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Conference

The 4th International Electronic Conference on Antibiotics

21-23 May 2025 | Online



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The 4th International Electronic Conference on Antibiotics

21–23 May 2025 | Online



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Welcome from the Chairs

On behalf of *Antibiotics* (ISSN: 2079-6382, Impact Factor: 4.3), I would like to welcome you to **the 4th International Electronic Conference on Antibiotics (ECA2025)**. This event aims to bring together researchers and scholars to discuss a wide range of topics covering the aim and scope of *Antibiotics*. We envision this conference as a highly interactive forum open to diverse interaction between its participants. Serves as a platform covering a broad range of topics, publishing papers on all aspects of antibiotics, and encompassing the general fields of biochemistry, chemistry, genetics, microbiology, and pharmacology. *Antibiotics* is the journal of choice for researchers needing a quick turnaround time to review and publish their papers. We can be proud that we have many repeat contributing authors, which sends a strong message to the research community that *Antibiotics* is recognized as a high-quality service provider with an impeccable reputation because of its peer review and revision process.

We expect that participants of this conference will be able to exchange novel, provocative ideas by presenting short oral presentations on research and development and discoveries, as well as emphasizing challenges facing antibiotic resistance as a public health crisis.

Download the conference banner and share it with your colleagues!

Kind regards,



Prof. Dr. Manuel Simões

Department of Chemical
Engineering, Faculty of
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Session Chairs



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Invited Speakers



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University of Technology,
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Program Overview

21st May	22nd May	23rd May
09:00-12:00 (CEST) Session 5. Multidisciplinary Antimicrobial Strategies: Materials, Peptides, Bacteriophages and Repurposing	09:00-10:50 (CEST) Session 7. Clinical and Environmental Impact of Bacterial Biofilms	09:00-11:10 (CEST) Session 3. Epidemiology, Prevalence and Mechanisms of Antibiotic Resistance and Cross-Resistance
12:00-13:05 (CEST) Session 6. Antibiotic Clinical Studies, Pharmacokinetics and Pharmacodynamics	14:00-16:20 (CEST) Session 8. Artificial Intelligence Strategies to Tackle Antibiotic Resistance	14:00 (CEST) Session 2. Antibiotics and One Health
14:00-17:10 (CEST) Session 4. Novel Antimicrobial Agents: Discovery, Design, Synthesis and Action		16:10 (CEST) Session 1. Antibiotics Stewardship and Antimicrobial Use in Healthcare Settings

ECA 2025 Program

(Day 1)

Session 5. Multidisciplinary Antimicrobial Strategies: Materials, Peptides, Bacteriophages and Repurposing

Date: 21 May 2025 (Wednesday)

Time: 9:00 (CEST, Basel) | 03:00 (EDT, New York) | 15:00 (CST Asia, Beijing)

Time (CEST)	Speaker	Title
9:00-9:10	Dr. Marc Maresca Editor in Chief, <i>Antibiotics</i>	<i>Opening Speech</i>
9:10-9:15	Prof. Dr. Serena Riela Session Chair	<i>Welcome from the Session Chair</i>
09:15-09:45	Assoc. Prof. Markus Weingarth Keynote Speaker	Cracking Nature's code to designing Lipid-targeting Antibiotics
09:45-10:05	Dr. Elena Maria Varoni Invited Speaker	Prescribing Antibiotics in Dentistry: Clinical Insights and Implications
10:05-10:25	Dr. Marina Massaro Invited Speaker	Nanomaterials Based on Clay Minerals to Fight Antibiotic Resistance
10:25-10:40	Caroline Black Selected Speaker	Conditions Mimicking Host Infection Environments Impact Antimicrobial Susceptibilities
10:40-10:55	Alibala Aliyev Selected Speaker	Modification of Polyvinylidene Fluoride (PVDF) Surgical Meshes with Bentonite-Based Nanocomposites for Enhanced Antimicrobial Performance and Drug Delivery Applications
10:55-11:10	Catarina Roma-Rodrigues Selected Speaker	Isolation of Soil Microorganisms for the Synthesis of Gold and Silver Nanoparticles for Antimicrobial Applications
11:10-11:25	Maphori Maliehe Selected Speaker	Evaluation of The Inhibitory Effects of Artemisinin on Cryptococcus Neoformans
11:25-11:40	Ângela Freitas Selected Speaker	Development of a Photodynamic Therapy Protocol to control Skin Infections by <i>Pseudomonas aeruginosa</i>
11:40-12:00	Hadiya Malik, Zoobaria Zahid, Vadym Poniatovsky	Flash Poster Presentations

S6. Antibiotic Clinical Studies, Pharmacokinetics and Pharmacodynamics

Date: 21 May 2025 (Wednesday)

Time: 12:00 (CEST, Basel) | 06:00 (EDT, New York) | 18:00 (CST Asia, Beijing)

Time (CEST)	Speaker	Title
12:00-12:05	Prof. Dr. Stefano Di Bella Session Chair	<i>Welcome from the Session Chair</i>
12:05-12:25	Dr. Vasiliki Koumaki Invited Speaker	New PK/PD Data on Old Antibiotics
12:25-12:40	Asma Aboelezz Selected Speaker	The Impact of Augmented Renal Function on Vancomycin Pharmacokinetics in Neuro-critically Ill Patients
12:40-12:55	Stella Babich Selected Speaker	Feasibility of 24 h Continuous Infusion of Cefiderocol Administered by Elastomeric Pump in Attaining an Aggressive Pharmacokinetic/Pharmacodynamic (PK/PD) Target in the Treatment of NDM-Producing <i>Klebsiella Pneumoniae</i> Otitis Media
12:55-13:05	Natasa Hulak, Mishaal Khawar	Flash Poster Presentations

S4. Novel Antimicrobial Agents: Discovery, Design, Synthesis and Action

Date: 21 May 2025 (Wednesday)

Time: 14:00 (CEST, Basel) | 08:00 (EDT, New York) | 20:00 (CST Asia, Beijing)

Time (CEST)	Speaker	Title
14:00-14:05	Prof. Dr. Jordi Vila Session Chair	<i>Welcome from the Session Chair</i>
14:05-14:20	Marie Hanot Selected Speaker	Novel Aminoquinoline Bi-Aromatic Hybrids as Anti-Biofilm Agents Against <i>Pseudomonas Aeruginosa</i>
14:20-14:35	Attilio Di Maio Selected Speaker	Aurones and Their Derivatives as Promising Antimicrobial Molecules
14:35-14:50	Ilaria D'Agostino Selected Speaker	A Multidisciplinary Study Towards Ciprofloxacin Hybrids: Harnessing Carbonic Anhydrase Inhibition in <i>Pseudomonas aeruginosa</i> for Next-Generation Antibacterial Agents
14:50-15:05	Marie Gréverie Selected Speaker	New 2,8-Bis(Trifluoromethyl)Quinoline-4-Carboxamides As Potential Antimycobacterial Agents
15:05-15:20	Younes Smani Selected Speaker	The Development of a New Antibiotic Class Targeting Enolase in <i>Acinetobacter Baumannii</i>
15:20-15:35	Joaquín Sandoval-Vargas Selected Speaker	Exploration and Identification of Bioactive Compounds from Antarctic Lichens: Contribution to Bioprospecting of New Antimicrobials
15:35-15:55	Prof. Dr. Mark G Moloney Invited Speaker	Natural Product Inspired Antibacterial Lactams and Tetramates
15:55-16:10	Letizia Bartolone Selected Speaker	Reviving GE23077: Investigating the Biosynthetic Pathways and Antimicrobial Potential of a Promising RNAP Inhibitor

16:10-16:25	Federico Bosetto Selected Speaker	Development of DNA Aptamers as Therapeutic Tools Against <i>Pseudomonas Aeruginosa</i>
16:25-16:40	Miguel Leitão Selected Speaker	Disruption of Quorum Sensing in <i>Pseudomonas aeruginosa</i> by Sinapic Acid: Impacts on Biofilm Formation and Virulence
16:40-17:15	Fazlurrahman Khan, Lília Soares Teixeira, Manuel Böhmman, Olga N. Sineva, Ana Maranhã, Yonghong Zhang, Nikolet Ilieva Pavlova	Flash Poster Presentations

(Day 2)**S7. Clinical and Environmental Impact of Bacterial Biofilms****Date: 22 May 2025 (Thursday)**

Time: 09:00 (CEST, Basel) | 03:00 (EDT, New York) | 15:00 (CST Asia, Beijing)

Time (CEST)	Speaker	Title
09:00-09:05	Prof. Dr. Manuel Simões Event (Session) Chair	<i>Welcome from the Session Chair</i>
09:05-09:25	Prof. Dr. Olivier Habimana Invited Speaker	High Risk of Pathogen and Antibiotic Resistance Transfer in Live Seafood Wet Markets
09:25-09:45	Prof. Dr. Zhenbo Xu Invited Speaker	Biofilm Formation of Staphylococcus Aureus Under Low Concentration of Antibiotics
09:45-10:00	Ana Rita Pereira Selected Speaker	Effect of Methylparaben Disinfection By-products on the Chlorine Tolerance of Biofilms
10:00-10:15	Sadeeva Zulfirya Selected Speaker	Biofilm Formation and Antibiotic Resistance in <i>Pseudomonas Aeruginosa</i> Isolated from Blood and Cerebrospinal Fluid of Children
10:15-10:30	Akanksha Mishra Selected Speaker	Biofilm formation on the surface of medical devices: a growing concern for hospital-acquired infections
10:30-10:50	Enea Ovedani, Zehra Irshad, Sunny Cui, DIVYA NAIR	Flash Poster Presentations

S8. Artificial Intelligence Strategies to Tackle Antibiotic Resistance**Date: 22 May 2025 (Thursday)**

Time: 14:00 (CEST, Basel) | 08:00 (EDT, New York) | 20:00 (CST Asia, Beijing)

Time (CEST)	Speaker	Title
14:00-14:05	Dr. Marc Maresca Event (Session) Chair	<i>Welcome from the Session Chair</i>

14:05-14:35	Prof. Dr. Octávio Luiz Franco Keynote Speaker	Antimicrobial Peptide DIGITAL Optimization Enables The Generation of Bioinspired Products
14:35-15:05	Prof. Dr. Cesar de la Fuente Keynote Speaker	TBC
15:05-15:25	Dr. Alessandro Perrella Invited Speaker	GPT-Based Drug-to-Disease (DtD) Checker as a Tool for Optimizing Antibiotic Use and Reducing Resistance
15:25-15:40	Ezgi Nur YUKSEK Selected Speaker	Artificial Intelligence in Antibiotic Stewardship: Optimising Prescribing Processes and Overcoming Ethical Challenges
15:40-15:55	Alizay Ashfaq Selected Speaker	Immersive Technologies in Healthcare: Virtual Reality's Role in Addressing Antibiotic Resistance
15:55-16:10	ISHANT DIWAKAR DAHAKE Selected Speaker	Using Artificial Intelligence to Combat Antimicrobial Resistance: Advancements and Challenges
16:10-16:20	Alexis Reinbold, Tatiana Makarova	Flash Poster Presentations

(Day 3)

S3. Epidemiology, Prevalence and Mechanisms of Antibiotic Resistance and Cross-Resistance

Date: 23 May 2025 (Friday)

Time: 9:00 (CEST, Basel) | 03:00 (EDT, New York) | 15:00 (CST Asia, Beijing)

Time (CEST)	Speaker	Title
09:00-09:05	Dr. Marc Maresca Event Chair	<i>Welcome from the Session Chair</i>
09:05-09:35	Prof. Dr. Ute Römling Keynote Speaker	TBC
09:35-09:50	Panagiota Tzevelekou Selected Speaker	Catalytic Production of Erythromycin Against COVID-19
09:50-10:05	Vanessa Silva Selected Speaker	Environmental Dissemination of Multidrug-resistant <i>Klebsiella</i> Spp.: Evidence from Genomic Surveillance of Surface Water
10:05-10:20	Antonia Charalampos Mataragka Selected Speaker	Antibiotic Susceptibility Testing of Escherichia Coli and Coliform Isolates Detected in Samples of Drinking Water from Central Greece
10:20-10:35	Amer Abdelgany Selected Speaker	Intermittent Antimicrobial Treatments Enhanced The Persistence And Transfer Of Antimicrobial Resistance Genes In The Gut Microbiota
10:35-10:50	Akamu Ewunkem Selected Speaker	Surviving the Greek Gift: Gallium Resistance
10:50-11:10	Eugene Y.H. Yeung, Marta Katkowska, Antonia Charalampos Mataragka, Marina Bubonja-Sonje	Flash Poster Presentations

S2. Antibiotics and One Health

Date: 23 May 2025 (Friday)

Time: 14:00 (CEST, Basel) | 08:00 (EDT, New York) | 20:00 (CST Asia, Beijing)

Time (CEST)	Speaker	Title
14:00-14:05	Dr. Efstathios Giaouris Session Chair	<i>Welcome from the Session Chair</i>
14:05-14:25	Dr. Cristian Piras Invited Speaker	TBC
14:25-14:45	Dr. Sara M. Soto González Invited Speaker	Antimicrobial Resistance from An One Health Perspective
14:45-15:00	Liang WANG Selected Speaker	Identification and Quantification of Mixed Antibiotics in Aqueous Solution Through Machine Learning Analysis of SERS Spectra
15:00-15:15	Davide Messina Selected Speaker	Correlation Between Use of Antibiotics and Prevalence of Resistant Strains of Coagulase-positive Staphylococci (<i>S. aureus</i>) in Dairy Farms in Apulia (Southern Italy)
15:15-15:30	Joana Paiva Selected Speaker	Antimicrobial Resistance and Biofilm Formation in <i>Staphylococcus Aureus</i> Isolated from Retail Meat: Implications for Food Safety
15:30-15:45	Andreia Garces Selected Speaker	Wildlife and Antibiotic Resistance: Exploring the Case of Bears
15:45-16:10	Ashly Chagua, Antonia Charalampos Mataragka, Carla Miranda, Hernan Nievas, Margarita Terentjeva	Flash Poster Presentations

S1. Antibiotics Stewardship and Antimicrobial Use in Healthcare Settings

Date: 23 May 2025 (Friday)

Time: 16:10 (CEST, Basel) | 10:10 (EDT, New York) | 22:10 (CST Asia, Beijing)

Time (CEST)	Speaker	Title
16:10-16:15	Prof. Dr. Reza Nassiri Session Chair	<i>Welcome from the Session Chair</i>
16:35-16:55	Dr. Márió Gajdács Invited Speaker	Knowledge and Attitudes of Nurses and Allied Healthcare Professionals Towards Antimicrobial Use and Resistance: A Cross-Sectional Survey in Hungary
16:55-17:10	Vinicius Pereira dos Anjos Selected Speaker	Fourier Transform Infrared Spectroscopy-Based Detection of Amoxicillin and Ampicillin for Advancing Antibiotic Monitoring with Optical Techniques
17:10-17:25	Eugene Y.H. Yeung Selected Speaker	Fosfomycin Sensitivity Among Enterobacterales and Enterococci in Urine Culture in British Columbia, Canada, 2023-2024
17:25-17:45	Jayasutha Jayram, Zhanar Kosherova, Eda Altınöz, Sávio Benvindo Ferreira	Flash Poster Presentations

17:45-17:

Prof. Dr. Manuel Simões
Dr. Marc Maresca
Event Chairs

Closing Speech

Session 1. Antibiotics Stewardship and Antimicrobial Use in Healthcare Settings

sciforum-125070: Knowledge and attitudes of nurses and allied healthcare professionals towards antimicrobial use and resistance: a cross-sectional survey in Hungary

Zita Livia Szabó ¹, Rita Eszter Major ¹, Regina Finta ², Edit Paulik ³ and Márió Gajdács ^{1,*}

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Introduction:

Antimicrobial resistance (AMR) is one of the most significant public health issues of the 21st century. Numerous professional guidelines highlight the role of nurses and allied healthcare professionals in enabling and promoting appropriate antibiotic use; however, there is limited data on their knowledge and attitudes regarding AMR, despite the fact that they make up 50–70% of the healthcare workforce globally. The aim of the present study is to assess the knowledge and attitudes related to AMR among nurses and allied healthcare professionals in Hungary.

Methods:

A quantitative, cross-sectional study was performed, using a 80-item, self-administered questionnaire, which was developed for the purposes of this study. The internal consistency of the instrument was determined during pilot studies (Cronbach's α : 0.737, Kuder-Richardson KR-20: 0.724). In addition to assessing knowledge and attitudes, the recognition of twelve AMR-related concepts by the participants was also assessed. Data collection was carried out between 01/03/2021 and 01/03/2022. Statistical analyses (descriptive statistics, non-parametric tests, Spearman's rank correlation, χ^2 test) were performed using IBM SPSS 25.0 software. Ethical approval ID (SZTE-RKEB): 170/2020-SZTE; 4851.

Results:

Among the $n=255$ participants in the study, 90.2% were female, 47.8% were employed in inpatient care, and their median age was 44 years (range: 21–67). The distribution of healthcare-related educational attainment was as follows: 30.6% held a vocational qualification (OKJ), 51.4% held a bachelors (BSc) degree, and 18.0% had a masters (MSc) degree. A majority (69.0%) identified their healthcare education as the primary source of their knowledge related to AMR. A positive self-assessment of academic achievement was associated with significantly higher knowledge scores (19.58 ± 5.37 vs. negative: 16.39 ± 5.42 ; $p=0.001$), more favorable attitudes (10.53 ± 3.06 vs. negative: 8.36 ± 2.66 ; $p=0.001$), and recognition of a higher number of AMR-related concepts (5.37 ± 1.95 vs. negative: 4.70 ± 1.55 ; $p=0.01$). No significant differences were observed in knowledge and attitude scores, or recognized AMR-related concepts based on age or level of educational attainment ($p>0.05$, respectively). Knowledge scores showed a positive, moderately strong, significant correlation with both attitude scores and the number of recognized concepts ($r=0.549$ and $r=0.470$; $p=0.001$ in both cases).

Conclusions:

Nurses and allied healthcare professionals play a key role in integrated, patient-centered healthcare and, within the framework of task-shifting, may acquire additional responsibilities and authorizations within healthcare systems, in the context of AMR. The knowledge and attitudes of healthcare professionals related to AMR may have important implications for their daily clinical practice, and these may be improved through targeted educational interventions.



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sciforum-117535: A Comprehensive Assessment of the Antimicrobial Resistance and Antibigram Profiles in Healthcare Settings Among the Indian Population

Dr. karthik sankar ^{1,*}, Dr. Mohathasim A Billah ¹, Dr. Sribal Selvarajan ², Dr.Madhumitha N ¹, Dr.Rangarajan S ¹, Dr.Monisha R L ¹ and Dr.Madesh L ¹

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Background:

Antimicrobial resistance is a critical global concern, impacting patient outcomes and healthcare costs. This study evaluates antibiogram data and resistance patterns among various sample cultures from a tertiary care center in India.

Methods:

A prospective cross-sectional study was conducted for the period of 2023 to 2025. Bacterial isolates from urine, blood, respiratory, and exudate cultures were identified using biochemical tests. The Kirby–Bauer disc diffusion method, which was recommended by CLSI's 2023 guidelines, was used to test for antibiotic susceptibility. The resistance patterns were analyzed for MRSA, ESBL, carbapenems, vancomycin, linezolid, tigecycline, and colistin. To look at the trends in resistance, antibiogram data were grouped for Gram-negative (*E. coli*, *Klebsiella*, *Pseudomonas*, *Enterobacter*, *Morganella*, *Acinetobacter*, and *Proteus*) and Gram-positive pathogens (*Enterococcus*, *Staphylococcus*, and *CONS*).

Results:

Among the Gram-negative bacteria, ESBL-producing *E. coli* (56%) and *Klebsiella pneumoniae* (62%) were predominant in the urine cultures, with *K. pneumoniae* showing 24% carbapenem resistance. The blood cultures showed that *K. pneumoniae* was resistant to 56% ESBL and 40% carbapenem. On the other hand, the respiratory cultures showed that *Enterobacter* spp. were resistant to ESBL the most (93.4%). The exudate cultures showed *E. coli* (75%) and *K. pneumoniae* (56%) with significant ESBL resistance. Among the Gram-positive bacteria, MRSA was found in 35.3% of blood infections and 27.3% of respiratory cultures. MRCONS exhibited 53.58% resistance in the blood, and VRE was detected in 9.1% of bloodstream infections. The antibiogram data showed that *E. coli* was highly susceptible to amikacin (93%) and imipenem (94%) in the urine, and *Pseudomonas* spp. were still highly susceptible to polymyxin B (100%) but not to ceftazidime (88%).

Conclusions:

This study shows that antimicrobial resistance is rising at an alarming rate, especially in bloodstream infections caused by ESBL-producing *E. coli* and *K. pneumoniae*, carbapenem-resistant *Acinetobacter* spp., and MRSA. These findings emphasize the need for stringent antibiotic stewardship to mitigate resistance spread, especially in developing countries.



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sciforum-115937: Prevalence of Antimicrobial Resistance Among Antibiotics in the WHO's AWaRe Classification Used to Treat Urinary Tract Infections in Diabetic Women

Ahmad Hamdan, Mohannad Natheef Abu Haweeleh *, Leena Al-Qassem, Amira Kashkoul, Izzaldin Alremawi, Umna Hussain, Sara Khan, Menatalla Elbadway, Tawanda Chivese, Habib Farooqui and Susu Zughaier

Qatar University, College of Medicine, Doha, Qatar

Abstract: Background and Objectives: Diabetes is linked to a higher risk of urinary tract infections (UTIs) in women, often leading to recurrent antibiotic treatment. Frequent antibiotic use for UTIs can contribute to antimicrobial resistance (AMR), a critical public health threat that increases treatment failure. This study investigated the prevalence of AMR and its associated factors among women with UTIs, comparing those with and without diabetes. **Results:** The study population had a mean age of 52 years (SD = 23) for women without diabetes and 68 years (SD = 14) for those with diabetes. Resistance was highest for cefazolin and levofloxacin in the Access and Watch antibiotic groups, while ciprofloxacin was the most frequently prescribed antibiotic. AMR prevalence was 35.7% among women with diabetes and 21.3% among those without. After adjustment, AMR was significantly associated with both uncomplicated diabetes (OR 1.14, 95% CI 1.08–1.21) and complicated diabetes (OR 1.54, 95% CI 1.45–1.64), as well as with higher numbers of prescribed antibiotics (OR 277.39, 95% CI 253.79–303.17). **Methods:** Using a cross-sectional cohort from the Physionet database, we analyzed data on 116,902 female participants treated for UTIs, including their antibiotic exposure, diabetes status, comorbidities, and hospital admission details. Antimicrobials were classified per the WHO's AWaRe criteria. The primary outcome was AMR identified in urine cultures, and the association with diabetes status was evaluated using multivariable logistic regression. **Conclusions:** Our findings highlight the need for focused antimicrobial stewardship in women with diabetes to reduce AMR rates in this vulnerable group.



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sciforum-115836: A systematic review: antimicrobial consumption surveillance and stewardship efforts in the former USSR countries

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Background/Objectives:

Antimicrobial consumption (AMC) and stewardship (AMS) are effective strategies to combat increasing antimicrobial resistance rates worldwide. Post-Soviet countries (Armenia, Azerbaijan, Belarus, Estonia, Georgia, Kazakhstan, Kyrgyzstan, Latvia, Lithuania, Moldova, the Russian Federation, Tajikistan, Turkmenistan, Ukraine, and Uzbekistan) have implemented essential components for AMC and AMS to different extents to inform and guide decision-making and amend their policies. This review assesses and characterizes the existing systems in post-Soviet countries.

Methods:

Papers were searched in PubMed, Google Scholar, Embase, CINAHL, CyberLeninka, and Scopus according to the inclusion criteria. This search also included gray literature covering the official sites of international and national health organizations. Three reviewers screened and then carefully assessed the articles using the JBI and AACODS appraisal checklists.

Results:

Eleven (73.3%) countries with updated national action plans for combatting antimicrobial resistance defined AMC and AMS as strategic directions or objectives. Fifteen (100%) countries submit antimicrobial consumption data to international networks. Yet considerable disparities exist in the complexity of the monitoring systems and data sources employed across the region, except for in Georgia, which does not use AMC data for policy adjustments. Across these nations, disparities exist in the implementation of key elements supporting AMS, with no related policies reported in Tajikistan; well-established guidelines and feedback mechanisms are reported in Belarus, Estonia, Kazakhstan, and the Russian Federation; ten countries (66.7%) document only the partial implementation of stewardship practices.

