors

WHO priority programs to tackle antimicrobial rsistance

Omid Zamani [1] © ℗

[1] World Health Organization

BACKGROUND AND OBJECTIVES: Antimicrobial resistance (AMR) is an increasingly serious threat to health and development. AMR needs to be tackled from many angles at multiple levels and across different sectors. The World Health Organization (WHO) is at the forefront of the global battle against antimicrobial resistance (AMR), a growing threat to public health and modern medicine. Employing a multi-pronged strategy, the WHO is orchestrating efforts at the global, regional, and country levels to curb the emergence and spread of drug-resistant pathogens.

MATERIALS AND METHODS: Review of WHO publications and strategic priorities since 2015.

RESULTS AND DISCUSSION: The Global Action Plan on Antimicrobial Resistance (GAP-AMR), adopted by the World Health Assembly in 2015. The WHO collaborates with Member States to develop and implement national action plans on AMR that align with this global plan. These national strategies are designed to address AMR across various sectors, including human health, animal health, and agriculture, guided by the GAP's five key strategic objectives: Improve awareness and understanding of AMR through effective communication, education, and training. Strengthen the knowledge and evidence base through surveillance and research. Reduce the incidence of infection through effective sanitation, hygiene, and infection prevention measures. Optimize the use of antimicrobial medicines in human and animal health. Develop the economic case for sustainable investment and increase investment in new medicines, diagnostic tools, vaccines, and other interventions. Underpinning this strategy is a people-centered approach that focuses on preventing infections and ensuring equitable access to quality healthcare.

Keywords: AMR, one health, antimicrobial resistance, global health, IPC, WHO

Zoonotic tuberculosis (ZTB)

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BACKGROUND AND OBJECTIVES: Bovine tuberculosis is a chronic bacterial disease of animals caused by members of the Mycobacterium tuberculosis complex, primarily by M. bovis and rarely by M.caprae. It is a major zoonotic disease, and cattle are the main source of infection for humans. Bovine tuberculosis (bTB) is characterized by the formation of granulomas in tissues and organs, more significantly in the lungs, lymph nodes, intestine, kidney, liver and spleen. Tuberculosis is recognized as one of the most important threat to human and animal health causing mortality, morbidity and economic losses. Tuberculosis (TB) is one of the major public health threats globally and cause infection among billions of peoples each year and ranks as second leading cause of death from an infectious disease worldwide after HIV/AIDS.

MATERIALS AND METHODS: Zoonotic TB can spread from infected animals to humans, typically by the inhalation of aerosols, close contact and ingestion of raw animal products, also, it represents a financial burden due to the loss of productivity of livestock through the reduction of milk production and carcass condemnation. Drinking raw milk is a primary route of M. bovis infection of humans. Naturally, the occurrence of zoonotic TB is greatly dependent on the presence of TB in animals.

RESULTS AND DISCUSSION: Global estimated prevalence of zoonotic TB is Of 10 million people currently with new active TB, 140,000 (range, 69,800–235,000) are estimated to be new cases of zTB (1.4%) of which an approximately 11,400 (8.1%, range 4,470-21,600) died (WHO, 2020a) for pulmonary and extra-pulmonary TB cases.

Keywords: M. bovis - M.caprae - zoonotic TB