Conclusions:

The review provides key insights into the existing AMC and AMS implementation in the former USSR countries. Further efforts are needed to strengthen and expand antimicrobial stewardship programs, improve surveillance systems, and address key challenges in these regions.



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sciforum-112802: Antibiotic Therapy in Patients with Bacteremia Caused by *Escherichia Coli* or *Staphylococcus Aureus*

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Introduction:

Infections involving bacteria in the bloodstream pose a significant public health risk, potentially progressing to sepsis, which is often fatal. *Staphylococcus aureus* and *Escherichia coli* are recurrent pathogens in these infections, and effective treatment depends on the proper choice of antibiotics due to the growing issue of antimicrobial resistance. **Objectives:** The aim of this study was to evaluate the clinical management of bacteremias caused by *E. coli* and *S. aureus*. **Methodology:** This is a literature review study that used the PubMed and Virtual Health Library (VHL) databases, employing the following descriptors: bacteremia AND antibiotics AND *Staphylococcus aureus* OR *Escherichia coli*.

Results:

The search yielded a total of 394 articles, and after applying the selection and exclusion criteria, 9 articles were deemed eligible. It was observed that the treatment for methicillin-sensitive *S. aureus* includes penicillinase-resistant semi-synthetic penicillins, first-generation cephalosporins, and daptomycin. Beta-lactam anti-staphylococcal therapy is effective for methicillin-sensitive *S. aureus*, but combining it with daptomycin did not show additional benefits, as it did not reduce mortality or recurrence. For methicillin-resistant *S. aureus* cases, vancomycin or daptomycin is recommended. The combination of daptomycin with fosfomycin showed a 12% higher success rate, but without statistical significance. Ceftobiprole showed efficacy similar to that of daptomycin in treating complicated *S. aureus* bacteremias, with a success rate of 69.8%, making it an effective alternative. In bacteremias caused by *E. coli* producing extended-spectrum β -lactamases, carbapenems such as meropenem are the standard treatment. Fosfomycin is an alternative, but it is not superior to meropenem. Piperacillin–tazobactam demonstrated comparable efficacy to carbapenems, provided that the co-production of OXA-1 by *E. coli* was rare. **Conclusions:** The management of bacteremias caused by *S. aureus* and *E. coli* requires continuous monitoring of antimicrobial resistance and therapeutic efficacy. New treatments and approaches are crucial to address the growing threat of these infections.



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sciforum-118724: Comparative study on the Efficacy and safety of Gemifloxacin Versus Amoxicillin/Clavulanate in the management of Chronic Bronchitis

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Introduction:

Chronic bronchitis is a significant public health concern, often leading to recurrent exacerbations and impaired lung function. Effective antibiotic therapy is crucial to manage bacterial infections that exacerbate symptoms. Gemifloxacin, a broad-spectrum fluoroquinolone, and Amoxicillin/Clavulanate, a beta-lactam/beta-lactamase inhibitor combination, are commonly prescribed antibiotics for respiratory tract infections. This study evaluates the therapeutic efficacy and safety of Gemifloxacin versus Amoxicillin/Clavulanate in chronic bronchitis patients.

Method:

A randomized open-label clinical trial was conducted on patients diagnosed with chronic bronchitis experiencing acute exacerbations. During the study period, a total of 102 patients were enrolled in this study. Of these, 33 patients were in the Gemifloxacin 320 mg group and 35 patients were in the Amoxicillin/Clavulanate 625 mg group, whereas 34 were in the Amoxicillin/Clavulanate 1 gram group, based on the inclusion and exclusion criteria. During the study period, three patients were excluded from the Gemifloxacin 320 mg group, five patients were excluded from the Amoxicillin/Clavulanate 625 mg group, and four patients were excluded from the Amoxicillin/Clavulanate 625 mg group due to a lack of exact information. The data of the remaining 90 patients—30 patients in each group—were analyzed. Clinical symptoms, X-ray, PFT (FVC, FEV₁, FEF, (FEV₁/FVC), and bacteriologic assessments were performed for all patients.

Results:

Both Gemifloxacin and Amoxicillin/Clavulanate (625 mg and 1 gm) effectively reduced symptoms and improved lung function. The bacteriological success rate was found to be better in the Gemifloxacin 320 mg group compared with the Amoxicillin/Clavulanate 1 gram and Amoxicillin/Clavulanate 625 mg groups.

Conclusion:

Gemifloxacin 320 mg offers an effective alternative to Amoxicillin/Clavulanate 1 gram and Amoxicillin/Clavulanate 625 mg in the treatment of chronic bronchitis. The incidence of side effects was found to be lower in Gemifloxacin 320 mg, suggesting better tolerability when compared with Amoxicillin/Clavulanate 1 gram and Amoxicillin/Clavulanate 625 mg.



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sciforum-113160: Fosfomycin Sensitivity Among Enterobacterales and Enterococci in Urine Culture in British Columbia, Canada, 2023-2024

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Introduction:

Fosfomycin is a commonly prescribed antimicrobial for the prevention and treatment of urinary tract infections. The current study aimed to show the fosfomycin sensitivity among Enterobacterales and enterococci urinary isolates in communities in British Columbia (BC), Canada. The population data will help clinicians in predicting the effectiveness of fosfomycin when patients' urine isolate susceptibility results are pending.

Methods:

LifeLabs BC regional microbiology laboratories, connected with 129 collection centres in urban and rural communities in the province, provided the laboratory data. An audit was conducted on all urine cultures from October 2023 to September 2024. Antimicrobial susceptibility testing was performed and interpreted using the Clinical and Laboratory Standard Institute M100 guidance. Breakpoints for *Enterococcus faecalis* and *Escherichia coli* were extrapolated to all enterococci and Enterobacterales, respectively. Species with 30 isolates tested were excluded to reduce the risk of selection bias.

Results:

Microorganisms (Susceptible Isolates/Total Number of Isolates = % Susceptible)
Enterobacter cloacae complex (16/65= 25%)
Enterococcus faecalis (249 / 266 = 94%)
Escherichia coli (49272/ 50329 = 98%)
Klebsiella oxytoca (32 / 62 = 52%)
Klebsiella pneumoniae (333 / 522 = 64%)
Proteus mirabilis (107 / 139 = 77%)
Vancomycin-resistant Enterococcus faecium (35 / 60 = 58%)
Vancomycin-sensitive Enterococcus faecium (55 / 112 = 49%)

Conclusion:

Based on population data in BC, fosfomycin is likely effective against *Enterococcus faecalis* and *Escherichia coli* in urine (sensitivity >80%). Fosfomycin effectiveness is questionable against *Klebsiella pneumoniae* and *Proteus mirabilis* in urine (sensitivity 60-80%). It is likely ineffective against the *Enterobacter cloacae* complex, *Klebsiella oxytoca*, and *Enterococcus faecium* in urine (sensitivity 60%).



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sciforum-115299: Fourier Transform Infrared Spectroscopy-Based Detection of Amoxicillin and Ampicillin for Advancing Antibiotic Monitoring with Optical Techniques

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Introduction:

Amoxicillin and Ampicillin are among the most widely used antibiotics for treating bacterial infections. While traditional drug monitoring methods often face challenges relative to accuracy and analysis speed, optical-based techniques offer a promising alternative. Fourier transform infrared spectroscopy (FTIR), a well-established tool, is particularly suited for this purpose. This study introduces a novel approach to the standard methods of antibiotic detection and monitoring, leveraging the capabilities of vibrational spectroscopy and helping in antimicrobial stewardship.

Methods:

Principal Component Analysis (PCA) was used in the fingerprint region to detect differences between the studied antibiotics. Additionally, absorbance intensity in the fingerprint region was monitored to assess the degradation of each antibiotic over time. To achieve this, the area under the curve was calculated and subjected to inferential statistical tests for both intragroup (degradation of the same antibiotic) and intergroup (degradation within the same time interval, comparing the two antibiotics) comparisons. All analyses were performed in OriginLab and using Python in the Google Colab and Orange environment. For the calculations of the limit of detection (LoD), the method based on the calibration curve was used.

Results:

Through the experiments, it was possible to identify the fingerprints of each antibiotic and statistically separate them, despite both belonging to the same class of antibiotics, where the spectral peaks appear in the same region. For degradation, all tests were conducted with a significance level of $\alpha = 5\%$. In this investigation, our results show several quantification characteristics with a detection limit of 186.40 mM for Ampicillin (using peak ratio) and 81.40 mM for Amoxicillin (using peak intensity).

Conclusions:

This research demonstrates that FTIR spectroscopy is effective for antibiotic detection and has the potential to be further developed into a monitoring protocol.



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sciforum-115017: From Policy to Practice: Field-Level Regulation for Sustainable Antibiotic Stewardship in Bangladesh

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Antimicrobial resistance (AMR) is a pressing global health and development crisis. Low- and middle-income countries (LMICs), like Bangladesh, are disproportionately affected due to the weak enforcement of antibiotic regulations, pluralistic healthcare systems, and limited access to healthcare facilities in a predominantly rural population. Contemporary studies highlight the limited judicious use of antibiotics, despite a higher density of pharmacies in rural areas of Bangladesh.

This study investigates the field-level dynamics of antibiotic regulation in Bangladesh and its role in fostering sustainable stewardship practices, emphasizing a bottom-up approach to regulation to complement traditional top-down mechanisms.

Employing a qualitative, case-oriented design, this study relies on both primary and secondary data. Primary data were collected through key informant interviews, focus group discussions, and semi-structured interviews with district drug inspectors, community members, and local pharmacists, supplemented by official reports.

The findings reveal a gap between policy and practice, driven by institutional inefficiencies, power dynamics, limited stakeholder engagement, and inadequate public awareness at the field level. Among community respondents, 47.06% reported using antibiotics in the last six months, with almost half engaging in self-medication, and 52% were unaware of the legal restrictions on antibiotic sales.

This study advocates for an integrated regulatory approach that fosters stakeholder participation, strengthens district-level regulatory capacity, and aligns antibiotic regulation with broader public health goals. Strengthening field-level regulation and bridging the gap between policy and practice is crucial to promoting sustainable and effective antibiotic stewardship in Bangladesh.



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sciforum-115961: Navigating the Challenges of Antibiotic Stewardship

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1. Introduction

Background:

Antimicrobial resistance (AMR) poses a significant global health threat, increasing morbidity, mortality, and healthcare costs.

The WHO has recognized the urgency of this issue and emphasized the need for multi-sectoral collaboration to combat AMR.

Significance:

Antibiotic Stewardship Programs (ASPs) are crucial for mitigating AMR by optimizing antibiotic use, reducing unnecessary prescriptions, controlling infection spread, and improving patient outcomes.

Effective ASPs can contribute to preserving the effectiveness of existing antibiotics for future generations.

Research Question:

What are the primary obstacles encountered in the successful implementation and long-term sustainability of ASPs within healthcare settings?

2. Methods

Literature Review:

A comprehensive literature review was conducted using major databases (PubMed, Scopus, Web of Science, Embase, and the Cochrane Library).

Relevant articles were identified using a combination of relevant keywords.

Data were systematically extracted from selected articles, including information on the types of challenges encountered, strategies to overcome these challenges, and the outcomes of implementation strategies.

Data Analysis:

Qualitative analysis was conducted to identify and categorize common themes and patterns in the challenges encountered during ASP implementation.

If applicable, quantitative analysis was performed to further analyze and interpret the extracted data.

3. Results

Key Challenges identified were as follows:

Resource Limitations;

Organizational Barriers;

Patient-Related Factors;

External Pressures.



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sciforum-118737: Prescribing Antibiotics in dentistry: clinical insights and implications

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Inappropriate use of antibiotics has become a critical global health concern, significantly contributing to the rise of bacterial resistance. This alarming phenomenon represents a threat to public health, as antibiotic-resistant infections become increasingly difficult to treat and life-threatening. In 2019, bacterial antimicrobial resistance was linked to approximately 4.95 million deaths worldwide.

Dentists play a substantial role in antibiotic stewardship, as recent studies indicate that dental prescriptions account for nearly 10% of all oral antibiotic prescriptions—a percentage that has shown little to no decline over time. Prescribing patterns in dentistry often rely on empirical decision-making rather than evidence-based guidelines, leading to overuse, misuse, and inappropriate prophylactic or therapeutic antibiotic administration. This widespread mismanagement exacerbates the development of resistance, highlighting the need for evidence-based prescribing protocols and enhanced education on antimicrobial stewardship to mitigate unnecessary antibiotic use in dental settings.

To complicate the picture, chlorhexidine (CHX), the most widely used antiseptic in dentistry, is commonly applied for oral healthcare in the form of mouthwashes, toothpastes, gels, varnishes, and sprays. However, in recent decades, studies have supported its bacterial resistance to CHX across various species. The possible contribution of CHX to antimicrobial resistance through selective pressure requires thorough evaluation, and further research should investigate CHX resistance and potential cross-resistance with antibiotics in both clinical and environmental isolates.

This talk will provide a comprehensive overview of antibiotic use in dentistry and its clinical implications, including considerations regarding its combined use with CHX.



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sciforum-115042: Restoration of Antibiotic Effectiveness with *P. hartigii* Extract Against Multidrug-Resistant *E. coli*

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Studies on multidrug-resistant microorganisms, especially *Escherichia coli* (*E. coli*) strains, continue worldwide. In addition to the discovery of new antibiotics, there is also significant research on resistance mechanisms. One such mechanism is the efflux pump, which rapidly expels substances (antibiotics) from the bacterial cell or reduces their concentration. Therefore, the effectiveness of antibiotics can be restored by preventing this mechanism, and studies on potential inhibitors in this direction are ongoing.

In this study, the potential inhibitory effect of acetone extract obtained from *Phellinus hartigii* (*P. hartigii*) against drug-resistant *E. coli* strains was investigated. This was done by using the extract in combination with the antibiotics aztreonam (ATM 30 µg), cefixime (CFM 5 µg), amoxicillin–clavulanate (AMC 30 µg), piperacillin–tazobactam (TZP 36 µg), and ceftriaxone (CRO 30 µg) (Oxoid, UK).

For the first stage of inhibition, the Ethidium Bromide (EtBr) test was used with *P. hartigii* acetone extract. After observing inhibition according to the test results, antibiotic disks were applied together with the extract, antibiotic, and resistant strains. As a result of this study, it was observed that activities against *E. coli*#3 strain ATM (MIC 4), *E. coli*#10 strain ATM (MIC 8), *E. coli*#7 strain TZP (MIC >16/4), and *E. coli*#8 strain TZP (MIC >16/4) were restored. Based on these findings, *P. hartigii* acetone extract may have a potential efflux pump inhibitory effect, but further studies are required to explain this effect more broadly.

Acknowledgement: This study was supported by the Kastamonu University Scientific Research Project (KUBAP-01-2021-47).



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Session 2. Antibiotics and One Health

sciforum-118793: *Galleria mellonella* as a model to evaluate the effect of tetracycline against *Campylobacter coli* strains

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Campylobacter spp. is one of the leading causes of foodborne bacterial gastrointestinal illnesses in humans, primarily through chicken meat. The prevalence of antibiotic-resistant *Campylobacter* strains in chicken is increasing worldwide. This fact makes it necessary to evaluate antimicrobial effectiveness, particularly through in vivo models such as *Galleria mellonella* larvae (GML). In this work, GML were infected with strains of *C. coli* and treated with tetracycline (8, 12, 15, 20, and 40 mg/mL); after that, all groups were cultivated at 37°C for 4 days without feeding. In this period, mortality, bacterial load in hemolymph, and hemocyte count were assessed. The results showed that the group treated with 8 and 12 mg/mL of tetracycline had its mortality reduced to less than 10% in the first 3 days. In contrast, higher doses (15, 20, and 40 mg/ml) showed no significant difference compared to the infected group without antibiotic treatment. Bacterial load decreased by more than 3 log₁₀ in the first 0.5 hours in the treated groups. No difference was observed in the number of hemocytes between treated and untreated larvae. Treatment with tetracycline at 12 mg/ml was the most effective in reducing larval mortality and controlling *C. coli* infection. These results suggest the usefulness of the *Galleria mellonella* larvae model in evaluating antibiotic dosages against *C.coli*.



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sciforum-115980: Antibiotic Resistance Genes in Aquaculture: Environmental Hotspots and Public Health Implications

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The role of fish farming in the dissemination spread of antibiotic resistance genes (ARGs) has become an urgent environmental and public health concern. Fish farms, particularly those using intensive or semi-intensive aquaculture practices, serve as hotspots for the selection and proliferation of antibiotic-resistant bacteria (ARB). Labella et al. demonstrated a significantly higher incidence of multi-resistant bacterial strains in aquaculture centers (10%) compared to coastal areas (4%) in the Adriatic Sea [1]. Tetracycline resistance was particularly prominent, with up to 50% of bacterial isolates from specific zones, showing resistance. In contrast, resistance to flumequine remained low (0.3%), highlighting selective pressures imposed by antibiotic use patterns. Horizontal gene transfer, facilitated by mobile genetic elements, allows for the spread of ARGs among bacterial populations in fish farm effluents, sediments, and biofilms. Effluent water from aquaculture systems has been identified as a critical matrix contributing to ARG dissemination.

The frequent use of oxytetracycline, flumequine, and trimethoprim–sulfadiazine in fish farms exacerbates ARG selection. Studies have also shown cross-resistance, where exposure to older antibiotics like flumequine induces resistance to clinically relevant fluoroquinolones (e.g., ciprofloxacin), posing a direct threat to human health [2]. Furthermore, elevated water temperatures during summer were correlated with increased resistance incidence, suggesting environmental factors may amplify the selective pressures within aquaculture systems [2].

This review highlights the role of aquaculture practices in driving antibiotic resistance, with fish farms acting as reservoirs for ARBs and ARGs.

Reference: Labella, A., et al (2013). High incidence of antibiotic multi-resistant bacteria in coastal areas dedicated to fish farming. *Marine pollution bulletin*, 70 1-2, 197-203. <https://doi.org/10.1016/j.marpolbul.2013.02.037>.

Jo, H., et al (2021). Fish farm effluents as a source of antibiotic resistance gene dissemination on Jeju Island, South Korea. *Environmental pollution*, 276, 116764. <https://doi.org/10.1016/j.envpol.2021.116764>.



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sciforum-115955: Third-generation Cephalosporin-resistant *Escherichia coli* Isolates Belonging to High-risk Clones Obtained From Fresh Pork Meat in La Plata City, Argentina

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A high-risk clone is defined as being globally distributed, associated with multiple antimicrobial resistance determinants, able to colonise and persist in the host, capable of effective transmission between hosts, has enhanced pathogenicity and fitness, and can cause severe and/or recurrent infections. Since 2024, third-generation cephalosporin-resistant (3GC-R) *E. coli* has been included in the critical group of the WHO Bacterial Priority Pathogens List. This study aimed to determine the presence of high-risk clones among the highest priority critically important antimicrobials (HPCIA)-resistant *E. coli* isolated from fresh pork meat from butcher shops in La Plata, Buenos Aires, Argentina. Whole genome sequencing was performed on 85 HPCIA-resistant *E. coli* isolates, obtained from 46 butcher shops in La Plata. Of these, 27 belonged to nine clones described as High Risk: ST101 (n=5), ST10 (n=4), ST48 (n=4), ST744 (n=4), ST23 (n=3), ST58 (n=2), ST88 (n=2), ST117 (n=2) and ST410 (n=1) and 12 of them were 3GC-R. Resistance was mediated by *bla*_{CTX-M-55} (n=7), *bla*_{CTX-M-14} (n=4) and *bla*_{CMY-2} (n=1). *E. coli* harbouring *bla*_{CTX-M-55} belonged to ST10, ST23, ST58, ST88 and ST117. These were also fosfomycin-resistant mediated by *fosA3* (n=3) and *fosL1* (n=2), and potentially ciprofloxacin-resistant by plasmid-mediated quinolone resistance genes *qnrB19* and *qnrS1* (n=4). *E. coli* harbouring *bla*_{CTX-M-14} (n=4) belonged to ST23 and ST101 and were potentially ciprofloxacin-resistant due to *qnrS1* carriage. *E. coli* harbouring *bla*_{CMY-2} belonged to ST48, and all were fluoroquinolone-resistant, with one carrying *qnrS1* (n=1). The detection of high-risk clones in food products underscores the risk of transmission and highlights the urgent need for control strategies to mitigate the spread of pathogens implicated in cross-contamination and food safety, highlighting the importance of implementing good manufacturing practices.



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sciforum-106845: Wildlife and Antibiotic Resistance: Exploring the Case of Bears

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Antibiotic resistance in bears, while not as widely studied as in humans or livestock, has received increasing attention in recent years. This phenomenon primarily arises from human activities introducing antibiotic-resistant bacteria into wild ecosystems, where animals such as bears can be exposed. Due to habitat destruction and a lack of available food, it is very common for bears to rummage through landfills, where they might ingest bacteria that have developed resistance from exposure to antibiotics that are used in human medicine or agriculture. Another source of contamination is when water systems are contaminated, through which these bacteria can spread into natural habitats. The objective of this review is to describe the presence of antibiotic-resistant bacteria in bear species, their sources and their possible impact on the population. Concerning the available data, it is possible to observe that existing studies have focused on Sloth bears (*Melursus ursinus*), black bears (*Ursus americanus*), giant panda (*Ailuropoda melanoleuca*), polar bear (*Ursus maritimus*) and brown bear (*Ursus arctos*). The most observed species of bacteria were *Escherichia coli*. While the direct impact of antibiotic resistance on bear populations is still unclear, the presence of resistant bacteria in wild bears is concerning. It could make them more susceptible to infections that are difficult to treat, potentially affecting their overall health and survival. Antibiotic resistance in bears is an emerging area of study that highlights the far-reaching consequences of antibiotic overuse in humans and livestock. It illustrates how environmental contamination can spread resistance even to remote wildlife populations, underscoring the need for responsible antibiotic use and better waste management to limit this global problem.



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sciforum-115697: A High Presence of CTX-M-2-Producing *Escherichia coli* in Chicken Meat Obtained from Butcher Shops in La Plata City, Argentina.

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Global widespread extended-spectrum β -lactamase (ESBL)-producing *Escherichia coli* poses a significant threat in human healthcare and community settings. Chicken meat may be one of the critical transmission routes for those bacteria in the community. This study aimed to characterise 72 ESBL-producing *E. coli* isolated from 92 samples of chicken meat from 46 butcher shops in La Plata, Argentina. Antimicrobial susceptibility was evaluated using the disk diffusion method according to Clinical and Laboratory Standards Institute (CLSI) guidelines. The Whole Genome Sequencing (WGS) of the isolates were analysed on the Galaxy platform version 23.1. The ESBL resistance was mediated by blaCTX-M-2 (n=42), blaCTX-M-55 (n=14), blaCTX-M-14 (n=5), blaCTX-M-15 (n=5), blaCTX-M-65 (n=3), blaCTX-M-8, blaCTX-M-27, blaCTX-M-2/blaCTX-M-55 (n=1 of each one). Thirty-nine ESBL-producing *E. coli* harboured other plasmid-mediated genes that confer resistance to highest-priority critically important antimicrobial fosfomycin and ciprofloxacin. The gene fosL1 was principally associated with blaCTX-M-2 (n=15) and fosA3 exclusively to blaCTX-M-55 (n=7). The gene qnrB19 was associated with blaCTX-M-2 (n=13) and to blaCTX-M-55 (n=3) since qnrS1 was associated with blaCTX-M-15 (n=3) and to blaCTX-M-14 (n=1). Fourteen *E. coli* harbour genes conferred resistance to all three highest priority critically important antimicrobials (HPCIA): 3GC, fosfomycin and fluoroquinolones. All isolates were sensitive to carbapenems and colistin. ESBL-producing *E. coli* were multidrug-resistant (MDR), showing resistance to other groups of antimicrobial agents such as tetracyclines, amphenicols and aminoglycosides. Our results show a high circulation of ESBL-producing *E. coli*, resistant to other HPCIA that belong to CTX-M groups predominant in poultry and humans in Argentina. Future studies will be necessary to determine the origin of contamination of chicken meat within the production chain. The information obtained supports the promotion of measures that allow the implementation of strategies for the correct handling of food and prevent its transmission to humans.



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sciforum-114822: A Survey of Antimicrobial Usage/Consumption in Animal Production: a Cross-Sectional Study of Kaduna Metropolis, Nigeria

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BACKGROUND:

The use of antimicrobials in animals is a global practice against infections and for the enhancement of productivity. This study was aimed at monitoring antimicrobial usage/consumption (AMU/AMC) in animal production in Kaduna metropolis. Measuring AMU in animal production can provide useful data for monitoring AMU over time, which will assist in setting benchmarks to promote antimicrobial resistance (AMR) reduction.

METHOD:

This study involved the daily collation and validation of active primary drug sales and prescription data from thirty-two veterinary pharmaceutical outlets and clinics out of forty-one (41) pre-identified points within Kaduna metropolis (78%) over a 12-week period.

RESULTS:

Classes and types of antimicrobials that were identified included macrolides, quinoxalines, polypeptides, streptogramins, glycolipids, oligosaccharides, phosphonic acids, and polymeric compounds. In total, 83.7% of the identified antimicrobials were in the forms of oral medication, and most were registered antibiotics (52.8%). Parenteral and topical forms were also identified, with 94% also being antibiotics. The estimated AMU/AMC was 282mg/kg population correction unit (PCU). Poultry were the most significant population, constituting 99% (31,502,004) of the study population. The class-specific AMU/AMC was antibiotics, with 274mg/kg PCU (with the tetracyclines constituting 24.1%). The antiprotozoal AMU/AMC was 418mg/kg PCU, of which triazenetrones (17.1%) were mainly applied in the treatment of coccidia infections. The anthelmintic AMU/AMC was the highest at 576mg/kg PCU, with albendazole, piperazine, and levamisole being the most commonly used. These constituted 95.8% of the volume of anthelmintics and 16.5% of the volume of antimicrobials that were used in animals in the study. Oxytetracycline had the highest sale/usage for a single active agent at 9.6% of the volume.

CONCLUSION:

This study has provided useful and practical information on the trends in antimicrobial usage in animals, with poultry being the most important animal population involved in AMU/AMC and oxytetracycline being the most abused antibiotic in animal production. Antimicrobial stewardship (AMS) should be targeted at poultry populations, with an emphasis on reducing antibiotic usage/consumption.



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sciforum-115617: Antibiotic Prescription In Food-Producing Animals—A Focus Group Study To Assess Portuguese Veterinarians' Knowledge And Attitudes

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Introduction:

The inadequate use of antibiotics in humans, animals, and agriculture has been associated with the emergence and dissemination of antibiotic-resistant bacteria. To successfully tackle the public health problem of antibiotic resistance (ABR), it is necessary to take a One Health approach.

Methods:

Focus groups were carried out among Portuguese veterinarians whose practice was in production animals (bovine, swine, ovine, and caprine). The topic guide was constructed based on the information obtained from a previous systematic review. Qualitative analysis was performed using NVivo software.

Results:

Six focus groups were conducted, with a total of 19 veterinarians. From this study, four main themes emerged: (1) a lack of control of antibiotic use/drug residues in food-producing animals: surveillance/monitoring should be improved by investing in human resources/tools. The illegal access to drugs should be more strictly controlled, as it undermines antibiotic stewardship; (2) challenges in guideline adherence: guidelines should be simplified and adjusted for ABR and production animals. Authorization/access to vaccines used in other countries is difficult and time-consuming; (3) limited ABR knowledge: fear of animal loss drives antibiotic overuse/misuse; (4) client resource constraints: poor husbandry and delayed veterinary intervention, combined with veterinarians' workload and stress, contribute to inappropriate antibiotic use.

Conclusions:

To promote responsible antibiotic use in veterinary medicine, we need better monitoring systems, simplified guidelines, and increased vaccine access. Educational interventions for veterinarians and clients are essential, and collaboration among all stakeholders is vital for enhancing governance and ensuring sustainable antimicrobial practices.

Funding: Project 2022.04568.PTDC, supported by the Foundation for Science and Technology (FCT) in its state budget component (OE).



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sciforum-115940: Antimicrobial Resistance and Biofilm Formation in *Staphylococcus Aureus* Isolated from Retail Meat: Implications for Food Safety

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Staphylococcus aureus is a significant pathogen that can be transmitted through the food chain, often linked to antimicrobial resistance (AMR) and virulence factors, which contribute to its persistence and pathogenicity. Biofilm formation enhances its survival under adverse conditions and contributes to AMR dissemination. This study aimed to evaluate the antimicrobial resistance profile and biofilm formation of *S. aureus* strains isolated from meat samples and its implications for food safety. Seventy-five meat samples, including fresh meats and meat-based products, were collected in Northern Portugal. *S. aureus* strains were isolated and antimicrobial resistance was determined using the Kirby–Bauer disk diffusion method, against 14 antimicrobial agents. Resistance and virulence genes were evaluated by PCR. All samples were tested regarding their biofilm formation using the microtiter biofilm assay at 24 and 48 hours. Biofilm biomass quantification was performed via Crystal Violet staining. The results were normalized against the reference strain *S. aureus* ATCC® 25923 to ensure consistent comparison. *S. aureus* isolates were resistant to penicillin (52.6%), tetracycline (44.4%), chloramphenicol (36.8%) and tobramycin (26.3%). Resistance genes found were: *tetK* (31.58%), *cat*_{pc223} (21.05%) and *blaZ* and *ant(a')-Ia* (15.79%). All isolates demonstrated the ability to form biofilms at both 24 and 48 hours. Biofilm production was lower at 24 h, with a percentage mean of 114.34% ± 12.51, when compared to 48 hours, where it increased to 115.04% ± 22.43. However, these differences were not statistically significant ($p > 0.05$). Additionally, our isolates showed a higher biofilm production capacity when compared to the reference strain used. These findings highlight the public health risks posed by food-adapted *S. aureus*, particularly their role in promoting bacterial survival through biofilm formation, and AMR in food environments, emphasizing the need for targeted strategies to mitigate these risks in the food industry.



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sciforum-118767: Antimicrobial Resistance and Virulence in *Escherichia coli* from Broilers: Genetic Insights for One Health

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The widespread use of antibiotics in livestock has significantly contributed to the emergence and spread of antimicrobial-resistant bacteria, posing a risk for zoonotic transmission. The presence of multidrug-resistant *Escherichia coli* in poultry emphasizes the need for a One Health approach in monitoring antimicrobial resistance. This study aimed to determine the prevalence of *E. coli* in fecal samples from broilers, characterize their antimicrobial resistance profiles, and assess their genetic traits, including resistance genes, virulence factors, integrases, and phylogenetic groups.

Genomic DNA was extracted from 19 *E. coli* isolates obtained from broiler fecal samples collected at Savinor (Trofa, Portugal) using the boiling method. Resistance genes, integrases, virulence factors, and phylogenetic groups were identified by PCR. Only two isolates lacked resistance genes. The most prevalent gene was *ampC* (17/19), followed by *tetA* (12/19), *bla*CTX-M (11/19), and *qnrS* (7/19). Other detected genes included *bla*SHV, *bla*TEM, *bla*VIM, *aadA1*, *aadA5*, *sul2*, *strB*, *sul1*, *bla*IMP, and *aac(3)-II*. All isolates carried the *fimA* virulence factor, with five also harboring *aer*. The *int1* integrase gene was found in six isolates. Phylogenetic analysis showed that 12 isolates belonged to group A, five to B1, and two to D.

This study reveals the high prevalence of antibiotic-resistant *E. coli* in broilers in Portugal, underscoring the importance of regional surveillance. The combined analysis of resistance, virulence factors, and phylogenetic groups provides a broader understanding of the genetic traits that may enhance zoonotic potential. Resistance was mainly observed in typically commensal phylogroups, suggesting an adaptation to selective pressure in poultry environments. Stronger antimicrobial stewardship, including restricting critically important antibiotics, promoting alternatives like probiotics and vaccination, and improving farm hygiene, is crucial. Future research should focus on tracking resistance gene mobility and transmission pathways to inform public health strategies within a One Health framework.



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sciforum-115890: Antimicrobial Resistance In Enterobacteriales Isolates From Wild Foxes (*Vulpes Vulpes*)

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Antimicrobial resistance (AMR) is recognized as a global public health threat. Resistant bacteria have been disseminated in ecosystems with AMR in isolates from wildlife which were not directly exposed to antimicrobials has been reported. The aim of the present study was to detect AMR in Enterobacteriales isolates recovered from wild red foxes (*Vulpes vulpes*) in Latvia. Identified microorganisms were confirmed with matrix-assisted laser desorption/ionization (MALDI-TOF MS), and antimicrobial resistance was detected with the minimum inhibitory concentration (MIC) test. Antimicrobial resistance genes were identified with whole-genome sequencing (WGS). A total of 27 isolates of Enterobacteriales, including *Enterobacter cloacea* (1), *E. asburiae* (1), *Enterobacter coli* (21), *Hafnia alvei* (3) and *Salmonella* Typhimurium (1), were identified in 32 red fox faecal samples. Among the isolates, 19 (70%) did not exhibit resistance to any of the tested antimicrobials. None of the strains exhibited multidrug resistance. Resistances to ampicillin (4/27, 15%), colistin (3/27, 11%), azithromycin (2/27, 7%), ceftazidime (2/27, 7%) and cefotaxime (2/27, 7%) were the most frequently reported; the antimicrobial resistance pattern differed between Enterobacteriales species. *S. Typhimurium* was susceptible against all antibiotics tested. The most prevalent AMR genes were *acrF*, *blaEC* and *mdtM*. One *E. coli* (1/21, 5%) isolate was confirmed as extended-spectrum beta-lactamase producing *E. coli* (blaTEM-1). The present study highlights the presence of AMR in Enterobacteriales in foxes from areas without direct exposure to anthropogenic factors.



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sciforum-114704: Assessment of Gut Microbiota in Post-COVID-19 Patients

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Gut dysbiosis, exacerbated by excessive antimicrobial use, is a significant concern in patients with post-COVID-19 syndrome, often persisting beyond the resolution of SARS-CoV-2 infection. Dysbiosis contributes to microbiota imbalance and antimicrobial resistance, necessitating alternative approaches for rehabilitating post-COVID-19 patients.

A pilot study included 24 post-COVID-19 patients with gut dysbiosis (men: 45%). The ages of patients ranged from 46 to 80 years, with a median of 58 (51; 71) years. Intestinal content samples were obtained on the first day of admission from the 24 patients, who had recovered from the disease and received outpatient or inpatient treatment for periods of two to six months by the time of the study. Antibacterial therapy was administered in most patients during the stage of acute illness (third-generation cephalosporins or amoxicillin in combination with beta-lactamase inhibitors). The composition of the gut microbiota was analyzed using Colonoflor-16 (biocenosis) kits (AlphaLab, St. Petersburg, Russia), and real-time PCR detection (CFX 96, BioRad, Hercules, CA, USA) was performed on patients on the day of admission.

The levels of the *Bacteroides fragilis* group, *Klebsiella oxytoca*, *K. pneumoniae*, *Candida* spp., *Staphylococcus aureus*, *Proteus vulgaris* / *Proteus mirabilis*, *Enterococcus* spp., *Enterobacter* spp., and *Citrobacter* spp. exceeded the reference values by 1.5–2 times in the stool samples of patients. Additionally, the presence of *Clostridium difficile*, *Clostridium perfringens*, *Fusobacterium nucleatum*, and *Parvimonas micra*, microorganisms that are absent in the gut microbiota of healthy subjects, was detected. A high ratio of the *Bacteroides fragilis*/*Faecalibacterium prausnitzii* group was also found, which is a sign of anaerobic imbalance and inflammation.

These results support the need for further studies aimed at identifying and correcting intestinal microbiota dysbiosis in patients who have recovered from COVID-19.



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sciforum-115283: Characterisation Of Resistant Enteric Bacteria Isolated From Poultry Faeces and Meat In Portugal—Is There A Risk To Public Health?

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Introduction:

Foodborne diseases associated with resistant and multidrug-resistant (MDR) bacteria represent a significant public health concern, with food-producing animals being a major source of these infections. The aim of this study was to identify and to characterise *E. coli*, *Salmonella* spp., and *Shigella* spp. isolated from turkeys and chickens of Portuguese origin produced for human consumption.

Methods:

Between 2023 and 2024, 201 faecal samples (108 turkeys; 93 chickens), collected in various slaughterhouses, and 66 raw meat samples (33 each of turkeys and chickens), purchased in different retail stores, were analysed. Isolation was performed in selective and non-selective media. All isolates underwent to antimicrobial susceptibility testing and whole-genome sequencing.

Results:

No cases of *Shigella* spp. were detected and *Salmonella* spp. (*S. Newport*) was isolated from one turkey faecal sample (0.9%). *E. coli* was detected in 97.5% of faeces (100% in turkeys; 94.6% in chickens) and in 92.4% of meat samples (90.9% in turkeys; 93.9% in chickens).

Virulence genes of enteropathogenic *E. coli* (EPEC), extraintestinal pathogenic *E. coli* (ExPEC) and avian pathogenic *E. coli* (APEC) were identified in both animals. *S. Newport* was susceptible to all tested antibiotics. For *E. coli*, 78.1% faecal (74.1% in turkeys; 83.0% in chickens) and 78.7% (90.0% in turkeys; 67.7% in chickens) meat isolates were resistant to at least one antibiotic. The most common resistances were to ampicillin, tetracycline, and ciprofloxacin, and all isolates were susceptible to meropenem, ceftiofur and temocillin. A MDR profile was observed in 58.6% isolates (56.5% in turkeys; 61.7% from chickens), corresponding to 59.1% isolates from faeces and 56.8% from meat samples. Seven *E. coli* isolates (five from turkeys and two from chickens) were identified as extended-spectrum beta-lactamase (ESBL) producers (*bla*CTXM-15, *bla*CTX-M-55 and *bla*SHV-12), and eight isolates from turkeys carried the *mcr-1.1* gene.

Conclusion:

This study highlights the role of poultry slaughtered for human consumption and poultry meat as potential sources of human contamination with pathogenic and/or MDR isolates, underscoring the importance of the One Health concept.



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sciforum-118785: Correlation between use of antibiotics and prevalence of resistant strains of coagulase-positive staphylococci (*S. aureus*) in dairy farms in Apulia (Southern Italy)

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The spread of multidrug-resistant bacteria is a concerning problem worldwide. This preliminary study investigated the correlation between antibiotic consumption and the antimicrobial resistance trends of coagulase-positive Staphylococci (*S. aureus*) in raw milk from 154 dairy farms located in two provinces of the Apulia region in Southern Italy: Bari and Taranto. Data concerning antibiotic consumption expressed in DDDAit (Defined Daily Dose Animal for Italy) were extracted from the VETINFO portal. Data on antibiotic resistance (percentage of antibiotic-intermediate or -resistant isolates) were obtained from raw milk analysis performed at the laboratory of the Istituto Zooprofilattico Sperimentale di Puglia e Basilicata, Putignano (BA). The data collected suggest a strong correlation between the quantities of some antibiotics used (i.e. penicillins, aminoglycosides, cephalosporins, macrolides, lincosamides, fluoroquinolones and third-generation cephalosporins) and the prevalence of *Staphylococcus aureus* strains resistant to the molecules used (i.e. oxacillin, ampicillin, penicillin, amoxicillin/clavulanic acid, rifampicin, kanamycin, gentamicin, cefazolin, erythromycin, pirlimycin, enrofloxacin and ceftiofur). These data are in agreement with a previous study by Parisi et al. (2016) and may indicate a possible positive correlation between the use of antibiotics and the development of antibiotic resistance. This study, although preliminary, must be interpreted in the broader context of safeguarding public health: the presence of antimicrobial-resistant bacteria in dairy products, particularly those produced from raw milk, poses a potential risk of infection and/or colonization for humans, with limited treatment options and complications in treatment outcome. The overall data present a discrete indicator of antibiotic use and resistance patterns in Apulian dairy farms. A continued review of databases and a more rigorous use of antimicrobials therefore appear critical to minimizing the risk of the emergence of resistant organisms.



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sciforum-115570: Correlation of In Vitro Antibiogram With In Vivo Anti-Pathogenic Efficacy of Different Antibiotics Against Three Gram-Negative Bacterial Pathogens in the *Caenorhabditis Elegans* Infection Model

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Introduction: Though antibiogram generated through disc diffusion assay is a widely used method to assist the clinician in selecting appropriate antibiotics for patient treatment, correlation of in vitro efficacy of antibiotics with their in vivo efficacy needs deeper investigations.

Methods: The model host *Caenorhabditis elegans* was challenged with three different antibiotic-resistant gram-negative bacterial pathogens (*Pseudomonas aeruginosa*, *Vibrio cholerae*, or *Escherichia coli*) in absence or presence of the MIC---levels of those antibiotics belonging to different classes, to whom these pathogens were shown to be sensitive in disc diffusion assay. Worm survival was quantified over a period of five days through microscopic live-dead count.

Results: While ampicillin, ciprofloxacin, and tetracycline could offer significant protection to the worm population in face of *V. cholerae* challenge, streptomycin and clindamycin failed to do so. Streptomycin also could not rescue worms against *E. coli*. As ampicillin and ciprofloxacin were effective against *E. coli* too, antibiotic-response of both these pathogens in worm model can be said to have some commonality. While ciprofloxacin, a fluoroquinolone antibiotic effective against remaining two pathogens, could not protect the worm population from *P. aeruginosa* attack, another quinolone antibiotic ofloxacin could do this. Cefotaxime, a third-generation cephalosporin also failed to confer any protection on worm population challenged with *P. aeruginosa*. The correlation between 'MIC' and 'in vivo efficacy (as per first-day endpoint)' was stronger in case of *E. coli* ($r: -0.97$) than *P. aeruginosa* ($r: -0.53$). In case of *V. cholerae* ($r: 0.23$), antibiotics with lower MIC exhibited lesser in vivo efficacy than those with higher MIC. Correlation between 'diameter of zone of inhibition' and 'in vivo efficacy (as per first-day endpoint)' was found to be better for *V. cholerae* ($r: 0.62$) than remaining two pathogens.

Conclusions: Further investigation with a broader range of antibiotics and pathogens should be conducted to check whether in vivo assays with simple model hosts can be a better predictor of clinical efficacy of antibiotics, than the conventional disc diffusion or broth dilution assays.



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sciforum-118781: Detection of extended-spectrum beta-lactamase (ESBL)-producing *Klebsiella pneumoniae* in samples from meat rabbits

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Klebsiella pneumoniae is an opportunistic pathogen that can acquire multiple antimicrobial resistance mechanisms. The presence of multidrug-resistant *K. pneumoniae* in food-producing animals raises concerns about its potential role in the dissemination of resistance genes. This study aimed to investigate the occurrence of *K. pneumoniae* in healthy meat rabbits and characterize its antimicrobial resistance and virulence profiles.

A total of 295 fecal samples were collected from 20 rabbit farms in northern Portugal. Samples were incubated in BHI broth and plated on Chromocult Coliform Agar with cefotaxime (2 µg/mL). Pink colonies were subcultured on BHI agar and identified by MALDI-TOF MS. Antimicrobial susceptibility was assessed by the Kirby–Bauer method, and whole-genome sequencing was performed to detect resistance and virulence genes, as well as clonal lineages.

Out of the 295 samples, only 6 (2%) ESBL-producing *K. pneumoniae* were isolated. All isolates were multidrug-resistant, as they were resistant to at least three classes of antibiotics. All isolates carried ESBL-related genes, including *bla*_{TEM-1}(5/6), *bla*_{CTX-M-15} (2/6), and *bla*_{SHV} variants (*bla*_{SHV-1}, *bla*_{SHV-28}, *bla*_{SHV-38}, *bla*_{SHV-61}), as well as *bla*_{OXA-1} in two isolates. Genes associated with aminoglycoside resistance were identified in all isolates, such as *aph*(3'')-Ib, *aph*(6)-Id, and *aac*(3)-Ile/IVa. Tetracycline resistance was mainly mediated by *tet*(A) and *tet*(D), while sulfonamide resistance was conferred by *sul*1 and *sul*2. Among fluoroquinolone resistance genes, *qnr*B1 and *qnr*S1 were detected. The *fosA* gene, conferring resistance to fosfomycin, was also present. Genes associated with heavy-metal resistance (*sil* and *pco*) were found in all isolates. All isolates carried regulators such as *ramA*, *marA*, and *baeR*, which modulate efflux pump. Isolates were ascribed to ST307, ST45, ST193, and ST2026.

These findings reinforce the need for the continuous monitoring of antimicrobial resistance in *K. pneumoniae* from food-producing animals, as their potential role in the spread of resistance genes poses a risk to public health.



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sciforum-118638: Detection of proteins involved in antimicrobial resistance (AMR) in Bovine Milk bacterial consortia through proteomics and mass spectrometry

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The increasing threat of antimicrobial resistance (AMR) necessitates novel and complementary approaches to monitor and mitigate its spread in animal-derived biofluids such as milk. Our research applies omics sciences, particularly proteomics and metaproteomics, to detect AMR-related proteins and antimicrobial peptides (AMPs), providing crucial insights into the microbial consortia present in raw milk. By integrating liquid atmospheric pressure matrix-assisted laser desorption/ionization (LAP-MALDI) mass spectrometry (MS) profiling, bottom-up proteomics, and metaproteomics, we characterized AMR-related proteins in milk from intensive (Pezzata Rossa, Bruna Alpina, and Frisona) and non-intensive (Podolica) farming systems. Our findings revealed the presence of β -lactamases and tetracycline resistance proteins in all samples, confirming raw milk as a potential bioindicator of AMR circulation.

In parallel, our research also explored sustainable antimicrobial strategies by evaluating the inhibitory potential of plant-derived essential oils (EOs) against *Staphylococcus xylosus*, an opportunistic pathogen associated with bovine mastitis. An EO blend composed of *Myrtus communis*, *Salvia officinalis*, and *Cistus ladanifer* was tested alongside erythromycin for its antimicrobial efficacy. MALDI-TOF MS confirmed strain identification, and disk diffusion assays demonstrated a dose-dependent inhibitory effect of the EO blend, suggesting its potential as a complementary strategy to mitigate AMR.

These findings highlight the importance of integrating proteomics-based AMR surveillance with alternative antimicrobial strategies, such as phytocomplexes, to enhance food safety and reduce reliance on conventional antibiotics. Future studies will further investigate the synergistic potential of plant-derived antimicrobials in combination with existing therapeutic options.



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sciforum-118776: Evaluation of bio-based alternatives and natural biocides against azoles to mitigate fungal resistance in crops

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The massive use of azoles in agricultural and horticultural production has been described as a determining factor in the emergence of resistant strains, particularly of *Aspergillus* spp, which pose a significant threat to human and environmental health, according to a recent EU report under the "One Health" approach. This fact is linked to the non-medical use of azoles, according to a recent European Food Safety Authority (EFSA) report under the "One Health" approach. Approximately 120,000 tons of azoles have been placed on the market in the EU/EEA for non-medical uses, mostly as phytosanitary products, according to data analyzed between 2010 and 2021. Some compounds, such as epoxiconazole, used mainly in EU cereal, fruit, vegetables, and other crops, have proved highly resistant. However, because of regulatory advancements, the use of these compounds could be subject to a ban, which would impact the global farming sector. Environmental hotspots for resistance selection have also been identified, including the use and storage of agricultural residues and biocide-treated wood. Therefore, this systematic review aims to evaluate bio-based alternatives, assessing their efficacy, mechanisms of action, impact on harvesting, and limitations. Through a benchmark study with azoles, our work seeks to identify sustainability strategies that reduce the dependence on synthetic fungicides and promote safer and more effective agricultural practices. In addition, regulatory guidelines will be discussed to promote integrated approaches that support robust food security.



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sciforum-115943: Exploring the Role of Autochthonous Portuguese Hens in Antimicrobial Resistance Dissemination: A Study of *Escherichia coli* in Cloacal and Eggshell Samples

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Introduction:

The use of antibiotics in intensive animal farming is a significant contributor to antimicrobial resistance (AMR), which is a global public health concern. However, the role of autochthonous Portuguese laying hens as reservoirs of antibiotic-resistant *Escherichia coli* remains underexplored. These breeds, raised in extensive systems with minimal antibiotic use, provide a unique opportunity to study AMR under lower selective pressure. This study investigated the role of autochthonous Portuguese laying hens (*Preta Lusitânica*, *Amarela*, *Branca*, and *Pedrês Portuguesa*) as carriers of antibiotic-resistant *E. coli*, using cloacal and eggshell swabs to assess their antimicrobial resistance profiles.

Methods:

A total of 64 cloacal and 64 eggshell swabs were collected from 31 selected flocks (2 per flock, 16 per breed), yielding 67 *E. coli* isolates (33 from cloaca, 34 from eggshell). The isolates' susceptibility against 10 antibiotics was assessed following EUCAST/CLSI guidelines.

Results:

All cloacal isolates (100%) and 94% of eggshells isolates exhibited resistance to gentamicin. Additional resistance in cloacal isolates was observed to tetracycline (29%, *Branca*, *Pedrês Portuguesa*, and *Amarela*), ampicillin (14%, *Branca*, *Preta Lusitânica*, and *Amarela*), trimethoprim+sulfamethoxazole (14%, *Branca*, *Pedrês Portuguesa*, and *Amarela*), and amikacin (7%, *Branca* and *Amarela*). In eggshell isolates, resistance was observed to tetracycline (38%, across all breeds), ampicillin (15%, *Pedrês Portuguesa* and *Amarela*), amikacin (6%, *Preta Lusitânica*), and trimethoprim+sulfamethoxazole (3%, *Branca*). Resistance to at least one antibiotic was found in 100% of cloacal isolates and 97% of eggshell isolates. Multidrug resistance was identified in 14% of cloacal isolates (*Branca* and *Amarela*) and 18% of eggshell isolates (*Preta Lusitânica*, *Amarela*, and *Pedrês Portuguesa*).

Conclusions:

As sustainable poultry farming gains importance, this pioneering study provides valuable insights into the role of autochthonous hens in AMR transmission, emphasizing their impact on food safety and global AMR mitigation. Additionally, it explores whether native hens' by-products contribute to the spread of antibiotic-resistant *E. coli* through the food chain.

Acknowledgements: SALMYTH_GI2-CESPU_2022; FCT/MCTES – UIDB/50006/2020 and UIDP/50006/2020.



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sciforum-115949: Genetic Insights into *Acinetobacter bereziniae* IJ5: A Comparative Genomics Perspective

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Abstract

Introduction : *Acinetobacter bereziniae* IJ5 is a Gram-negative bacterium notorious for multidrug resistance and poses a significant risk for nosocomial infections. This study focuses on the genomic characterization of *A. bereziniae* strain IJ5, recovered from drinking water in Dhaka, Bangladesh. Through comparative genome analysis with other global strains, we determine its pathogenicity, virulence, and adaptation strategies.

Methods:

The genome of *A. bereziniae* was sequenced using Illumina MiniSeq, followed by assembly with Shovill on Galaxy and annotation through RAST and PGAP in NCBI. The bioinformatics analyses carried out revealed antibiotic resistance genes, virulome, toxin–antitoxin systems, secondary metabolites, and prophage sequences, with the goal of identifying the factors that contribute to its pathogenicity.

Result:

A unique combination of MDR genes such as qacG, adeF, OXA-355, and vanG was identified, coupled with diverse toxin–antitoxin systems consisting of RelE/RelB, ParE/ParD, and HigB/HigA, underscoring the high survival capability of IJ5. The genome of *A. bereziniae* IJ5 has a GC content of 38% and a total size of 4.4 Mb. The presence of distinct metabolic pathways, such as Ni-siderophores, RiPP-like compounds, and arylpolyenes, contributes to the resilience of IJ5 in clinical environments. IJ5's pathogenicity score of 77.2% indicates a strong potential to infect humans, enhanced by regulatory elements. IJ5 is closely related to the AB839 (Taiwan) and FFMG-36-12-21 (Tanzania) strains of *A. bereziniae*, as they share a common ancestor; additionally no other strains cluster with IJ5, portraying its unique sub-lineage.

Conclusion:

The genomic analysis of *A. bereziniae* reveals a distinctive mixture of MDR genes and toxin–antitoxin systems, showing an enhanced adaptability in clinical settings. A high pathogenicity score of 77.2% indicates strong infection potential, likely reinforced by regulatory elements. Comparative analysis further shows the genomic plasticity and persistence of IJ5, highlighting the necessity for continuous surveillance and research to develop targeted infection control and treatment strategies within Bangladeshi healthcare facilities.



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sciforum-108810: Identification and Quantification of Mixed Antibiotics in Aqueous Solution Through Machine Learning Analysis of SERS Spectra

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Introduction:

The accumulation of antibiotic residues in natural environments poses critical risks to public health and ecosystem stability due to their biochemical and physiological impacts. Ensuring water safety by preventing antibiotic contamination necessitates the development of rapid and reliable detection methods. Surface-enhanced Raman spectroscopy (SERS) offers high sensitivity and specificity in identifying small molecules but faces challenges in distinguishing individual antibiotics within complex mixtures.

Methods:

This study introduces a deep-learning-based model to analyze SERS spectra for the efficient identification of antibiotics in mixtures and precise determination of their concentrations. A simulated water environment with residues of ciprofloxacin, doxycycline, and levofloxacin was prepared. A computational framework combining a convolutional neural network (CNN) for classification and a non-negative elastic network (NN-EN) for quantification was applied to the SERS spectra data.

Results:

The CNN model achieved 98.68% accuracy in identifying individual antibiotics in mixtures. Additionally, the Shapley Additive exPlanations (SHAP) analysis highlighted the model's capacity to target specific spectral peaks, while the NN-EN model accurately quantified each antibiotic's concentration within the mixtures.

Conclusion:

The combined use of SERS with CNN and NN-EN models presents a promising solution for the rapid and accurate detection and quantification of antibiotic residues in water, potentially enhancing efforts to monitor and control aquatic contamination.



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sciforum-115960: Multidrug-Resistant *Klebsiella Pneumoniae* in Native Portuguese Cattle Breeds: A Public Health Concern

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Introduction:

The global increase in antibiotic-resistant bacteria, particularly multidrug-resistant strains, is diminishing antibiotic effectiveness. Livestock animals serve as reservoirs for these bacteria, threatening public health via the food chain and environmental contamination. *Klebsiella pneumoniae* is a significant pathogen, linked to fatal human infections, veterinary concerns, and multidrug resistance. This study aimed to phenotypically and genotypically characterize *Klebsiella* spp. isolated from fecal samples of four cattle breeds, Holstein–Friesian and three native Portuguese breeds—Barrosã, Cachena, and Minhota—in the Northern Region of Portugal.

Methods:

A total of 640 fecal samples were collected from 40 farms, pooled by age group (8 calves and 8 cows per farm) and inoculated on MacConkey and HiCrome *Klebsiella* Selective agar. *Klebsiella* spp. isolates (43 out of 63) representing breeds/age groups were selected for antibiotic susceptibility testing (CLSI guidelines) and PCR assays for identification and detection of resistance genes.

Results:

All 43 isolates were identified as *Klebsiella pneumoniae* and showed resistance to at least one antibiotic, with 100% of them being resistant to ampicillin. Barrosã and Cachena isolates displayed resistance only to ampicillin, while 17% (calves) and 13% (cows) of Minhota isolates demonstrated resistance to amoxicillin+clavulanic acid and tetracycline, respectively. Holstein-Friesian isolates exhibited resistance to multiple antibiotics, including amoxicillin+clavulanic acid (20%), cefotaxime (50%), aztreonam (30%), ciprofloxacin (20%), gentamicin (10%), tetracycline (80%), and trimethoprim+sulfamethoxazole (50%), all obtained from calves. Multidrug resistance was observed in 14% isolates, all from Holstein-Friesian cattle. ESBL activity was detected in 21% of the 43 *K. pneumoniae* isolates. From 42 tested isolates, the *bla*_{SHV} gene was detected in 67% of isolates, followed by *sul2* (43%), *aac*(3')-IV (43%), *bla*_{TEM} (33%), *bla*_{CTX-M} (14%), *tetB* (10%) and *aac*(6')-Ib-cr (10%), with a higher prevalence in calves.

Conclusions:

This work underscores, for the first time, the presence of multidrug-resistant *K. pneumoniae* in native Portuguese cattle breeds, highlighting potential risks to food safety and public health.

Acknowledgements: CoRECattle-GI2-CESPU-2022, EnteroGEN_GI2-CESPU_2023, FCT/MCTES-UIDB/50006/2020 and UIDP/50006/2020.



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sciforum-116060: Phenotypic Characterization and Serotyping of *Salmonella* Spp. and *Listeria Monocytogenes* Isolates From Feed Samples

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In addition to its presence in foods for human consumption, the foodborne pathogenic bacteria *Salmonella* spp. and *Listeria monocytogenes* can also be detected in animal feeding stuff.

The aim of this work was to phenotypically confirm the presence of the above microorganisms in feed samples, through biochemical and/or serological testing of the microbial isolates following the microbiological analysis for the detection of these pathogens. Thus, 15 strains of *Salmonella* spp. and 9 strains of *L. monocytogenes* were confirmed. Multiplex PCR was utilized to assign the isolated strains to the four most prevalent and most important public health-related *Salmonella* serotypes as well as to the four most frequently identified PCR-serogroups of *L. monocytogenes*.

Serotyping revealed the presence of *Salmonella* serotypes Thompson (60%), Typhimurium (6.7%) and Enteritidis (6.7%), whereas four strains were identified as *Salmonella* spp. (26.6%) but were not assigned to any of the detected serotypes. *L. monocytogenes* isolates were classified into the PCR-serogroups IIa (44.5%), IIb (11.1%), IIc (11.1%) and I/b (33.3%).

Furthermore, the bacterial isolates were screened for AMR. Strains of *Salmonella* spp. were susceptible to five of the antibiotics tested (tetracycline, norfloxacin, ciprofloxacin, gentamicin, meropenem), while they showed resistance to ampicillin (2/15), cefotaxime (7/15) and ceftazidime (5/15), without any multi-drug resistance being recorded whatsoever. *L. monocytogenes* strains were only susceptible to erythromycin and ampicillin, while one strain of the pathogen was multi-drug resistant to the remaining five antibiotics (tetracycline, penicillin, sulfamethoxazole, ciprofloxacin, meropenem). Moreover, the recorded AMR of *L. monocytogenes* isolates was as follows: tetracycline (11.1%), penicillin (11.1%), sulfamethoxazole (55.5%), ciprofloxacin (22.2%) and meropenem (11.1%).

The results of the present study demonstrate the presence of important foodborne pathogenic bacteria with increased AMR to antibiotics caused at the primary production and at the farm level by the inappropriate use of pharmacological substances used to treat animal diseases, resulting in the potential detection of resistant bacterial strains of the pathogens to animal-originated food products.



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sciforum-115130: Prevalence And Antibiotic Sensitivity Patterns Of Extended-Spectrum Beta-Lactamase-Producing *Escherichia Coli* In Selected Chicken Processing Plants In Ibadan.

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Poultry products are essential to global food security, yet they can also harbor foodborne pathogens, such as *Escherichia coli* (*E. coli*). While *E. coli* is a common bacterium in human and animal intestines, certain strains can cause severe gastrointestinal illness if consumed. Given the widespread consumption of poultry in Nigeria, ensuring the safety of chicken products is crucial for public health. Increasing antimicrobial use and expanding reservoirs in food animals like chickens have been associated with the rise in the prevalence of Extended extended-spectrum beta-lactamase-producing *E. coli* (ESBL-EC). This study aimed to assess the prevalence and antibiotic resistance patterns of *E. coli* strains and determine the antibiogram of Extended Spectrum Beta-Lactamase-producing *E. coli* isolated from chicken processing plants in Ibadan, Nigeria.

A total of 100 swab samples were collected from the packaging stage of the processing line of five chicken processing plants across three local government areas: Oluyole, Lagelu, and Ibadan Southwest in Ibadan, Nigeria. Samples underwent standard microbiological techniques for *E. coli* isolation and identification, followed by antibiotic susceptibility testing using the Kirby–Bauer disk diffusion method. The obtained data were analysed using descriptive statistics.

The investigation revealed concerning results, with 45 out of 100 samples yielding *E. coli* isolates. Overall, 40 were identified as ESBL-producing strains, and 5 as non-ESBL *E. coli*. Prevalence rates varied among processing plants and local government areas, with Ibadan Southwest Local Government showing the highest prevalence at 60% and Plants B and D showing the highest prevalence per plant. High resistance rates were observed among the isolates against commonly used antibiotics, including 93.33% resistance to cefotaxime and 88.89% resistance to ceftazidime. Additionally, 77.78% and 75.56% resistance rates were recorded for tetracycline and pefloxacin, respectively. Multidrug resistance (MDR) was also prevalent among 84.45% of isolates, with 12.5% demonstrating extended-drug resistance (XDR).



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sciforum-108072: Prevalence and associated risk factors of Vancomycin-resistant *Enterococcus faecium* in well water used for domestic purposes in Ile-Ife, southwestern Nigeria

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Introduction:

Vancomycin-resistant *Enterococcus faecium* (VREf) has become a major public health concern worldwide. Although hospital-based transmission is generally associated with outbreaks, contaminated water may play a role in the spread of VREf. This study determined the prevalence of VREf and identified associated risk factors in domestic wells in the study area.

Methods:

We assessed 350 wells for VREf, and questionnaires were administered to obtain information about well characteristics and owners' biodemographic data. Isolates were identified using biochemical and molecular methods. The isolates were tested against eight antibiotics using the Kirby–Bauer disc diffusion method, and the vancomycin minimum inhibitory concentration (MIC) was determined by the agar dilution method. The resistance (*vanA*, *vanB*, *msrA/B*, *mefA*, *mph (ABC)*) and virulence (*esp*, *gelE*, and *hla*) genes of VREf were detected by polymerase chain reaction. Data analysis was conducted with R statistical software.

Results:

Thirty-eight (10.9%) wells were contaminated by VREf, with counts ranging from 100 to 5000 CFU/mL. Wells sited near dumpsites, with ponding within three meters and split water collection, significantly harbored VREf ($p < 0.05$). All isolates (100%) exhibited resistance to tetracycline, linezolid, penicillin, erythromycin, and vancomycin. The vancomycin MIC of the isolates varied from 64 to 512 µg/ml. Twenty-seven of the thirty-eight isolates harbored only the *vanA* gene, while one harbored both the *vanA* and *vanB* genes. Five isolates harbored the *msrA/B* gene, three isolates harbored only the *mph(ABC)* gene, one harbored the *mph(ABC)* and *mefA* genes, and four harbored only the *mefA* gene. The virulence determinants *esp*, *gelE*, and *hla* were found in 2.6%, 29%, and 28.9% of the isolates, respectively.

Conclusion:

The presence of VREf in well water highlights the risk to human health associated with the use of untreated water. There is a need for periodic sanitation and inspection of wells to prevent ponding, split water collection, and possible outbreaks of waterborne diseases.



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sciforum-118119: Recent Knowledge on the Probiotic *Saccharomyces cerevisiae* in Aquaculture: A Narrative Review

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Aquaculture is a key food production sector responsible for meeting the nutritional needs of a rapidly growing global population. However, the emergence of disease outbreaks has become a major challenge for the aquaculture industry, resulting in significant economic losses. The use of costly and toxic antibiotics for treatment has a negative impact on the aquatic environment. Consequently, there has been growing interest in probiotics as a non-antibiotic approach to managing disease outbreaks and improving fish performance. The use of the yeast probiotic *Saccharomyces cerevisiae* has shown remarkable benefits in aquaculture. In February 2025, a narrative search was conducted on the Web of Science (WoS) database for the period 2015-2025 to identify relevant studies investigating the beneficial effects of *S. cerevisiae* in aquatic species. After searching WoS, 644 articles were found, and the most relevant articles were reviewed, summarized, and discussed. The probiotic *S. cerevisiae* has shown a wide range of benefits, including an improved growth performance, improved feed efficiency, enhanced diversity of the gut microbiome, and a superior immune response. The implementation of *S. cerevisiae* has been a recent trend, and its efficacy in aquatic environments has been thoroughly investigated. This review aims to provide a valuable insight into *S. cerevisiae* as one of the most important aquaculture probiotics and highlights the need for more research to fully understand its benefits and mechanism of action.



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sciforum-115911: The Emergence of Carbapenem-Resistant *Enterobacteriaceae* from *Camelus dromedarius* in the UAE: the first report of bla_{NDM}-positive *Escherichia coli*.

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Introduction:

The rising prevalence of carbapenem-resistant *Enterobacteriaceae* (CRE) poses a major public health threat, impacting the efficacy of last-resort antibiotics. In the United Arab Emirates (UAE), camels, vital to culture and the economy, may act as CRE reservoirs. However, the CRE carriage in farm animals across the UAE and Gulf Cooperation Council countries remains largely unexplored.

Objectives:

This pilot study aimed to evaluate the prevalence and genetic characteristics of carbapenem-resistant *Enterobacteriaceae* in camels in the UAE.

Methods:

Fecal samples from 12 camels on a Dubai farm were screened for carbapenem- and extended-spectrum β -lactamase-producing Gram-negative bacilli using selective culture techniques. The antimicrobial susceptibility testing followed the CLSI guidelines, while multiplex PCR was used to identify Carbapenemase genes. Whole-genome sequencing (WGS) revealed detailed genetic profiles, including the sequence types and global relatedness of the isolates. In total, 20 bacterial isolates were tested, and based on their plasmid profiles, WGS of 4 isolates was performed.

Results:

CR *Escherichia coli* was found in 8.33% (1/12) of the camels. The isolates carried the bla_{NDM} gene, conferring carbapenem resistance, but lacked the other tested Carbapenemase genes. Antimicrobial susceptibility testing showed multidrug resistance to multiple antibiotic classes. Among the four isolates, the **S101-C1** isolate (the ST648 complex) displayed an extensive resistance profile, harboring bla_{NDM-5}, bla_{CTX-M-15}, bla_{OXA-1}, bla_{TEM-1}, and resistance genes for aminoglycosides (aac(6)-Ib-cr5, aadA5), sulfonamides (sul1), tetracyclines (tet(B)), and macrolides (mph(A)). Resistance was augmented by efflux-associated genes (acrF/emrD/emrE) and mutations (ftsI_N337NYRIN, gyrA_D87N/S83L). Another isolate, **S101-E1** (ST155 complex), exhibited MDR, with the resistance genes bla_{CTX-M-15}, bla_{TEM-1}, tet(A), qnrS1 and a colistin resistance mutation (pmrB_Y358N). Efflux-related genes (acrF/mdtM) were also present.

Conclusion:

This study is the first to report the presence of *bla*_{NDM}-positive *E. coli* in camels in the UAE, suggesting that camels may serve as reservoirs for antimicrobial-resistant bacteria, including CRE. It highlights the potential risks of zoonotic transmission through direct contact or via the food chain.



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Session 3. Epidemiology, Prevalence and Mechanisms of Antibiotic Resistance and Cross-Resistance

sciforum-118484: Antibiotic susceptibility testing of *Escherichia coli* and coliform isolates detected in samples of drinking water from central Greece

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The drinking water cycle consists of the stages of untreated water, potable water, and sewage. *Escherichia coli* is considered an indicator of the faecal contamination of water, since it is a common bacterium of the intestinal flora of humans and warm-blooded animals and is a carrier of many antibiotic-resistance genes. The aim of this investigation was to assess the level of drug resistance of coliforms and *E. coli* isolates in samples of drinking water submitted from various sites of Central South Greece during the period 2018–2022. The highest resistance rates among both *E. coli* and coliform isolates were observed against ampicillin. The analysis of drug resistance conducted with reference to antibiotic groups indicated that most AMR and/or MDR isolates of *E. coli* or coliforms exhibited resistance against group A (ampicillin and amoxicillin/clavulanic acid). The most frequent phylogroup of the *E. coli* isolates was B1 followed by groups A and B2. The genus assignment for the coliform isolates other than *E. coli* was *Enterobacter*, *Citrobacter*, *Klebsiella*, and *Serratia*. In conclusion, various bacteria can be transferred from one stage of the drinking-water cycle to the next, either through the normal operation of the cycle or due to system failures, with the consequence that even drinking water contains various bacteria, pathogenic or non-pathogenic.



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sciforum-118725: Antibiotic resistance of *Staphylococcus aureus* isolated from raw beef sold in meat processing plants and markets

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Staphylococcus aureus (*S. aureus*) is a pathogenic bacterium capable of colonizing human and animal hosts while persisting on environmental surfaces. Due to its ability to spread via direct and indirect transmission, it poses a major risk for food contamination, necessitating stringent hygiene control throughout food storage, processing, and distribution.

This study aimed to detect the *S. aureus* contamination in raw beef and surface swabs from meat markets and assess antibiotic resistance. A total of 372 samples were analyzed: 160 from a meat processing plant and 212 from meat markets. *S. aureus* was identified using polymerase chain reaction (PCR) targeting the *nucA* gene, following the ISO 6888-1:2021 standards. Antibiotic susceptibility was assessed using the Kirby–Bauer disk diffusion method, with the results interpreted according to the CLSI M100-S27 guidelines. Resistance genes (*mecA*, *mecC*, *vanA*, and *vanB*) were detected using PCR.

No *S. aureus* was detected in the meat processing plant samples. However, 31.3% of the raw beef and 17.3% of the surface swabs from markets tested positive. The isolates from the raw beef exhibited the highest resistance to oxacillin, ampicillin, and penicillin. Over 50% of the surface swab isolates demonstrated resistance to oxacillin, tetracycline, azithromycin, and clindamycin. The *mecA* gene was found in 24.4% of the raw meat isolates and 35.7% of the surface swab isolates, whereas *vanA*, *vanB*, and *mecC* were not detected.

The high prevalence of *S. aureus* contamination and antibiotic resistance in meat markets presents potential public health risks. These findings emphasize the need for improved food safety measures, strict hygiene regulations, and responsible antibiotic use. Continuous surveillance and novel therapeutic strategies are essential for mitigating the risks associated with antibiotic-resistant bacteria.



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sciforum-117558: Antibiotic Susceptibility Profile Of Bacteria Isolated From Abacha Sold Within Ebonyi State University (EBSU) And Alex Ekwueme Federal University Ndufu-Alike Ikwo (FUNAI).

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Introduction:

Abacha, a traditional African salad made from processed cassava, is widely consumed in southeastern Nigeria, including Ebonyi State. Its preparation often involves exposure to open air, inadequate hygiene, and unregulated water sources, making it susceptible to bacterial contamination and foodborne illnesses. This study examines the antibiotic susceptibility of bacteria isolated from Abacha sold at Ebonyi State University (EBSU) and Alex-Ekwueme Federal University, Ndufu-Alike, Ikwo (FUNAI).

Methods:

Samples were collected from six vendors on both university campuses. Standard microbiological techniques were used for bacterial isolation and confirmation, while the disc diffusion method was applied for antibiotic susceptibility testing.

Results:

All six Abacha samples showed microbial contamination, with the highest levels found at the FUNAI front gate and the lowest levels found at EBSU Presco campus. Total bacterial and coliform counts exceeded tolerable limits, with counts above 10^4 (total viable count) and 10^1 (total coliform count). Identified bacteria included *Staphylococcus aureus* (20.0%), *Pseudomonas aeruginosa* (16.7%), and others. High resistance was observed against erythromycin, cefotaxime, and ampicillin (up to 80%).

Conclusion:

Ciprofloxacin (96.7%), colistin, and gentamycin showed the highest efficacy, likely due to their broad spectrum and lower resistance rates. These findings highlight the need for improved hygiene among street food vendors to reduce bacterial contamination and antibiotic resistance risks.



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sciforum-105269: Antifungal Resistance Profile of Yeast Involved in Vulvovaginal Candidiasis Infections in Pregnant Women in the Buea Regional Hospital

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Background:

Antifungal resistance is gradually becoming a much more frequent problem. The limited number of available drugs and growing resistance especially as it is a common infection with pregnant women mostly caused by *Candida albicans* has become a serious issue worldwide. Previous studies have shown that approximately 70-75% of women will have at least one episode of vulvovaginal candidiasis with half of that percentage having recurrent infection.

Objective:

The aim of this study was to determine the antifungal resistance profile of yeast involved in vulvovaginal candidiasis infections in pregnant women in the Buea Regional Hospital.

Method:

This cross-sectional study was carried out from the 20th of May to the 30th of June. The volunteers were given questionnaires in order to obtain their socio-demographic data and vaginal swab samples. The samples were cultured on Sabouraud Dextrose Agar, gram stain microscopy was done and susceptibility tests carried out to identify *Candida* strains. The data was recorded in Microsoft Excel 2010 and analyzed using SPSS version 20.

Results:

A total number of 92 participants took part in this research of varying ages with the highest percentage of 48(52.2%) being women within the age range 26-36 years. The prevalence was 51(55.4%) for positive cases and 41(44.6%) for negative cases. The prevalence of the species determined from the positive cases were 40(78.4%) for *C. albicans* and 11(21.6%) were non-*albicans* *candida* species. The sensitivity differed with the species that is, *C. albicans*: KCA-10 21(52.5%), and FLC-25 12(30%). None of the drugs were sensitive for non-*albicans* *candida* species (NAC).

Conclusion:

The limited antifungal drugs are growing highly resistant to yeast infections especially for NAC and the rate of infection amongst pregnant women remain quite high.



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sciforum-116994: Antimicrobial Resistance Profiles of Biofilm-forming *E. coli*, *Pseudomonas Aeruginosa*, and *Klebsiella Pneumoniae* Isolates from Chronic Wound Infection.

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Background

Antimicrobial-resistant (AMR) bacteria in chronic wound infections contribute to delayed healing, prolonged treatment, increased mortality, and rising healthcare costs. In resource-limited settings like Abakaliki, Southeastern Nigeria, improper antibiotic use worsens wound infection management. This study evaluates the antimicrobial resistance profiles of biofilm-forming *E. coli*, *Pseudomonas aeruginosa*, and *Klebsiella pneumoniae* and identifies antimicrobial resistance genes in chronic wound infections.

Materials and Methods:

From February to September 2024, pus samples from chronic wounds (≥ 12 weeks) were collected at Alex Ekwueme Federal University Teaching Hospital, Abakaliki. Bacteria were isolated using standard microbiological techniques, biofilm formation was assessed via Congo Red Agar (CRA), and antimicrobial resistance genes were detected through Polymerase Chain Reaction (PCR).

Results:

Of 600 samples analyzed, 476 (79.3%) had bacterial growth: *E. coli* (31.8%), *P. aeruginosa* (26.2%), and *K. pneumoniae* (21.3%). Biofilm formation was observed in 41.8% of the isolates, predominantly *P. aeruginosa* (19.8%), followed by *E. coli* (12.2%) and *K. pneumoniae* (9.8%). All isolates were resistant to amoxicillin–clavulanic acid (100%). *E. coli* showed high resistance to ceftriaxone (86.3%) and ampicillin (87.6%), while *P. aeruginosa* resisted colistin (100%) and cefotaxime (84.0%). *K. pneumoniae* exhibited resistance to ceftazidime (67.8%). No resistance was found against imipenem, ofloxacin, and gentamicin. *E. coli* carried *bla*CTX-M-9 (63%), *bla*TEM (54.7%), and *bla*SHV (41.1%), all *P. aeruginosa* harbored *bla*CTX-M-9, *bla*SHV and *bla*TEM (100 %) while *K. pneumoniae* harbored *bla*CTX-M-9 (100%) and *bla*TEM (49.1%). The *mcr-1* gene was present in all isolates.

Conclusion:

The AMR burden in Abakaliki presents a significant challenge in treating chronic wound infections. Addressing this issue requires antimicrobial stewardship, infection control, routine surveillance, education, and research to improve regional wound infection management.



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sciforum-108107: Antimicrobial Resistance Reduction challenges in Nigeria

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Antimicrobial resistance (AMR) poses a severe threat to public health and economic stability in Nigeria, contributing to the global estimate of 700,000 annual deaths, with projections of 10 million by 2050, if unaddressed. This study examines the challenges and drivers of AMR in Nigeria, alongside strategies and their outcomes. Key factors fueling AMR include public knowledge gaps, patient non-compliance, cultural misconceptions about antibiotic use, inappropriate prescribing, and irrational drug use in humans and animals. Despite institutional efforts to curb AMR through surveillance, infection control, and awareness campaigns, success has been limited due to persistent and evolving challenges. Results indicate that low public awareness and inadequate regulation enforcement continue to undermine reduction schemes, with antibiotic misuse remaining prevalent in both healthcare and agricultural settings. Compliance issues and cultural beliefs further complicate efforts, as patients often fail to complete prescribed treatments or misuse antibiotics based on misinformation.

To address these findings, this study proposes targeted recommendations. Sponsored ads and programmatic advertising during AMR Awareness Week can enhance public education, reaching diverse Nigerian demographics. Localized AMR-centered health talks at the community level, as well as the integration of foundational AMR courses into educational curricula, aim to bridge knowledge gaps. The continuous evaluation and adaptation of these strategies are critical to tackle emerging challenges effectively. While national strategies and research investments show some promises, their suboptimal impact highlights the need for innovative approaches. Implementing these recommendations could significantly reduce AMR's burden in Nigeria, improving public health outcomes, supporting economic development, and contributing to global security. This study highlights the urgency of adapting dynamic, inclusive interventions to combat the rising tide of antimicrobial resistance.



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sciforum-115803: Antimicrobial Susceptibilities of *Salmonella* and *Shigella* species isolates in stool culture in British Columbia, Canada, 2020-2023

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Introduction:

Hospital microbiology laboratories do not routinely allow for testing for community gastrointestinal stool pathogens in hospitalized patients who develop diarrhea after day 3 of hospitalization. In contrast, community microbiology laboratories routinely collect data on gastrointestinal stool pathogens, including their antimicrobial susceptibility profiles. To assist community antimicrobial stewardship, the current study aimed to summarize the susceptibilities of *Salmonella* and *Shigella* isolates in stool cultures performed in regional community microbiology laboratories in British Columbia (BC), Canada.

Methods:

LifeLabs BC microbiology laboratories, connected with 129 collection centres in urban and rural communities in the province, provided the laboratory data for the *Salmonella* and *Shigella* species that were isolated in stool cultures. An audit was conducted from January 1, 2020, to December 31, 2023.

Results:

Table 1: Antimicrobial Susceptibilities of *Salmonella* and *Shigella* species isolates in stool culture in British Columbia, Canada, 2020-2023

ORGANISM	Ampicillin	Trimethoprim-Sulfamethoxazole	Ciprofloxacin	Azithromycin	Ceftriaxone
<i>Salmonella</i> Paratyphi A, % susceptible	100	100	0	100	100
n =	6	10	8	6	11
<i>Salmonella</i> Typhi, % susceptible	100	100	0	100	100
n =	2	9	7	8	9
Other <i>Salmonella</i> species, % susceptible	91	94	89	0	98
n =	318	273	303	1	318
<i>Shigella boydii</i> , % susceptible	36	62	36	71	86
n =	14	13	11	7	14
<i>Shigella dysenteriae</i> , % susceptible	0	0	0	0	50
n =	2	2	1	1	2
<i>Shigella flexneri</i> , % susceptible	5	22	27	40	92
n =	95	87	92	45	95
<i>Shigella sonnei</i> , % susceptible	27	1	15	20	91
n =	131	122	125	59	131

(Results could be skewed for antibiotic susceptibility results with 30 isolates.)

Conclusion:

Salmonella Paratyphi A and *Salmonella* Typhi isolates in stool were universally susceptible to ampicillin, trimethoprim-sulfamethoxazole, azithromycin, and ceftriaxone. Choosing an oral antimicrobial agent for *Shigella* species is a challenge, as the sensitivities of oral agents were 50%. However, *Shigella boydii*, *Shigella flexneri*, and *Shigella sonnei* were >80% susceptible to intravenous ceftriaxone.



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sciforum-116129: Antimicrobial Susceptibility and Carbapenemases in *Pseudomonas Aeruginosa* Isolated From Children with Cystic Fibrosis

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Introduction:

P. aeruginosa is an opportunistic pathogen that is a major cause of morbidity and mortality in patients with cystic fibrosis and immunocompromised individuals. The eradication of *P. aeruginosa* is becoming increasingly difficult due to its ability to resist antibiotics.

Aim:

The aim of this study was to study the susceptibility to antimicrobial drugs and the presence of carbapenemases in *P. aeruginosa* isolates from patients with cystic fibrosis.

Methods:

Antibiotic susceptibility was determined by the broth microdilution method, whereas carbapenemases were determined by real-time PCR.

Results:

A total of 95 *P. aeruginosa* strains isolated in 2022-2023 were studied. Resistance to meropenem and imipenem was 14% and 56%, respectively. Sensitivity with increased exposure was 19% and 44%, respectively. Between 22% and 27% of isolates were resistant to aminoglycosides. A total of 21% and 14% were resistant to ceftolozane/tazobactam and ceftazidime/avibactam, respectively. Resistance to aztreonam, ciprofloxacin, ceftazidime and piperacillin/tazobactam was 16%, 37%, 29% and 28%, respectively. It is worth noting that we identified 2% of strains resistant to colistin. When performing PCR for strains resistant to meropenem and/or imipenem, it was determined that six isolates had VIM carbapenemase (NDM, IMP carbapenemases were not detected). All VIM+ isolates retained susceptibility to colistin, four isolates were also susceptible to amikacin and five isolates showed susceptibility with increased exposure to aztreonam.

Conclusions:

The resistance of *P. aeruginosa* to antibiotics of different classes ranged from 2 to 56%. Only six isolates were found to have metallo- β -lactamase VIM. Resistance to meropenem was demonstrated by 13 isolates and to imipenem by 52 isolates. Resistance to carbapenems in *P. aeruginosa* isolated from cystic fibrosis patients is probably associated with other properties of the bacterium.



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sciforum-114149: Antimicrobial Susceptibility Profiles of *Neisseria Gonorrhoeae* in British Columbia, Canada, 2023

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Introduction:

Nowadays, molecular testing is the gold standard for laboratory diagnosis of gonorrhea due to its superior sensitivity compared to culture. However, unlike culture, specimens collected for molecular testing cannot have susceptibility testing performed. The current study aimed to show the antimicrobial susceptibility profiles of *Neisseria gonorrhoeae* isolates identified by culture in British Columbia (BC) communities. The data helps answering whether the Canadian Guidelines on Sexually Transmitted Infections empiric preferred treatment (ceftriaxone monotherapy) or alternative treatment (cefixime plus doxycycline or cefixime plus azithromycin) require amendment.

Methods:

An audit was conducted on the susceptibility profiles of all culture-positive *Neisseria gonorrhoeae* isolates identified by LifeLabs BC regional microbiology laboratories, connected with 129 community collection centres, the largest network in the province of British Columbia, Canada. In 2023, 98 culture-positive *Neisseria gonorrhoeae* isolates underwent antimicrobial susceptibility testing in the provincial laboratory. Their results were interpreted using the Clinical and Laboratory Standard Institute (CLSI) M100 guidance.

Results:

The susceptibilities of *Neisseria gonorrhoeae* isolates were as follows: azithromycin 97%, cefixime 100%, ceftriaxone 100%, ciprofloxacin 27%, penicillin 7%, and tetracycline 39%. As per CLSI, organisms that are susceptible to tetracycline are also considered susceptible to doxycycline and minocycline.

Conclusion:

The preferred treatment of ceftriaxone with monotherapy is likely effective against *Neisseria gonorrhoeae* in the BC communities as 100% sensitivity was observed. Combination therapy with cefixime and azithromycin are also likely effective as 100% and 97% sensitivities were observed, respectively. Doxycycline should not be recommended as a monotherapy treatment or post-exposure prophylaxis of *Neisseria gonorrhoeae*, as its sensitivity was only 39%. Penicillin and ciprofloxacin did not appear to be effective treatment options in most cases.



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sciforum-115791: Bacterial Pathogen Profiles and Antibiotic Resistance in Pediatric Leukemia Patients: Insights for Optimizing Infection Management in Immunocompromised Children

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Background:

This study investigates bacterial etiology and antibiotic resistance in pediatric leukemia patients to determine the impact of chronic pathology on treatment efficacy. The study was made in Romania.

Methods:

Thirty cases of children aged 1–16 years (18 boys, 12 girls) were analyzed, identifying 13 pathogens, including 8 Gram-positive and 5 Gram-negative bacteria.

Results:

Among the patients, 11 girls presented with acute lymphoblastic leukemia (ALL) type B, while one boy and one girl had acute myeloid leukemia, and, as for boys, three had ALL type T and two had pre-B ALL. The most common pathogens were methicillin-resistant *Staphylococcus aureus* (MRSA, 11 patients), methicillin-sensitive *Staphylococcus aureus* (MSSA, 6 patients), *Klebsiella* spp., and *Staphylococcus epidermidis*. Due to the patients' compromised health, most required intensive care and strong antibiotic regimens, including linezolid, vancomycin, and ertapenem, which showed limited resistance.

Conclusions:

These findings highlight the critical importance of understanding bacterial resistance patterns to guide effective treatments in vulnerable populations. Knowing specific resistance profiles can be lifesaving, allowing for tailored therapies that improve survival rates in children with leukemia facing serious bacterial infections. Focusing on the dual aspects of pediatric patients and multidrug-resistant bacterial infections, this study aims to highlight the importance of addressing these factors together to enhance therapeutic approaches in vulnerable populations.



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sciforum-103781: Catalytic Production of Erythromycin Against COVID-19

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The outbreak of COVID-19 and the need to alleviate the virus's symptoms prompted the scientific community to explore alternative treatment methods, aiming to surpass the effectiveness of traditional medicine. This study examines the overall structure and catalytic mechanism of erythromycin's synthesis, as well as its industrial production, emphasizing its value against infectious diseases like COVID-19. Key points include the discovery of erythromycin, its broad clinical applications, and the pivotal role of P450eryF in its production. The significance of erythromycin and its biosynthesis catalyst, P450eryF, has led to collaboration between many countries with the World Health Organization (WHO) and the health industry. Between 2011 and 2021, erythromycin production increased globally. In particular, in Asia, South America, and Africa, the exportation of erythromycin antibiotics rose during the COVID-19 outbreak. In 2021, China was the top exporter of erythromycin (USD 185 M). Meanwhile, the leading importers were India (USD 104 M), with Japan and Croatia following. In the same decade, 60,046 erythromycin-related patents were published worldwide, with the U.S. holding the largest share at 36.88%. This analysis utilizes current production rates and published patents to review the latest statistics, highlighting global collaboration in erythromycin's production and its critical role in addressing global health challenges, as it remains a crucial antibiotic for treating diverse infectious diseases.



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sciforum-115332: Clinical Validation of New Rapid Molecular Diagnostic Method for Bloodstream Infections

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Introduction:

Bloodstream infection (BSI) is critical medical emergency associated with a high mortality rate. Rapid and accurate identification of the infectious agent and antimicrobial susceptibility is critical to initiating the appropriate, targeted therapy and improving patient outcomes. The aim of this study was to evaluate the performance of a Molecular Mouse System (MMS) for the rapid identification of Gram-negative bacteria (GNB) and their resistance genes directly from a positive blood culture (BC).

Methods:

A total of 80 positive BC samples from different clinical departments with microscopically detected GNB were analyzed using rapid molecular multiplex assays.

Results:

Compared to the routine culture methods, the MMS achieved a sensitivity and specificity of 98% for GNB detection. Only 2 out of 80 GNB (*Pseudomonas putida* and *Acinetobacter calcoaceticus*) were not identified by the MMS, as they were off-panel bacteria, while *Enterobacter aerogenes* was identified at the genus level (*Enterobacteriaceae*). However, in 2 out of 80 BC samples, the MMS revealed GNB that were not identified using culture-based methods but were later confirmed using the FILMARRAY™ multiplex PCR panel. In one polymicrobial sample, the MMS detected multidrug-resistant *Stenotrophomonas maltophilia*, which was not detected by the routine culture. The type of extended-spectrum beta-lactamase resistance gene (ESBL) detected using the MMS was mostly CTX-M-1/9 (n=19/20), alone or in combination with SHV-type β-lactamase or/and with one of the three different types of carbapenemase resistance genes (OXA-48, KPC, NDM). Furthermore, the MMS identified the resistance gene for the carbapenemase OXA-23 in an *Acinetobacter baumannii*-positive BC sample.

Conclusion:

These results suggest that the MMS is considered an effective and beneficial diagnostic method for faster therapeutic decision-making in patients with BSIs.



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sciforum-115920: Decoding Bel-1: Structural Insights into an Extended-Spectrum Beta-Lactamase with Carbapenemase-Like Disulfide Features from *Pseudomonas aeruginosa*

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Pseudomonas aeruginosa, a notorious pathogen, is responsible for severe human infections such as respiratory tract infections, soft tissue infections, and urinary tract infections. Beta-lactams are the cornerstone of treatment for these infections; however, the rise of beta-lactamase enzymes has steadily eroded their efficacy. Among these, **Bel-1**, a Class A extended-spectrum beta-lactamase (ESBL), stands out due to its unusual features resembling Class A carbapenemases, including a distinct Cys69-Cys238 disulfide bond. Despite this, Bel-1 primarily exhibits ESBL-like activity. To uncover its evolutionary trajectory towards carbapenemase activity, we conducted a detailed biochemical characterization of Bel-1 with various beta-lactam drugs. Interestingly, oxacillin inhibited Bel-1, consistent with its ESBL nature. Using isothermal titration calorimetry (ITC), we studied oxacillin binding and further explored substrate interactions by employing a deacylation-deficient mutant (E166A), enabling substrate-binding analysis without catalytic turnover. We crystallized the wild-type Bel-1 (PDB: 8JK3) and its E166A mutant (PDB: 8JOI), performing thermal melting and molecular dynamics simulations at various temperatures to examine the role of E166 in enzyme stability. These experiments revealed E166's crucial contribution to maintaining enzyme stability and its involvement in deacylation water positioning within the active site. While deacylation water was present in wild-type Bel-1, it was absent in the E166A mutant, underscoring E166's role in substrate processing. This study provides significant insights into Bel-1's behavior, delineating its distinctions from Class A carbapenemases and advancing our understanding of beta-lactamase evolution and function.



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sciforum-115916: Efficiency Of Routine Methods In the Detection Of Methicillin-Resistant Coagulase-Negative Staphylococci.

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Introduction:

Among the multiple mechanisms of acquired drug resistance in coagulase-negative staphylococci (CoNS), methicillin resistance appears to be the most important from a clinical and epidemiological perspective. According to the Clinical and Laboratory Standard Institute (CLSI) guidelines, the detection of *mec* genes is the gold standard for identification of staphylococcal methicillin resistance. In this study, we tested the efficiency of routine methods in the detection of methicillin-resistant coagulase-negative staphylococci strains (MRCoNS).

Methods:

Methicillin resistance was identified using cefoxitin (30 µg) and oxacillin (1 µg) by the disk diffusion method (DDM) on Mueller–Hinton agar (Becton Dickinson, Franklin Lakes, NJ, USA) per CLSI recommendations. Oxacillin MICs (Minimal Inhibitory Concentrations) were determined by the agar dilution method (ADM) according to CLSI recommendations [M07-A10]. To detect the *mecA* gene, *mecA* primers were designed. For *mecA*-negative CoNS strains, the *mecC* and *mecB* genes were tested by simplex PCR.

Results:

The sensitivity of the disk diffusion method to oxacillin compared to the detection of the *mecA* gene was 100%, while the serial dilution method for oxacillin had a lower value (87.1%). A lower sensitivity was obtained for the disk diffusion method for cefoxitin (69.7%), while the specificity of the disk diffusion method for cefoxitin was the highest, at 95.4%. A slightly lower specificity was obtained for oxacillin by the serial dilution and disk diffusion methods, at 90.6% and 87.1%, respectively. According to CLSI guidelines, the reference for phenotypic methods was the detection of *mec* genes by PCR.

Conclusions:

Oxacillin-based methods were highly sensitive in detecting *mecA*-positive CoNS strains. Due to the heterogeneity of MRCoNS, confirmation of methicillin resistance by different methods seems crucial. This can prevent the misidentification of MRCoNS and failed antibiotic therapy.



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sciforum-118780: Environmental dissemination of multidrug-resistant *Klebsiella* spp.: evidence from genomic surveillance of surface water

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Klebsiella spp. are opportunistic pathogens capable of acquiring antimicrobial resistance genes, posing a public health concern. Surface water can act as a reservoir for resistant bacteria, facilitating their dissemination in the environment. This study aimed to identify *Klebsiella* species in surface water and characterize their antimicrobial resistance and virulence profiles through whole-genome sequencing.

Water samples were collected from 77 sites in the Douro River Basin, Portugal, including rivers, streams, wells, and fountains. Water was filtered through a 0.45 µm membrane and incubated in BHI broth at 37°C for 24 h. Cultures were plated on Chromogenic Coliform Agar and subcultured on HiChrome *Klebsiella* Selective Agar. Purple colonies were subcultured on BHI agar and identified by MALDI-TOF MS. Antimicrobial susceptibility was evaluated using the Kirby–Bauer disk diffusion method, while whole-genome sequencing was conducted to identify resistance and virulence genes, along with clonal lineages.

Out of the 77 samples, 21 (27.3%) *Klebsiella* spp. were isolated. Among the isolates, thirteen *K. pneumoniae*, five *K. aerogenes*, two *K. michiganensis*, and one *K. oxytoca* were identified. Among *K. pneumoniae*, *bla*_{CTX-M-15}, *bla*_{TEM-1}, *bla*_{SHV} variants, and *bla*_{KPC-3} (3/13) were detected. Aminoglycoside resistance genes (*aph*(3'')-Ib, *aph*(6)-Id) and fluoroquinolone resistance genes (*qnrB1*, *qnrS1*) were present. All isolates carried *fosA* and heavy-metal resistance genes (*sil*, *pco*). Regarding the molecular typing, *K. pneumoniae* isolates belonged to a wide range of sequence types, including ST34, ST716, ST45, ST198, ST39, ST234, ST276, ST422, ST6, and ST37, while *K. oxytoca* was ascribed to ST155. *K. aerogenes* harbored *ampC*, *fosA9*, and efflux pump regulators (*ramA*, *marA*, *baeR*). *K. michiganensis* carried *bla*_{OXY-1}, *fosA*, and *qnrS1* (1/2), while *K. oxytoca* had *bla*_{OXY-2-8}, *fosA*, and *oqxA/B* efflux genes.

These findings highlight the presence of multidrug-resistant *Klebsiella* species in surface water, emphasizing the potential role of aquatic environments in the dissemination of antimicrobial resistance genes.



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sciforum-114904: ESBL-Producing *E.coli* in Ready-to-Eat Stuffed Mussels

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Foodborne bacteria play an important role in the spread of antibiotic resistance and complicate treatment processes. Regarding antibiotic resistance, extended-spectrum beta-lactamase (ESBL)-producing *E. coli* and carbapenem-resistant *Enterobacterales* are among the issues highlighted by the WHO. In this study, 200 ready-to-eat stuffed mussels from Istanbul were collected from various sales points (street vendors, kiosks, and restaurants) in 2024, and the presence of ESBL-producing *E. coli* was investigated. A total of 3.5% (7/200) *E. coli* was confirmed by PCR with 16S rRNA-specific primer. Antibiotic susceptibilities of the isolates to cefotaxime, ceftazidime, amoxicillin-clavulanic acid, meropenem, and ampicillin were measured by disk diffusion method. ESBL production in *E. coli* isolates was investigated using a double disk synergy test for phenotypic confirmation and *bla*_{OXA}, *bla*_{CTX-M}, *bla*_{SHV}, and *bla*_{TEM} gene presence by mPCR, and one isolate was found to contain the *bla*_{TEM} gene. The disk diffusion test and PCR investigated related carbapenem resistance, and *bla*_{NDM-1}, *bla*_{OXA-48}, *bla*_{VIM}, and *bla*_{IMP} genes were not observed in any isolate. This study is the first report of ESBL-producing *E. coli* isolate from ready-to-eat stuffed mussels in Türkiye. The presence of foodborne ESBL-producing *E. coli* threatens public health. It is necessary for food safety and global health to report the threats detected, especially in ready-to-eat products, and to take necessary measures.



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sciforum-115217: Evaluation of Antimicrobial Resistance in Magdalena, Colombia: Findings from a Retrospective Descriptive Study

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Antimicrobial resistance poses a critical challenge to global public health, complicating the treatment of common and life-threatening infections caused by bacteria, viruses, fungi, and parasites. This issue is particularly severe in developing regions, where factors such as the inappropriate use of antibiotics and inequalities in healthcare access contribute to the rise of multidrug-resistant strains. Unfortunately, Colombia is no exception to this growing problem. Nationally, hospital-associated infections caused by *Klebsiella pneumoniae* and *Pseudomonas aeruginosa* have become increasingly frequent, with resistance to broad-spectrum antimicrobials such as carbapenems being on the rise. Additionally, a descriptive analysis of bacterial isolates from intensive care units (ICUs) across twenty hospitals in twelve Colombian cities from 2019 to 2021 revealed a significant increase in the prevalence of multidrug-resistant microorganisms. In the most recent report (2019) on laboratory surveillance of antimicrobial resistance in healthcare-associated infections (HAIs) by the National Institute of Health (INS) of Colombia, the department of Magdalena exceeded national resistance rates for *Escherichia coli*, *K. pneumoniae*, *P. aeruginosa* (resistant to at least one carbapenem), and *Staphylococcus aureus* (oxacillin-resistant). However, no updated epidemiological data on antibacterial resistance in this region are currently available. This study presents an epidemiological analysis of the resistance profiles of pathogenic bacterial strains in the department of Magdalena, Colombia, during 2023–2024. A retrospective descriptive study was conducted using data from the Julio Méndez Barreneche University Hospital (HUIJMB) in Santa Marta D.T.C.H. The findings allow us to identify the most prevalent Gram-positive and Gram-negative bacterial strains in the region and explore potential risk factors.



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sciforum-115964: Genomic Insights Into Multidrug Resistance In *Pseudomonas Aeruginosa*, *Klebsiella Pneumoniae*, And *Escherichia Coli*: Implications For Cancer Patient Care

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Introduction:

Antimicrobial resistance is a critical concern, especially in immunocompromised cancer patients, where multidrug-resistant (MDR) and extensively drug-resistant (XDR) infections limit treatment options. This study investigates the resistance profiles of *Pseudomonas aeruginosa*, *Klebsiella pneumoniae*, and *Escherichia coli* isolated from cancer patients at a tertiary hospital.

Methods:

Clinical isolates from urine, blood, and sputum samples were collected from a tertiary hospital in Abu Dhabi. Antibiotic susceptibility testing was conducted using the disc diffusion method according to CLSI guidelines. Isolates were classified as CRE, MDR, or XDR based on resistance profiles. Genomic DNA was extracted using the Promega Kit, and whole-genome sequencing was performed on the Illumina platform. Resistance genes were identified using ResFinder, and plasmid incompatibility types were determined with PlasmidFinder. The genetic context of resistance genes, including IS elements and transposons, was assessed using ISfinder. Data analysis focused on resistance profiles, plasmid types, and potential clonal transmission.

Results:

A total of six *P. aeruginosa*, three *K. pneumoniae*, three *E. coli*, and additional isolates of *Aeromonas dhakensis*, *Salmonella enterica*, and *Stenotrophomonas maltophilia* were analyzed. *P. aeruginosa* isolates exhibited widespread resistance, including blaNDM-1 (carbapenem resistance), aph(3')-IIb (aminoglycoside resistance), and tet(A) (tetracycline resistance). *K. pneumoniae* isolates carried blaOXA-181 and blaCTX-M-15. *E. coli* strains harbored blaNDM-5 and blaCTX-M-15, along with aminoglycoside and fluoroquinolone resistance genes, with blaNDM-5 located on plasmids (MGEs) together with other resistance genes, facilitating their spread. Additional isolates included *Aeromonas dhakensis* from a leukemia patient, *Salmonella enterica* with IncFIB/IncFII plasmids from a breast cancer patient, and MDR *Stenotrophomonas maltophilia* from a cervical cancer patient.

Conclusion:

This study highlights the prevalence of MDR and XDR pathogens in cancer patients and the significance of plasmid-mediated gene transfer in resistance. Improved infection control and novel therapeutic strategies are critical to addressing these complex resistance mechanisms.



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sciforum-115679: Increased Prevalence of Invasive Pneumococcal Isolates and Reduced Penicillin Susceptibility of Non-Invasive Pneumococcal Isolates in Patients from Primorje-Gorski Kotar County (Croatia)

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Introduction:

Streptococcus pneumoniae is an important human pathogen responsible for both localized infections and invasive pneumococcal disease (IPD). Of particular concern is the increasing resistance to penicillin, the antibiotic of choice for the treatment of pneumococcal infections. As antimicrobial susceptibility varies by geographic location and the site of infection, the treatment guidelines must be derived from the local epidemiology.

Methods:

Surveillance was conducted at the Department of Clinical Microbiology, the Clinical Hospital Center Rijeka, in the period of January 2020 to December 2024. Invasive isolates were defined as strains collected from normally sterile sites (blood, pleural fluid, cerebrospinal fluid). The total number of pneumococcal isolates collected from inpatients and outpatients from Primorje-Gorski Kotar County, Croatia, was 925, of which 156 were invasive strains. All strains were tested for their antimicrobial susceptibility, with a focus on penicillin resistance.

Results:

The number of invasive isolates was twice as high in the period from 2022 to 2024 than that in the previous two years. More than 50% of invasive strains were isolated from adults over 65 years of age. The resurgence of pneumococcal infections can be explained by the gradual withdrawal of anti-COVID pandemic measures. A large number of all isolates showed a reduced susceptibility to penicillin, with significant differences between invasive and non-invasive strains (28% reduced susceptibility in invasive and 49% in non-invasive strains).

Conclusions:

The increasing trend of decreased susceptibility to penicillin observed in non-invasive pneumococcal strains is of great concern, as these strains, which have successfully spread in the population, are an important source of invasive infections and a reservoir of antimicrobial resistance. Rising penicillin resistance rates are affecting the treatment of IPD, especially pneumococcal meningitis. Nevertheless, parenteral penicillin is still the drug of choice for the treatment of pneumococcal pneumonia in Croatia.



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sciforum-115834: Intermittent Antimicrobial Treatments Enhanced The Persistence And Transfer Of Antimicrobial Resistance Genes In The Gut Microbiota

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Antimicrobial resistance (AMR) poses a significant threat to public health by compromising the effectiveness of infection treatments. Consuming food or water contaminated with AMR bacteria can lead to the transmission of resistant strains within the gut microbiota. However, the impact of intermittent clinical doses and prolonged sub-clinical exposure to antimicrobials on the persistence and transfer of AMR genes remains unclear.

To investigate this, five groups of mice were treated with ampicillin (Amp) administered in four intermittent clinical doses, with intervals of 20, 48, and 27 days between sequential treatments. During the intervals, the mice received additional tetracycline treatment in drinking water at concentrations ranging from 0 to 100 mg/L. The mice were orally inoculated with beta-lactam-resistant *Salmonella* Heidelberg carrying a mobile AMR plasmid (donor) following the first Amp treatment, *E. coli* labeled with green fluorescent protein (EC-GFP) as a recipient after the second Amp treatment, and beta-lactam-susceptible *S. Heidelberg* as another recipient after the third Amp treatment. Fecal samples were collected to enumerate donor, recipient, and transconjugant bacteria on selective agar media. Transconjugants were confirmed using qPCR targeting AMR genes.

The donor *S. Heidelberg* persisted throughout the experiment in all mice. Following each Amp treatment, the donor population reached a high density, but gradually declined until it became undetectable. The AMR plasmid was successfully transferred to commensal *E. coli*, EC-GFP, and the recipient *S. Heidelberg* after the first, second, and third Amp treatment, respectively. Tetracycline exposure enhanced both the persistence of the donor and the transfer of the AMR plasmid.

These findings underscore the significant impact of intermittent selective pressure on the persistence and transfer of AMR genes within the gut microbiota, reinforcing the need for more judicious antibiotic use to mitigate the spread of resistance.



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sciforum-115002: Prescribing Patterns and the Pharmacoeconomic Evaluation Of Antibiotics in the Pediatric Population Of A Tertiary Care Teaching Hospital—A Prospective, Observational Study

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Background:

Antibiotics are the most commonly prescribed drugs in pediatrics, which focuses on the medical treatment of newborns, children, and adolescents. Understanding and monitoring antibiotic prescribing patterns are crucial to ensuring their appropriate use, maximizing their benefits and minimizing harm. Cost minimization analysis is an effective tool for evaluating cost-effective strategies in pediatric healthcare.

Methodology:

This prospective observational study was conducted over ten months at Parul Sevashram Hospital, Vadodara, Gujarat. Following institutional ethics committee approval, 155 participants were enrolled based on the study-specific inclusion criteria. Data collected from the participants were evaluated against the WHO core prescribing indicators. A cost minimization analysis was performed on the antibiotic data. Statistical analyses were conducted using MS Excel and GraphPad Prism, and the findings were presented through percentages, tables, and graphical formats.

Results:

Our study involving 155 participants at Parul Sevashram Hospital, Vadodara, observed a higher proportion of males (65.16%) compared to females (34.84%). Most of the participants were aged 2 to 11 years (60.65%). Amoxicillin and Potassium Clavulanate were the most commonly prescribed antibiotics, with E. Coli being a prevalent pathogen. Polypharmacy was evident, with an average of 10.87 medications per prescription and many patients receiving more than three antibiotics. Injectable antibiotics were frequently used, though generic prescribing was below the WHO recommendations. The cost analysis revealed a significant price difference of 26% between the prescribed brands (INR 572,929.14/USD 6,851.20) and the suggested brands (INR 425,329.61/USD 5,086.05). This highlights the importance of cost-effective antibiotic choices.

Conclusion:

This study analyzed the antibiotic use in pediatric patients, focusing on the WHO's core indicators and pharmacoeconomic factors. It highlights polypharmacy and the prevalence of parenteral antibiotic treatment. Despite using generic names, the hospital does not meet the WHO's recommended range of antibiotics. A cost minimization analysis revealed significant differences between the prescribed and suggested brand formulations, highlighting opportunities for cost savings through generic or recommended substitutes.



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sciforum-113885: Prevalence And Antibiotic Sensitivity Pattern Of Extended-Spectrum Beta-Lactamase-Producing *Salmonella* Spp. In Poultry Meat From Selected Processing Plants In Ibadan, Nigeria

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Background:

Poultry meat constitutes a global food supply. *Salmonella* spp., a major foodborne disease, poses economic and public health risks. Extended-Spectrum Beta-lactamase (ESBL)-producing *Salmonella* spp. have consistently posed a challenge to antibiotic therapy. There is a dearth of information on the prevalence of ESBL *Salmonella* in poultry processing plants in Ibadan, Nigeria. This study investigated the prevalence of ESBL-producing *Salmonella* spp. in poultry processing plants in Ibadan, Nigeria, and determined its antibiotic resistance pattern.

Methods:

A total of 153 chicken swab samples were collected from processed birds at packaging points in five processing plants with high processing capacity (2000-6000) in Ibadan, Nigeria. Isolation of *Salmonella* spp. was performed using standard procedures. Antibiotic sensitivity testing, ESBL isolates, and data analysis were conducted using the Kirby-Bauer disc diffusion method, the double disc diffusion test, and descriptive statistics, respectively.

Results:

Overall, the prevalence of *Salmonella* spp. was 56 (36.6%). The antibiotic susceptibility profile revealed a high prevalence of multidrug resistance, MDR (64.3%; 36/56), and extensive drug resistance, XDR (20/56; 35.7%), among all *Salmonella* spp. isolates. The prevalence of ESBL *Salmonella* spp. and non-ESBL *Salmonella* spp. was 2.6% (4/153) and 34% (52/153), respectively. Furthermore, all ESBL *Salmonella* (100.0% 4/4) isolates were MDR and XDR, while 57.7% (30/52) and 28.8% (15/52) of non-ESBL *Salmonella* spp. were MDR and XDR, respectively. Five different antibiotypes of non-ESBL *Salmonella* were found, with MEM-TE-SXT-PEF (54%; 28/52) being predominant. However, ESBL *Salmonella* spp. presented one antibiotype (MEM-CAZ-CTX-SXT-TE-PEF) (100%; 4/4) resistance to all antibiotics tested.

Conclusion:

The high rate of MDR and XDR ESBL *Salmonella* isolates highlights the need for control over antibiotic use. A 50% reduction in antimicrobial use in food by 2030 and the development of new therapies like bacteriophages, peptides, and probiotics are crucial. Enforcing rational antibiotic use, strict hygiene, and national surveillance systems are essential to combating antimicrobial resistance.



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sciforum-108588: Prevalence and Antibiotic Sensitivity Patterns of Methicillin-resistant and Methicillin-sensitive *Staphylococcus aureus* in Dogs in Ibadan, Nigeria

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Background:

Staphylococcus aureus is among the leading causes of bacterial infections worldwide. Methicillin-resistant *Staphylococcus aureus* (MRSA), which is of public health importance, is gaining interest in veterinary medicine due to its zoonotic potential. Dogs are a major reservoir for zoonotic-infection-causing bacteria, including MRSA. This study investigated the prevalence of MRSA and MSSA in dogs in Ibadan, Oyo State, Nigeria, and determined their antibiotic resistance patterns.

Methods:

A total of 173 nasal swab samples were collected from dogs in residential areas of Ibadan, Nigeria. *S. aureus* was isolated using standard microbiological procedures. Furthermore, Antibiotic Sensitivity Testing was performed using the Kirby–Bauer disc diffusion method. The data obtained were analysed using descriptive statistics.

Results:

Overall, the prevalence of *Staphylococcus aureus* was 44/173 (25.4%). The prevalence of MRSA was 11.6% (20/173), while that of MSSA was 13.9% (24/173). Also, the frequency of antibiotic resistance in the MRSA (75%) isolates was higher than that in the MSSA (59.5%) isolates. The antibiotic susceptibility profiles revealed a high prevalence of multidrug resistance, MDR (79.5%; 35/44), and Extensive Drug Resistance, XDR (11.4%; 5/44), in all *S. aureus* isolates. Additionally, 100% (20/20) of MRSA and 66.7% (16/24) of MSSA showed MDR. Also, 25% (5/20) of MRSA and none of the MSSA showed XDR. This study revealed five different MRSA antibiotypes, where FOX-TE-P-AMP-E, at 60% (12/20), was predominant; likewise, five different MSSA antibiotypes were found, and TE-P-AMP-E, at 45.8% (11/24), was predominant.

Conclusion:

The high multidrug resistance and the occurrence of MRSA and MSSA are evidence of continuous antimicrobial exposure, indiscriminate access to and use of antibiotics, and a dense urban population, making the transfer and acquisition of resistance genes easy. It is strongly advised to implement and enforce infection control measures and promote responsible antibiotic usage at all levels to enhance overall public health outcomes.



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sciforum-114856: Prevalence and phenotypic and genotypic characteristics of *Staphylococcus aureus* isolated from small ruminants with mastitis in Sardinia, Italy

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Mastitis is a prevalent condition affecting small ruminants, leading to significant economic losses, attributed to decreased milk production and inferior milk quality at a global scale. This issue is particularly pronounced in the rural regions of the Mediterranean, where nearly two-thirds of the world's sheep and a quarter of the global goat milk supply is generated. The present study sought to explore the epidemiology, genetic diversity, antimicrobial resistance profiles, and virulence factors associated with *Staphylococcus aureus* isolated from sheep and goat suffering from clinical mastitis in Sardinia, Italy.

A total of thirty-four isolates obtained from clinical mastitis cases across 26 dairy farms were characterized through whole genome sequencing and phenotypic assessments of antibiotic resistance.

All isolates were confirmed to be phenotypically methicillin-sensitive *S. aureus* (MSSA). A small proportion of the isolates exhibited resistance to tetracycline (12.5%) and erythromycin (3.12%). The isolates were categorized into seven distinct sequence types, with ST133 (n = 15) and ST700 (n = 9) being the predominant types. All isolates that were resistant to tetracycline contained either the *tetM* or *tetK* gene.

The distribution of certain clusters across various regions demonstrates the ongoing presence of cluster-related infections. Despite all isolates being derived from clinical mastitis cases, they exhibited minimal resistance to the antimicrobials tested. This suggests that the farms surveyed have implemented highly effective hygiene practices, alongside routine antimicrobial resistance testing and the judicious use of antimicrobials to prevent the development of resistance. This approach aligns with the current agricultural regulations, particularly the enforcement of EU legislation. This could result in a reduction in the disease burden and an improvement in animal welfare.



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sciforum-116925: Serological Typing and Antibiograms of *Listeria Monocytogenes* Strains Isolated from Raw Milk, Whey and Ice cream

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Listeria monocytogenes is a well-known foodborne pathogenic bacterium responsible for severe diseases in humans and animals. Additionally, the increase in antibiotic resistance rates of *L. monocytogenes* strains after exposure to preservatives, antibiotics, and stress conditions has become another major public health issue. This study focuses on the serological identification of 11 *L. monocytogenes* isolates from milk (n=1), whey (n=2), and ice creams (n=8) and the investigation of the pathogen's antibiotic resistance. The serological typing of the strains involved using multiplex PCR for each of the strains, with 63.6% of them belonging to serogroup IVb, 27.3% to serogroup IIb, and 9.1% to serogroup IIa. It was noteworthy that all the strains of serogroup IVb, which includes serotype 4b, most commonly responsible for listeriosis outbreaks in humans, were isolated from one of the three companies from which the samples were taken, and concerned the ice cream production line. Regarding the antibiotic resistance of the strains, antibiograms of the pathogen isolations were assessed against a group of seven selected antibiotics (erythromycin, tetracycline, penicillin, trimethoprim–sulfamethoxazole, ampicillin, ciprofloxacin, and meropenem) which showed that six strains exhibited resistance to at least one of the examined antibiotics, while no strain exhibited resistance to ampicillin and meropenem, with the former being the drug of choice for the treatment of listeriosis. Two strains of serogroups IIb and IVb exhibited resistance to four and three antibiotics, respectively. The findings of this study are useful and could be utilized for epidemiological research on *L. monocytogenes* in the food-processing environment, revealing potential contamination scenarios, resistance to sanitization, and the persistence of the pathogen in the food-processing environment, as well as acquired microbial resistance along the food production chain.



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sciforum-115070: Surviving the Greek Gift: Gallium Resistance

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The public health crisis of antibiotic resistance has spurred studies of nonconventional antimicrobial approaches. Gallium is a promising and emerging approach to treating multidrug-resistant bacteria via a Trojan horse-like antimicrobial strategy or the physical disruption of bacterial activity. This study utilized experimental evolution to test the evolvability of gallium resistance in *Staphylococcus aureus* and potential correlated traits in metals, antibiotics, and polyfluorinated compounds and their genomics foundations. Whole-genome sequencing was utilized to reveal the functional networks of mutations associated with gallium resistance. Additionally, scanning electron microscopy (SEM) observation was used to visualize the distinct morphological changes on the surface of the gallium-resistant populations and compared to the control populations. As demonstrated by these studies, *S. aureus* evolved resistance to gallium after 20 days of selection. Furthermore, these populations displayed correlated traits to heavy metals, and polyfluorinated compounds. In contrast, the gallium-resistant populations were very sensitive to antibiotics. Whole-genome analysis revealed significant polymorphisms in the gallium (III)-resistant populations including, staphyloferrinA export MFS transporter/D ornithine citrate ligase (*sfaA/sfaD*), teichoic acid D Ala esterase (*fntA*), DUF3169 family protein (KQ76_RS01520), and adenine phosphoribosyltransferase (KQ76_RS08360), while the following polymorphisms in ABC transporter permease subunit (*pstC*) and acyltransferase family protein (KQ76_RS04365) were unique to the control populations. Polymorphisms directly affected the cell's morphology. SEM images showed significant external ultrastructural changes in the gallium-selected bacterial cells compared to the control cells. Our study confirmed that using gallium as antimicrobials can have significant health and environmental implications.



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sciforum-115726: The Antimicrobial Susceptibility Of Cefiderocol, A Novel Siderophore Cephalosporin, Against Clinically Isolated Carbapenem-Resistant Gram-Negative Bacilli From A Tertiary Care Hospital Of Punjab, Pakistan

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INTRODUCTION:

With the increasing prevalence of carbapenem-resistant isolates, it is imperative to identify and evaluate alternative treatment options to improve patient outcomes. Cefiderocol, a novel siderophore cephalosporin, is highly effective against these organisms and studies advocate its preferred use in clinical practice. A lack of local published material necessitated the present study, which is aimed to determine the antimicrobial susceptibility of cefiderocol against carbapenem-resistant Gram-negative bacilli isolated from various clinically significant specimens.

METHODS:

This cross-sectional study was carried out in the Microbiology Laboratory of the Combined Military Hospital, Lahore, Pakistan over a duration of 6 months. The clinical samples from 145 patients with carbapenem-resistant isolates were tested for susceptibility against cefiderocol (CLSI 2022). The results were then compared across various subgroups.

RESULTS:

The mean age of the patients was 45.8 ± 15.8 years. There were 114 (78.6%) male and 31 (21.4%) female patients with a male-to-female ratio of 3.7:1. The majority of the samples comprised blood ($n=40$, 27.6%) followed by pus in 35 (24.1%) and non-directed bronchial lavage in 21 (14.5%) cases. Among the carbapenem-resistant isolates, carbapenem-resistant enterobacteriaceae were more common and comprised 119 (82.1%) isolates, followed by pseudomonas aeruginosa in 26 (17.9%) cases. Cefiderocol susceptibility was observed in 133 (91.7%) carbapenem-resistant isolates. When compared, there was no statistically significant difference in cefiderocol susceptibility across various subgroups based on age (p -value=1.000), gender (p -value=0.720), type of clinical specimen (p -value=0.992), or carbapenem-resistant isolate (p -value=0.694).

CONCLUSION:

Cefiderocol demonstrated a high susceptibility rate against carbapenem-resistant isolates, regardless of patient demographics and microbial organism, which underscores the potential of cefiderocol as an effective alternative treatment option for such cases in future clinical practice.



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Session 4. Novel Antimicrobial Agents: Discovery, Design, Synthesis and Action

sciforum-118018: Cell-free supernatants from foodborne lactic acid bacteria isolates disrupt the AI-2 bacterial quorum-sensing system and inhibit biofilm formation in monocultures of *Listeria monocytogenes* and *Staphylococcus aureus*

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Biofilms composed of foodborne bacterial pathogens pose a significant challenge to food safety, as they enhance the microbial persistence in processing environments. Quorum sensing (QS), particularly the autoinducer-2 (AI-2) signaling system, which is widely conserved among both Gram-positive and Gram-negative bacteria and is involved in both intra- and inter-species bacterial communication, is employed to regulate group behaviors based on cell density and plays a crucial role in biofilm formation by pathogens such as *Listeria monocytogenes* and *Staphylococcus aureus*. Lactic acid bacteria (LAB) have been used for centuries in food fermentation to improve the sensory and nutritional profiles and preserve against detrimental microflora. The use of LAB and/or their metabolites as natural quorum-sensing inhibitors (QSIs) may represent a promising, eco-friendly antibiofilm strategy. This study investigates the ability of LAB-derived cell-free supernatants (CFSs) to interfere with AI-2-mediated QS and inhibit biofilm formation in monocultures of *L. monocytogenes* and *S. aureus*. To achieve this, a collection of 89 foodborne LAB isolates was initially screened for either AI-2 production or inhibition using *Vibrio harveyi* luminescence assays. Twenty CFSs displaying AI-2 interference activity were then selected and further evaluated for their antibiofilm potential at sub-minimum inhibitory concentrations (sub-MICs) using microtiter plate biofilm assays based on crystal violet staining. The results revealed that 61.8% (55/89) of the tested CFSs contained AI-2-like signals, while 28.1% (25/89) demonstrated significant AI-2-QSI activity. Almost all of the tested CFSs exhibiting AI-2 QS interference, except for one, significantly limited *L. monocytogenes* biofilm formation, while one of them also reduced the biomass accumulation of *S. aureus* biofilms significantly (by 47.8%). These findings highlight the potential of crude LAB extracts to disrupt QS and serve as novel antibiofilm agents in food safety applications. Further research will examine their efficacy against multi-species biofilms under food-relevant conditions.

This project was funded by the National Recovery and Resilience Plan Greece 2.0, European Union—NextGenerationEU (HFRI Project 15572).



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sciforum-115777: Reviving GE23077: Investigating the Biosynthetic Pathways and Antimicrobial Potential of a Promising RNAP Inhibitor

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Discovered in the 1990s as a product of the metabolism of the so-called ‘rare’ filamentous actinomycete *Actinomadura lepetitiana* DSM 10909 [1], GE23077 is a non-ribosomally synthesised cyclic heptapeptide antibiotic that inhibits a wide range of bacterial RNA polymerases (RNAP) in vitro while not affecting mammalian enzymes [2]. After its discovery, the molecule was later overlooked due to its more limited in vivo antimicrobial activity, which has mainly been exerted against *Moraxella catarrhalis*, *Neisseria gonorrhoeae*, and *Mycobacterium smegmatis* isolates [3]. However, with an increasing number of bacteria becoming resistant to antibiotics, including the major currently approved RNAP inhibitors (i.e., fidaxomicin and rifamycin), the development of new drugs to fight bacterial infections is essential. In this context, GE23077 might prove promising, as its target includes functionally critical residues of the RNAP that are different from those targeted by other inhibitors [4].

Therefore, our collaborative project aims to better understand the production of GE23077 using multiple approaches as an essential step for its further development. A high-quality genome sequence of *A. lepetitiana* was recently obtained using Illumina MiSeq and MinION, followed by the identification and annotation of a putative biosynthetic gene cluster (BGC) for the production of GE23077. Following the development of new methods for the genetic manipulation of this recalcitrant actinomycete, knock-out studies of key genes in the BGC and overexpression studies of two putative regulatory genes are currently ongoing. In parallel, in vitro studies are being performed on purified *A. lepetitiana* RNAP to evaluate its susceptibility to GE23077.

Elucidating the mechanisms behind the synthesis of this promising RNA inhibitor may also open the way to combinatorial biochemistry approaches to modify the molecule and potentially improve its in vivo antimicrobial activity.

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sciforum-112541: WGS of Two Novel *Streptomyces* Isolates with Interesting Secondary Metabolite Gene Clusters

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Streptomyces sp. bear antibiotics, antifungal and antitumor compounds. Anthracyclines and angucyclines are antitumor drugs with cytotoxic effects. During an artichoke cover cropping experiment at Rodale Organic Institute in Camarillo, actinomycetes were quantified and isolated. The purpose was to identify microbes with antibiotic qualities and unusual spore pigmentation in soil. Two *Streptomyces* sp. isolates, 37-AD-D4 and 42-E-JU, were from plots treated with polyethylene covers. The 16S rRNAs from the cultures were Sanger sequenced and analyzed on the DNA Subway Blue Line; there was low % similarity of partial 16S sequences. Strains were sent to Innomics for Whole genome sequencing (WGS) on BGI DNBseq. WGS reads were analyzed for quality and taxonomic classification using MiGA. WGS reads were assembled using SPAdes. Putative secondary metabolite gene clusters were identified with antiSMASH. Ketosynthase gene predictions were generated with NaPDoS2. The percentage of actinomycetes in the plots was between 6.2 and 6.45% in PLFA analysis; the Total Living Microbial Biomass was 2134.66-2258.31 ng/g. 16S microbial metabarcoding analysis was performed on soil. MiGA classification results from WGS indicated the closest relative to 37-AD-D4 was *Streptomyces viridodiataticus* (88.68% AAI, p=0.39); 42-E-JU was most closely related to *Streptomyces nigrum* (84.16% AAI, p=0.549). *Streptomyces* sp. 37-AD-D4 contained an anthracycline domain 87% similar to mithramycin, an aromatic spore pigment domain 80% similar to the *Streptomyces collinus* reference, and a PK spore pigment gene cluster 83% ID to the known *Streptomyces avermitilis* cluster. WGS of 42-E-JU contained a spore pigment polyketide 75% similar to *S. avermitilis* and kinamycin, an angucycline (73% ID). The 16S Illumina metabarcoding output from soil sample 42-JU contained 256 rarified reads of *Streptomyces* that were unassigned to a species. The output from sample 37-AD contained 34 rarified reads assigned to unclassified species of *Streptomyces*. The secondary metabolite biochemical analysis should be explored. Volatiles should be analyzed and potential antitumor effects tested.



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sciforum-115725: A Comparative Analysis of the Secondary Metabolites and Antibacterial Properties of a Small Number of Medicinal Plants Available in Dhaka city, Bangladesh

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Introduction:

Medicinal plants are a great source of bioactive compounds, such as secondary metabolites, with diverse biological activities, including antibacterial properties. The rise of antibiotic-resistant bacteria poses a significant threat to public health, necessitating the search for novel antibacterial agents. This research explored the presence of secondary metabolites such as flavonoids, tannins, saponins, and carotenoids, followed by the identification of *CHS*, *SQS*, *PSY*, and *LAR* genes and the antibacterial potential of medicinal plants such as *Aloe barbadensis* and *Mentha piperita*. The aim was to identify promising candidates for further investigation and development of antibacterial therapies.

Methods:

This study was conducted using triplicates of *Aloe barbadensis* and *Mentha piperita* leaves. Both ethanolic and methanolic crude extracts of these plants were used. The methanolic and ethanolic crude extracts of the selected plants were used, as both have good solubility. The antibacterial profiling was also conducted using agar well diffusion, and the Minimum Inhibitory Concentrations (MICs) against four bacterial strains (*Klebsiella pneumoniae*, *Escherichia fergusonii*, *Enterobacter cloacae* & *Citrobacter amalonaticus*) were established. The presence of *CHS*, *SQS*, *PSY*, and *LAR* genes was investigated using Polymerase Chain Reaction (PCR) of secondary metabolites.

Results:

Both extracts showed almost consistent phenotypic results. None of the samples contained all four screened classes of secondary metabolites. The methanolic extracts showed higher antibacterial activity than the ethanolic extracts. Mint leaf was found to have a higher antibacterial potency compared to aloe vera. On the other hand, aloe vera showed positive results in the genotypic analysis, containing all four secondary metabolites. The mint did not contain any of the targeted genes in this study.

Conclusion:

According to this study, the findings of the two samples were not aligned with the phenotypic and genotypic results. However, both samples were found to be a potential target in different analyses, suggesting their therapeutic potential. Further research can be conducted using larger number of samples to explore the underlying mechanisms.



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sciforum-106718: A Multidisciplinary Study Towards Ciprofloxacin Hybrids: Harnessing Carbonic Anhydrase Inhibition in *Pseudomonas aeruginosa* for Next-Generation Antibacterial Agents

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Among the current antibiotics in clinical practice, fluoroquinolone ciprofloxacin (CPX) stands out for its broad-spectrum antimicrobial activity. However, the emergence of multidrug-resistance phenomena significantly undermines its therapeutic efficacy, with several bacterial strains, including *Pseudomonas aeruginosa*, acquiring a resistant phenotype, making them no longer susceptible to CPX. Being a leading opportunistic bacterium, this pathogen is reported to cause severe, often life-threatening infections, especially in hospitalized immunocompromised patients. Pieces of evidence have highlighted the huge potential of targeting *P. aeruginosa* (Ps) carbonic anhydrase (CA, EC: 4.2.1.1) metalloenzymes, which play a critical role in the bacterium virulence and have recently emerged as attractive innovative pharmacological targets for the development of novel antibacterial agents.

This work provides a response to this challenge, based on the design and development of an extensive library of CPX hybrid derivatives incorporating recognized CA-inhibiting chemotypes, i.e., benzenesulfonamides and coumarins. Enzymatic and biological assays revealed the potent nanomolar inhibition of PsCA activity, along with remarkable antibacterial effects, including bactericidal and anti-biofilm properties for some compounds. Suboptimal PK properties for two representative compounds emerged from a preliminary study *in vitro*. Moreover, no toxicity was observed in the 3R-compliant *Galleria mellonella* larvae model, indicating a safety profile. *In silico* docking simulations and crystallization studies were helpful to gain valuable insights into the binding modes of such compounds to CA enzymes, guiding further optimization efforts. Altogether, our findings underscore the potential of CPX CA-inhibiting hybrids as a valuable strategy to fight *P. aeruginosa* infections, particularly in the context of rising antibiotic resistance.

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sciforum-115505: Antibacterial Activity and Safety Assessment of *Agrimonia Eupatoria* Ethanolic–Aqueous Extract

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Bacterial infections are difficult to treat due to multi-drug resistance, a global health challenge. Plant secondary metabolites, known for their broad spectrum of biological activities, offer a promising alternative. These compounds, particularly phenolics, are recognized for their antibacterial mechanisms and their potential to enhance the efficacy of conventional antibiotics. *Agrimonia eupatoria*, a plant from the Rosaceae family, is rich in phenolics and demonstrates a range of bioactivities, including antibacterial activity [1]. This study aimed to evaluate the antibacterial and antibiofilm properties of a 70% ethanolic–aqueous extract of the *Agrimonia eupatoria* herb, as well as its cytotoxicity and bacterial selectivity to assess its safety. The microdilution assay results demonstrated the extract to be significantly active against *Staphylococcus aureus*, *Staphylococcus aureus* MRSA, *Listeria monocytogenes*, and *Shigella flexneri*, with MIC values of 0.31 mg/mL for all strains, interpreted according to the MIC classification of Tamokou et al. [2]. Further, crystal violet staining of the biofilm biomass demonstrated the most notable antibiofilm effect against *S. aureus* MRSA, with a decrease in the biofilm biomass of up to 85.40%, followed by the effects against *S. aureus* (63.67%) and *L. monocytogenes* (62.24%). An increase in the biofilm biomass was observed in *S. flexneri*, which could be attributed to a stress response. To evaluate the safety of the extract, the selectivity index was calculated as the ratio between the cytotoxic (IC₅₀) and antimicrobial effect (MIC). The positive values obtained showed the higher selectivity of the extract towards bacteria compared to that for normal human fetal lung fibroblasts, i.e., MRC-5 cells (IC₅₀ = 1.52 mg/mL). The obtained results show that *A. eupatoria* possesses antibacterial and antibiofilm activity, which supports further research into its molecular mechanisms of action and potential synergistic effects with the available antibiotics. This strategy could target different sites of the bacterial cells and the pathways involved in biofilm formation, thereby improving antibacterial activity and preventing the development of resistance.



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sciforum-114793: Antibacterial Activity of Ethyl Acetate Extracts of Metabolites Produced by Endophytic Bacteria Isolated from *Moringa oleifera* Leaves against Antibiotic-Resistant Bacteria

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Introduction:

Endophytes are microorganisms colonizing healthy plants tissue without causing any apparent symptoms and noticeable injury to the host. They are reported as reservoir of various classes of broad spectrum bioactive compounds. Hence this study was conducted to evaluate the antibacterial activity of endophytic bacteria isolated from *Moringa oleifera* leaves against Methicillin Resistant *Staphylococcus aureus* and multidrug-resistant *Escherichia coli*.

Methods:

Endophytic bacteria were isolated from healthy leaves of *Moringa oleifera* and were identified based on their cultural, microscopic and biochemical characteristics. The endophytic bacteria were screened for antibacterial against Methicillin Resistant *Staphylococcus aureus* and multidrug-resistant *Escherichia coli*. Ethyl acetate extracts of metabolites produced by endophytic bacteria with activities were evaluated for antibacterial activity against MRSA and MDR *E. coli* using agar well diffusion assay with dimethyl sulfoxide as control. The Minimum Inhibitory Concentration and Minimum Bactericidal Concentration of the ethyl acetate extracts were determined.

Results:

Eleven endophytic bacteria were isolated from healthy leaves of *Moringa oleifera*. Four of the endophytes exhibited antibacterial activities against the test isolates. Ethyl acetate extracts of metabolites produced by endophytic bacteria showed a wide range of antibacterial activity with the inhibitory zone ranging from 11.0 to 27.0 mm for MRSA and 13.0 to 30.0 mm for MDR *E. coli* with MIC values between 50 mg/mL and 100 mg/mL. Dimethyl sulfoxide had no zone of inhibition against test isolates.

Conclusion:

Ethyl acetate extracts of metabolites produced by endophytic bacteria isolated from leaves of *Moringa oleifera* exhibited antibacterial activity against antibiotic-resistant isolates and can serve as source of novel therapeutic agents.



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sciforum-115765: Antibacterial Activity of Three Essential-oil-loaded Nanoemulsions Against Six Pathogenic Bacterial Strains

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Finding antibiotic substitutes through ecological synthesis methods based on natural compounds is becoming a necessity for the treatment and prevention of microbial infections. In the present study, three essential-oil-loaded nanoemulsions (NEs) were prepared using the high-energy method. The obtained oil-in-water emulsions were characterized by determining the droplet size, PDI, zeta potential, and transmittance. Their stability against thermodynamic conditions and conservation was also investigated. Subsequently, the NE's antibacterial activities were assessed against Gram-positive (*Staphylococcus aureus*, *Enterococcus faecalis*, *Listeria monocytogenes*) and Gram-negative (*Salmonella typhimurium*, *Escherichia coli*, *Pseudomonas aeruginosa*) pathogenic bacterial strains. Our results revealed that NEs were successfully formed, with mean sizes ranging from 13.12 to 24.74 nm, confirming the nanometric size of the droplets. PDI values ranged from 0.278 to 0.317 and the percentages of transmittance exceeded 96.40%, indicating the optical clarity of the formulation. The thermodynamic stability study revealed a homogeneous size dispersion of the prepared NE1 and NE2, confirming their stabilities. Regarding NE3, an instability to centrifugal forces was registered, with phase separation observed, suggesting a heterogeneous dispersion of this preparation. The results of the antibacterial activity revealed that all tested NEs exerted a bactericidal effect against the majority of the tested strains (5 out of 6). However, a bacteriostatic effect by the tested substances against the *E. coli* strain was registered. NE3 exhibited the highest effect with MIC values ranging between 6.25 and 25% (v/v). The obtained NEs remain an efficient natural tool to fight against pathogenic bacteria and could be valorized as a potent drug delivery system.



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sciforum-115576: Antibacterial Activity Screening Of an Imine Compound Synthesized Using a Cinnamaldehyde Derivative Against Staphylococcus Aureus Strains

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Imine pharmacophore groups offer the advantage of serving as the foundation for various drug representatives. Examples include furazolidone for bacterial or protozoal diarrhea, nitrofurantoin for uncomplicated urinary tract infections, and imbruvica for chronic lymphocytic leukemia and mantle cell lymphoma. Cinnamaldehyde, a major constituent of cinnamon oil, is an aromatic compound with a benzene ring and an aldehyde group attached to an unsaturated C=C bond at both ends. Studies on cinnamaldehyde have shown that it exhibits a broad range of biological activities. A novel imine compound, created using trans-cinnamaldehyde and polyamines such as tris (2-aminoethyl) amine (compound 5), was synthesized. The antibacterial activity of the compound was tested against clinical isolates (*S. aureus*, *S. aureus* ATCC 6538, *S. aureus* ATCC 25923, *S. aureus* UAMS-1, and *S. aureus* UAMS -929) using the two-fold microdilution method. The obtained results were compared with the results of the ampicillin and gentamicin. It was revealed that the MIC of F2-112B in the case of *S. aureus* (8 µg/mL) were lower than the MIC of ampicillin (16 µg/mL). The MIC value of compound F2-112B was equal (16 µg/ml) to ampicillin in the case of *S. aureus* ATCC 6538. According to the results, compared with other strains, compound 5 showed similar activities against UAMS-929 and ATCC 25923, and its MIC values were 64 µg/ml for each strain. The MIC value was 128 µg/ml when compound 5 was tested against the *S. aureus* strain UAMS-1. We also examined the potential binding mode between compound 5 and bacterially derived target proteins and carried out a protein–ligand docking simulation. The docking results for PBP2a (5M18) indicated that compound 5 successfully binds to the allosteric binding site of the protein, which aligns with the binding site of Cefepime, demonstrating a high binding affinity of -8.42 Kcal/mol.



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sciforum-118647: Antibiotic producers associated with the bark beetle *Ips typographus*

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The rapid development of antibiotic resistance has led to a constant search for and development of new antibiotic drugs. One way to search for antibiotics is to study microorganisms associated with insects [1]. For example actinomycetes isolated as insect symbionts are producers of many antibiotics and antifungal drugs [2].

In this study, samples of the remains of the inner part of spruce bark that was fed on by the bark beetle typographus (*Ips typographus*) were studied. Preliminary bark samples were washed with sterile water and suspended for inoculation. The inoculum was spread on 9 × 9 cm Petri dishes with solid nutrient medium brain heart infusion (with nystatin 50 µg/mL), potato dextrose (with tobramycin 25 µg/mL), nutrient agar (with nystatin 50 µg/mL), nutrient agar (with nystatin 50 µg/mL and nalidixic acid 30 µg/mL). 46 microbial isolates were isolated. Further, initial screening of antibiotic activity was done using agar diffusion method against a wide range of test microorganisms.

Based on the screening results, 10 isolates of microorganisms with pronounced antibiotic properties were selected for further study. Cultivation in liquid media led to identification of active metabolites by LC-MS for two strains. The production of the known antibiotics trichorozin and gliotoxin was observed for strain SK1-7. Trichorozin is a linear peptide belonging to the peptaibol class. The spectrum of activity of peptaibols is quite broad. Gliotoxin is a sulfur-containing mycotoxin that belongs to the class of natural 2,5-diketopiperazines with a broad spectrum of activity. The production of terreic acid, which is a covalent inhibitor of the bacterial cell wall biosynthetic enzyme UDP-N-acetylglucosamine 1-carboxyvinyltransferase, was produced by the strain SK3-18.

This work was supported by the Russian Science Foundation, project no. 25-14-00281.

M.I. Hutchings et al., Microbiota and Host 2023, 1, e230008.

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sciforum-115687: Antifungal activity of Metabolites of *Streptomyces* sp. strain SVP-71 Against *Trichosporon* sp.

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Introduction:

Representatives of the genus *Trichosporon* are basidiomycetous yeast-like microorganisms that are widely distributed in nature. The genus *Trichosporon* includes species capable of causing both superficial and invasive infections associated with high mortality rates. A notable characteristic of the *Trichosporon* species is their resistance to many antifungal agents that are commonly used for the treatment of invasive fungal infections.

Materials and Methods:

Trichosporon sp. were isolated from samples of the affected skin of a patient with a chronic infection. Identification was performed using MS (mass spectrometry).

The producer *Streptomyces* sp. strain SVP-71 was isolated from bentonite samples. The antifungal antibiotic was extracted from the culture fluid and biomass using butanol. Primary purification and metabolite separation were carried out using TLC. The obtained antibiotic was applied to sterile paper discs (14 µg per disc). Specific activity control was performed using discs with dried butanol.

The susceptibility of the clinical isolate to the obtained antibiotic was determined using the DDM, according to CLSI M44 guidelines. Caspofungin discs (5 mg, HiMedia), one of the most effective antifungal antibiotics, were used as a reference.

Results:

Screening studies revealed the antagonistic activity of *Streptomyces* sp. strain SVP-71 against a wide range of yeast-like and filamentous fungi that are pathogenic to humans, including the emerging pathogen *Candida auris*. The disc diffusion method also confirmed the activity of secondary metabolites from *Streptomyces* sp. strain SVP-71 against the clinical isolate of *Trichosporon* sp., with growth inhibition zones reaching up to 20 mm. In contrast, echinocandin antibiotics (caspofungin) showed no specific activity against this microorganism.

Conclusions:

The strain *Streptomyces* sp. SVP-71 demonstrates promise as a source of new antifungal agents, particularly for treating infections caused by fungi with natural resistance to standard antibiotics, such as echinocandins. This is of significant importance in the fight against mycoses that present as severe invasive infections.



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sciforum-115264: Antifungal Effect of Intimate Gel Based on Hydro-Ethanolic Extract of *Cyperus Esculentus* L. and Probiotic Bacteria in Wistar Rat

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Vulvovaginitis is most common in reproductive-aged women, where candidal vulvovaginitis accounts for roughly one-third of cases. Because of the increased interest from doctors and patients, the use of probiotics in reproductive-related dysbiosis is an area of continuing growth. The purpose of this study was to explore the effect of a natural intimate gel based on *Cyperus esculentus* L. hydro-ethanolic extract and beads of *Lactobacillus rhamnosus* SL42 on the treatment and prevention of recurrent vulvovaginitis induced by *C. albicans* (RVVC) in vivo. Wistar rats treated with oestrogenic substances were divided into 6 groups: 2 control groups (infected or not with two separate vulvovaginal infections of 5×10^4 cells/mL of *C. albicans*), 2 treatment groups (*Lactobacillus rhamnosus* Lcr35 or Econazole), and 2 prevention groups (10^8 CFU/g of *L. rhamnosus* SL42 in xanthan beads embedded or not in the intimate hydro-ethanolic plant gel). The fluctuation in microbial colonization and the change of bacterial flora in rat vaginal mucosa after sowing probiotic bacteria were investigated by colony-forming units (CFUs) and microflora analysis. Histological evaluation, myeloperoxidase (MPO) assay, and ELISA analysis for Prostaglandin E2 on vaginal tissues were also performed. The data obtained highlighted that the intimate gel based on tigernut extract and containing *L. rhamnosus* SL42 beads significantly preserved vaginal tissue architecture and prevented vaginal inflammation, proving its efficacy for the management of RVVC and reducing the adhesion of *C. albicans*, as did the probiotic bacteria Lcr35. Hence, *L. rhamnosus* SL42 was proven to be a potential probiotic for VVC treatment and prevention in vivo, and it may have potential application in RVVC prevention products.



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sciforum-118741: Antimicrobial activity evaluation of *N*-(aryl/heteroaryl)-2-chlorobenzenesulfonamide derivatives

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Antibiotic resistance is currently a global problem for modern civilization. Microorganisms become resistant to drugs through acquired mechanisms. Six pathogens are responsible for the majority of deaths: *Escherichia coli*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Streptococcus pneumoniae*, *Acinetobacter baumannii* and *Pseudomonas aeruginosa*. Growing drug resistance makes basic antibiotic therapy ineffective and increases the costs of polytherapy [1]. In recent years, there has been increasing interest in organic compounds that contain an aryl or a heteroarylsulfonamide group in their structure, which are characterized not only by anticancer activity but also by antimicrobial activity [2]. The presented studies follow the trend of searching for new hybrid molecules resulting from the combination of different pharmacophores with interesting biological profiles.

The antibacterial activity of compounds that had previously shown interesting anticancer activity was assessed [3]. The compounds were subjected to an assessment of their antibacterial activity in vitro tests against the Gram-positive bacterium *Staphylococcus aureus* (MIC = 8 µg/mL) and the Gram-negative *Escherichia coli* (MIC > 125 µg/mL). The most active derivative (**16**) was tested against the Gram-positive bacteria *S. epimermidis*, *E. faecalis*, and *B. subtilis* (MICs in a range from 2 to 125 µg/mL) and clinical strains of MRSA (MICs between 0.5 and 1 µg/mL). Ampicillin was used as the standard. The activity of the tested compound against a bacterial biofilm was also tested, and its hemolytic activity was assessed in the peripheral blood of domestic sheep.

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sciforum-118424: Antimicrobial Activity of Thymus vulgaris Essential Oil Evaluated In Vitro Against 21 Isolated Strains of Gram-negative and Gram-positive Bacteria

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Antimicrobial-resistance (AMR) is a 'natural phenomenon' based on a selection of microorganisms able to survive in an unfavourable environment, owing to genetic mutations or the acquisition of "pre-established" resistance genes. The overuse and misuse of antibiotics can favour the emergence and spread of AMR, with negative impacts on the management of bacterial infections and economic implications for healthcare systems. Research and development of natural antibacterial molecules, which exhibit multiple bio-functionalities and are less likely to induce resistance in bacteria, could represent a priority in the coming years to improve the antibacterial activity of existing molecules and counteract AMR. The present study identified the most effective concentration and contact time of Thymus vulgaris L. essential oil (TEO) to achieve in vitro bactericidal activity against twenty-one bacterial strains isolated from different specimens. In total, 10 µl of a solution containing the TEO and the bacterial strains isolated was sown in Petri-dishes for successive assessments of antibacterial efficacy, in terms of minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC), after 24 and 48 hours, respectively. The identified strains (*Mammaliicoccus lentus*, 2*Escherichia coli*, *Salmonella enterica* subsp.*enterica* sieroovar derby, 2*Staphylococcus*, *S.xylosus*, *S.chromogenes*, *S.epidermidis*, *S.enterica* subsp.*diarizonae*, *S.enterica* subsp.*salamae*, *S.enterica* subsp.*houtenae*, *E.coli*(b), *S.aureus*(b), *Citrobacter freundii*, *Enterococcus feciorum*, *Proteus mirabilis*, *Acinetobacter cioffi*, *Pseudomonas putrefaciens* and *Klebsiella pneumoniae*), each with different resistance profiles, and two ATCC strains (*S.aureus* and *Streptococcus mutans*) were tested after 6, 12, 24, and 48h of contact with TEO at different concentrations, from 5% to 2.5% to 1.25%(v/v), corresponding to 450, 225, and 112.5g/mL, respectively. We observed a complete inhibition of all bacterial strains after 12h of incubation at all TEO concentrations, demonstrating the efficacy of TEO against several Gram-positive and Gram-negative bacteria with different AMR. Further studies are needed to define the exact molecular mechanisms of TEO and its possible uses.



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sciforum-118728: Antimicrobial potential of *Emericellopsis* sp. E102 strain and isolation of new compound with antibacterial activity against Gram-negative bacteria

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In recent decades, the interest in the *Emericellopsis* genus as producers of bioactive molecules has increased significantly due to the isolation of new compounds with potential pharmaceutical applications. The species of this genus produce a spectrum of peptide antibiotics with antibacterial and antifungal activity.

Evaluation of the spectrum of antibiotic activity has allowed us to choose a promising producer of new antibacterial compounds, the *Emericellopsis* sp. E102 strain derived from saline soils. Strain E102, based on molecular and phylogenetic constructions, is allocated into a separate clade within the marine clade of *Emericellopsis* and is presumably a new species. In this research, three previously undescribed compounds were isolated from the fungal strain E102, grown in both Czapek–Dox and PDB liquid culture media. The ethyl acetate extract of the E102 strain demonstrated significant efficacy against a concentration of 1,000 µg/mL, resulting in inhibition zones measuring 20 - 30 mm against *Escherichia coli*, ATCC 25922; *Klebsiella pneumonia*, ATCC 700603; *Pseudomonas aeruginosa*, ATCC 27853; *Bacillus subtilis*, ATCC 6633; *Staphylococcus aureus*, ATCC 29213; and *Enterococcus faecalis*, ATCC 29212. Based on HPLC separation of the ethanol concentrates, an active compound was obtained and investigated further. The monoisotopic mass of the compound, determined using MS, was 724.5 g/mol. Using the Chemcalc.org service, the most probable gross formulas for the required component were determined. Based on the calculations presented, there is a high probability that the substance has a sterane framework.

The work of Vladimir V. Sokolov and Marina L. Georgieva was supported by the Russian Science Foundation (grant #25-24-00291). The work of Ivan V. Mironov was carried out with institutional funding from the Gause Institute of New Antibiotics.



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sciforum-118783: Antimicrobial Potential of *Camellia japonica* Flowers (var. Dr Tinsley) against Foodborne Pathogens

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Antibiotic resistance has become one of the biggest threats to modern medicine. The World Health Organization (WHO) and other health organizations warn that if antibiotic resistance is not brought under control, even simple infections can become deadly. The overuse and misuse of antibiotics lead to the emergence of resistant bacterial strains, creating a major challenge, especially in the treatment of foodborne pathogens. In response to this growing crisis, researchers are increasingly turning to natural antimicrobial alternatives. Consumer demand for organic and sustainable products has increased interest in the use of plant-derived bioactive compounds as natural preservatives. *Camellia japonica* flowers contain bioactive molecules such as phenolic compounds, anthocyanins, and polyphenols and may exhibit antimicrobial properties. In this study, the antimicrobial activity of *C. japonica* flowers (var. Dr Tinsley) against foodborne pathogens was evaluated using the agar diffusion method. The extracts were obtained by a conventional maceration technique (50 °C, 1 h) using 60% methanol solvent and were then lyophilized and re-suspended in dimethyl sulfoxide (DMSO). The results revealed that *C. japonica* (var. Dr Tinsley) extract showed significant antimicrobial activity against *Staphylococcus epidermidis* (11.24 mm), *Staphylococcus aureus* (10.98 mm), *Pseudomonas aeruginosa* (10.03 mm), *Salmonella enteritidis* (6.30 mm), and *Bacillus cereus* (6.54 mm). However, no inhibition was observed against *Escherichia coli*. A total of 15 µL of 40% lactic acid was used as a positive control, producing inhibition zones of 17.53 mm for *E. coli*, 16.4 mm for *S. aureus*, 18.41 mm for *S. enteritidis*, 12.53 mm for *P. aeruginosa*, and 14.76 mm for *B. cereus*. Meanwhile, 15 µL of DMSO served as the negative control, showing no inhibition. These findings suggest that *C. japonica* (var. Dr Tinsley) flowers have the potential to be used as bioprotectants in the food and pharmaceutical industries. Further research is needed to isolate and characterize the active compounds responsible for these effects.



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sciforum-115605: Assessing The Antimicrobial Activity Of Gemmotherapy Extracts

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Currently, antimicrobial resistance is one of the major threats to healthcare as multidrug-resistant strains of bacteria, yeasts, and molds continue to emerge. To address this issue, innovative solutions are needed, and one promising approach is the development of gemmotherapy extracts (GTEs) from plant parts such as buds and young shoots. In the current study, the antimicrobial activity of eight GTEs—raspberry, blackthorn, sea buckthorn, dog rose, lingonberry, hawthorn, common grapevine, and boxwood—was analyzed using agar diffusion and broth microdilution methods. The latter technique was used to determine the minimum inhibitory concentration (MIC) and the minimum bactericidal concentration (MBC). The antimicrobial efficacy was tested against seven bacterial strains, five mold strains, and two yeast strains, which can cause different health conditions in the human body. Using the agar-diffusion method, we found that Gram-positive bacteria showed good susceptibility, as lingonberry and dog rose GTEs formed inhibition zones even at a concentration of 10-20% in the case of *Bacillus cereus* and *Staphylococcus aureus*. On the contrary, none of the GTEs showed activity against Gram-negative bacteria, molds, or yeasts. By the broth microdilution method, we observed that dog rose and lingonberry GTEs were the most effective, inhibiting the growth of Gram-positive bacteria even at relatively low concentrations (10-40%). Gram-negative bacteria were more resistant to most GTEs, as only concentrations above 40-50% showed bacteriostatic effects. Yeast strains were the most resistant, as only concentrations above 60% were effective. Although the bactericidal effects were minimal, the GTEs from the lingonberry and the common grapevine were effective against five strains of bacteria, such as *Enterococcus faecalis*, *Listeria monocytogenes*, *Enterococcus faecalis*, *Pseudomonas aeruginosa*, and *Salmonella enterica*, with an MBC of 60-70%. Based on the antimicrobial properties observed, especially for dog rose and lingonberry GTEs, these extracts could be considered as potential agents to enhance the efficacy of antibiotic therapies.



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sciforum-118639: ASSESSING THE IMPACT OF DECANOYL-RVKR-CHLOROMETHYL KETONE ON *CRYPTOCOCCUS NEOFORMANS* CELLS

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Cryptococcus neoformans is a basidiomycetous yeast that rose from being an obscure fungus to an important fungal pathogen. Part of its success is attributed to its arsenal of virulence factors that allow it to subvert the immunological response in a susceptible host, including the production of proteases that can permeabilise the phagosomal membrane, leading to internalised cells escaping. This project sought to assess if a protease inhibitor, decanoyl-RVKR-chloromethyl ketone (DEC-RVKR-CMK), could decrease cryptococcal growth and increase their susceptibility towards macrophage phagocytosis. This compound is used to control unwanted proteolysis in model viral entry studies, including HIV entry studies. The in vitro susceptibility of cryptococcal cells was assessed by measuring the optical density of the cells following exposure to different DEC-RVKR-CMK concentrations. Additionally, the DEC-RVKR-CMK-treated and non-treated cells were co-cultured with macrophages to assess their susceptibility to macrophage phagocytosis. The pHrodo stain was used to assess the internalisation of cryptococcal cells by macrophages. The macrophages were lysed to liberate the internalised cryptococcal cells. A 10-fold increase in DEC-RVKR-CMK concentration led to the growth of cryptococcal cells being inhibited in a dose-dependent manner. In this study, 0.1 mM was defined as the minimum inhibition concentration and led to over 75% growth inhibition. There was no difference in the efficiency of macrophages to internalised DEC-RVKR-CMK-treated and non-treated cells. However, no colonies of DEC-RVKR-CMK-treated cells could be recovered on mycological agar, while the non-treated cells yielded colonies on the agar. The in vitro preliminary data obtained in this study suggest that DEC-RVKR-CMK may be ideal for controlling cryptococcal growth. The clinical relevance of the study may lie in impairing the ability of cryptococcal cells to escape from macrophages, avoiding immunoprocessing. It is suggested to investigate if this quality can be observed in other *C. neoformans* strains and elucidate the molecular mechanism underpinning the reported observations.



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sciforum-118537: Aurones and their derivatives as promising antimicrobial molecules.

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Resistance to conventional antibiotics used in medicine is rising dangerously high worldwide, and could lead to more than 10 billion deaths per year by 2050 according to the World Health Organisation (WHO). New types of antibacterial molecules have to be developed and should be i) nontoxic to humans, ii) active against bacteria already resistant to conventional antibiotics, and iii) unable or less likely to cause resistance compared to conventional antibiotics. Natural plant flavonoids are known to be effective molecules, but their activity and selectivity have to be increased. Among them, aurones have attracted attention due to their good antimicrobial activity associated with limited toxicity. Various aurone derivatives were chemically synthesized and tested for their biological activity on microorganisms (bacteria and fungi) and for their toxicity on human cells. Whereas some derivatives were found to be inactive or active only on some strains, others were found to have a larger spectrum of activity with Minimum Inhibitory Concentration (MIC) values as low as 0.78 μ M. Limited toxicity on human cells was found, giving high therapeutic indexes (> 100 and up to 600) for the best candidate. The data show that 5-acetamidoaurones are far more active and safer compared with 5-aminoaurones, and that benzyloxy and isopropyl substitutions at the B ring are the most promising strategy in the exploration of new antimicrobial aurones.



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sciforum-115972: Blue-Light Photoactivation of Berberine-Gentamicin Combination: A Synergistic Strategy Against *Staphylococcus aureus* Acute Wound Infections

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Background:

Methicillin-resistant *Staphylococcus aureus* (MRSA) poses a significant challenge in managing acute wound infections due to its high resistance to conventional antibiotics. The persistence of these infections not only complicates treatment but also increases the likelihood of chronicity. This study investigates the potential of the blue-light photoactivated berberine-gentamicin (Ber-Gen) combination as a novel strategy to enhance bacterial inactivation and overcome antibiotic resistance in *S. aureus*.

Methods:

A clinical strain of MRSA isolated from a diabetic foot ulcer was used. The antibacterial activity of Ber and Gen was screened individually and in combination. The photodynamic activity of the Ber was assessed using a light-emitting diode (LED) system with blue light (420 nm), at 30 mW/cm² (light doses of 9, 18, 27 J/cm²). The photodynamic activity of the Ber-Gen combination was evaluated after 6 h of incubation by the reduction of the culturability (colony forming units (CFU)/mL).

Results:

Ber significantly enhanced Gen activity, exhibiting a potentiating effect against MRSA. Blue-light activation of Ber (420 nm, 18 J/cm²) reduced its bactericidal concentration by 80-fold. The photodynamic activation of the Ber-Gen combination (420 nm, 10 min, 18 J/cm²) resulted in a ≈9-log CFU/mL reduction in *S. aureus* culturability, with a 2048-fold decrease in the bactericidal concentration of Gen.

Conclusion:

The dual approach of antimicrobial photodynamic inactivation combined with phytochemical-antibiotic combinations demonstrated a strong synergistic effect, effectively reducing *S. aureus* culturability and restoring the efficacy of Gen against MRSA. This approach shows promise as an innovative solution for managing antibiotic-resistant infections.



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sciforum-117875: Ciprofloxacin potentiation using the phytochemical 1,8-cineole against *Klebsiella pneumoniae* in planktonic and biofilm growth

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The increasing incidence of antibiotic resistance among *Klebsiella pneumoniae* isolates, along with their ability to form biofilms, places this pathogen in the critical priority group for which new antimicrobial treatments are urgently needed. The combination of plant compounds and antibiotics is a promising approach for enhancing antimicrobial activity. The phytochemical 1,8-cineole, which is effective against *K. pneumoniae*, is a good candidate for the development of novel antibacterial combination therapies. The aim of this study was to evaluate the combined action of 1,8-cineole with ciprofloxacin against *K. pneumoniae* in both planktonic cultures and biofilms. For this purpose, the planktonic growth (OD_{600nm}) of a clinical *K. pneumoniae* strain was quantified after treatment with the individual compounds or their combinations. Based on the obtained data, two types of drug interaction analyses were performed: 1) the fractional inhibitory concentration index (FICI) was calculated after determining the minimum inhibitory concentrations and 2) the BLISS model in the Combenefit software was used. A synergistic effect of 1,8-cineole with ciprofloxacin was revealed based on both analyses. In addition, the minimum bactericidal concentrations (MBCs) were determined by means of colony-forming unit (CFU) counting. The anti-biofilm effects of ciprofloxacin and 1,8-cineole, either alone or in combination, were assessed on pre-formed (24 h old) *K. pneumoniae* biofilms. The biomass was measured by means of crystal violet staining, and the cell viability was quantified using CFU counting. The most effective combined treatment was obtained using five-times ciprofloxacin MBC and half the 1,8-cineole MBC, resulting in a 90% biomass decrease and 4 Log_{10} reduction in cell viability. In contrast, these anti-biofilm effects were not observed when the same concentrations of the individual compounds were assayed. Taken together, our findings indicate that 1,8-cineole is a promising candidate for combinatorial therapies with clinically relevant antibiotics to treat *K. pneumoniae* infections.



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sciforum-115905: Combinations of Riboflavin with Antiseptics for Tackling *Staphylococcus aureus* Methicillin Resistant Infections by Photodynamic Inactivation

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Antibiotic-resistant pathogens, such as methicillin resistant *Staphylococcus aureus* (MRSA), pose significant challenges in managing chronic wound infections. Antibacterial photodynamic inactivation (aPDI) has emerged as an alternative to antibiotics by offering localized and resistance-independent bacterial elimination. Natural compounds with photosensitizing properties are particularly attractive due to their biocompatibility and sustainability. Therefore, this study investigates the potential of aPDI using riboflavin (RB), a vitamin and vital micronutrient commonly found in various animals and plants. RB is known to be a promising natural photosensitizer, capable of causing bacterial cell damage by reactive oxygen species (ROS) generation. Additionally, the potential synergistic combinations with the commonly used wound antiseptics, namely octenidine dihydrochloride (OCT) and polyhexamethylene biguanide (PHMB) against *S. aureus* clinical strain (MJMC568-B: MRSA) was assessed. The approach aimed to improve antiseptic efficiency by reducing the necessary concentrations. The antibacterial efficacy of RB, OCT and PHMB were determined independently by minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC). The photodynamic activity of RB was assessed by irradiating with blue light (420 nm) using a light-emitting diode (LED) system and quantification through colony-forming unit (CFU) analysis. An evaluation of the potential synergistic interactions of RB-mediated aPDI, with OCT and PHMB was conducted by a disk diffusion assay, and a checkerboard assay. The results highlight the potential of combining aPDI with antiseptics to achieve enhanced antibacterial effects against *S. aureus*. This dual approach could offer a promising solution for managing chronic wound infections, reducing the reliance on traditional antibiotics, and mitigating the risk of resistance development.

Acknowledgments: This work was supported by: Project InnovAntiBiofilm(ref. 101157363) financed by European Commission(Horizon-Widera 2023-Acess-02/Horizon-CSA); LEPABE, UIDB/00511/2020((DOI: 10.54499/UIDB/00511/2020)) and UIDP/00511/2020(DOI: 10.54499/UIDP/00511/2020); ALiCE, LA/P/0045/2020(DOI: 10.54499/LA/P/0045/2020); funded by national funds through the FCT/MCTES(PIDDAC; Lisbon, Portugal). Lília S. Teixeira acknowledges individual PhD fellowship from FCT(2023.04774.BDANA).



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sciforum-118417: CRYPTOCOCCAL MENINGITIS, WHAT IT IS, AND TREATMENT ISSUES RELATED TO ITS MANAGEMENT

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Introduction:

Cryptococcus (C.) *neoformans* is a pathogen capable of breaching the blood–brain barrier (BBB) and localising in the brain, presenting challenges for treatment. This is, in part, because amphotericin B cannot cross the BBB, and while fluconazole can cross the BBB, its use is limited by non-fluconazole susceptibility. This study aimed to reformulate aspirin by encapsulating it into D- α -tocopheryl polyethylene glycol succinate (TPGS), to characterise the formulation, and to evaluate its in vitro efficacy against *C. neoformans*.

Methods:

Aspirin was encapsulated into TPGS using a colloidal dispersion method. The aspirin–TPGS micelles were characterised using Fourier transform infrared spectroscopy (FTIR) and a Zeta particle analyser. The EUCAST protocol was used to assess the cryptococcal growth susceptibility to aspirin–TPGS at 0, 1, 2, and 4 mM concentrations. For a comparative analysis, cells were also treated with standard aspirin, TPGS, fluconazole, and amphotericin B at the same concentrations.

Results:

The FTIR spectra analysis confirmed the successful encapsulation of aspirin into TPGS. The aspirin–TPGS nanoparticles were 10.97 nm in size with a polydispersity index of 0.175 and a zeta potential of 3.668. Aspirin in TPGS was found to be more potent than standard aspirin powder at 1, 2, and 4 mM, which may have been due to increased lipophilicity that facilitated cellular entry. The aspirin–TPGS formulation was more effective than fluconazole at 1, 2, and 4 mM based on the calculated p values and showed a similar efficacy to that of amphotericin B. The results showed that aspirin–TPGS significantly reduced the cryptococcal growth after 48 hours compared to that in the untreated controls.

Conclusion:

These findings indicate that aspirin–TPGS micelles exhibit a potent inhibitory effect on *C. neoformans*, offering potential as a treatment for cryptococcal infections. Further studies will investigate aspirin–TPGS's ability to traverse the BBB using an in vitro model of hCMEC/D3 cells, enhancing our understanding of its therapeutic potential in complex biological systems.



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sciforum-118706: Design of novel antisense oligonucleotide targeting the flavin mononucleotide riboswitch in *Staphylococcus aureus*

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Introduction:

The Flavin mononucleotide riboswitch (FMN riboswitch) is the second most prevalent riboswitch, presented in more than 4300 bacterial species. Sensing FMN, it regulates the synthesis of vital cellular metabolites in *Staphylococcus aureus* (*S. aureus*) and seven more pathogenic bacteria included in the priority list of the World Health Organization important for combating antimicrobial resistance. The following study presents the process of the rational design of an antisense oligonucleotide (ASO) with bacteriostatic effects targeting the FMN riboswitch in *S. aureus*.

Methods:

The rational design of ASO, targeted to the multidrug-resistant bacterium *S. aureus*, is based on bioinformatics and genomic studies, encompassing the following: an analysis of international databases, Clustal X multiple alignments, a selection of appropriate motifs, BLAST analysis in human, probiotic, and other pathogenic bacteria, biochemical pathways, and RNA folding analysis (MFE and PF).

Results:

The bioinformatics study results show how the FMN riboswitch is highly suitable for ASO design, as it controls the expression of the *fmnP* gene in *S. aureus* (FMN transporter) by translation prevention, and the *ribD* operon (enzymes for FMN synthesis) by transcription termination. This allows us to design an ASO, which is recognized by both the riboswitch responsible for FMN synthesis and the one for the transporter protein. Its bacteriostatic effect in *S. aureus* is observed in 700nM, 4.5 µg/mL. Cytotoxicity tests confirm that it is not inherent in the human cell lining of non-small cell lung cancer A549 at this concentration.

Conclusions:

Since FMN is not presented in the human genome and regulates the synthesis and transport of essential proteins for the survival and division of bacterium metabolites, it provides the potential as target for designing antibacterial drugs against the most severe human pathogenic bacteria. Our proprietary bioinformatics protocols for suitability and for ASO design allow us to introduce novel ASO as potential effective antimicrobial therapeutic with a growth inhibitory effect in *S. aureus*.



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sciforum-115705: Development of DNA Aptamers as Therapeutic Tools Against *Pseudomonas Aeruginosa*

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Antibiotic resistance is posing a serious threat to human health. Therefore, innovative therapeutic tools are needed to efficiently treat resistant bacteria. Aptamers are small synthetic oligonucleotides which show high specificity and affinity for a designated target. They evolve from random DNA oligonucleotide pools by means of an in vitro selection process called Systemic Evolution of Ligands by EXponential enrichment (SELEX). Aptamers have multiple applications in the biotechnological field and can be considered as biological drugs to target resistant microorganisms. In this work, we selected DNA aptamers to target the hemophore of the haem assimilation system (HasA) from *Pseudomonas aeruginosa*. The selection was performed with a DNA library with a random region of 40 nucleotides, and with HasA, which was produced in house. Twelve rounds of SELEX were performed, and the selection was monitored using qPCR and melting curve analysis. From round 1 to 12, the main fluorescence signal peak at 70°C, typical of the library, and then gradually shifted to 84°C. Selected oligonucleotides were sequenced by means of Next-Generation Sequencing, and one single sequence was found to be enriched at 75% in the pool. The most abundant candidates are currently being tested for their binding affinity and specificity. Meanwhile, our group is working on the aptamer selection towards the receptor of the haem assimilation system (HasR). Since iron is an essential micronutrient for *P. aeruginosa*, as for many bacteria, targeting and potentially blocking elements of the bacterium's iron acquisition mechanisms, such as HasR and HasA, can put the bacterium at a significant metabolic disadvantage.



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sciforum-117767: Development of Naphthalimidehydrazide Derivatives as Potent Antibacterial Agents Against Carbapenem-resistant *A. baumannii*

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As per the WHO's "Bacterial Priority Pathogen List", Carbapenem-resistant *A. baumannii* (CRAB) is categorized as belonging to the critical priority pathogen group due to the extreme paucity of treatment options (1). *A. baumannii* causes several nosocomial infections such as pneumonia, sepsis and bacteraemia; skin and soft tissue infections; and meningitis (2). To respond to the urgent and unmet need of identifying novel antibiotics that are active against CRAB, we designed, synthesized and tested 29 naphthalimide derivatives by incorporating the hydrazine group against CRAB BAA-1605. From these compounds, 5b, 5c, 5d and 5e exhibited MICs ranging between 0.5 and 1 µg/ml, and all compounds except 5e displayed >200 selectivity indices (SIs) against Vero cells. Compound 5d was chosen as a representative and tested against an MDR clinical strain panel, with strains that are resistant to meropenem, levofloxacin and minocycline. In these tests, 5d displayed equi-potent activity. In addition, 5d demonstrated synergy with tobramycin, and the synergy was confirmed by means of a combination time kill assay against CRAB BAA-1605. From the above data, 5d exhibits promise as a potential antibacterial scaffold against CRAB (3).

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sciforum-115970: Disruption of Quorum Sensing in *Pseudomonas aeruginosa* by Sinapic Acid: Impacts on Biofilm Formation and Virulence

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Background:

Quorum sensing (QS) is a bacterial intercellular communication mechanism mediated by extracellular signalling molecules that regulate gene expression. The *las* system, consisting of LasI and LasR, is a fundamental QS component in *Pseudomonas aeruginosa* and plays a crucial role in the formation and maintenance of biofilms as well as in the regulation of virulence factors. Phenolic acids such as sinapic acid are plant secondary metabolites that exhibit antibacterial properties and low toxicity. The aim of this study was to evaluate the potential of sinapic acid as inhibitors of the *las*-QS system in *P. aeruginosa*, focussing on their effects on biofilm structure and virulence factor production.

Methods:

The inhibitory effect of sinapic acid on the *las* system was evaluated using bioreporter strains and bioluminescence-based assays. The architecture of the biofilm was analysed using optical coherence tomography (OCT), while the production of virulence factors (pyoverdine, pyocyanin, total proteases, lipases, and gelatinases) and motility was analysed by absorbance measurement and plate agar method.

Results:

Sinapic acid inhibited *las* QS activity by 90 % at a concentration of 1000 µg mL⁻¹. The production of N-3-oxododecanoyl-homoserine lactone, the autoinducer of the *las* system, was reduced by 60 % at a concentration of 6.25 µg mL⁻¹. This phenolic acid significantly disrupted the biofilm architecture and reduced the biofilm thickness from 25 µm to 14 µm. In addition, sinapic acid significantly reduced the production of important virulence factors and impaired bacterial swarming motility.

Conclusion:

Sinapic acid demonstrated strong inhibitory effect on the *las* QS system, leading to a disruption of the biofilm structure and reduced virulence of *P. aeruginosa*. These findings support their potential as antipathogenic and antivirulence agents for the treatment of biofilm-associated infections.



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sciforum-116156: Effect Of Ethyl Acetate Extracts of the Roots And Aerial Parts of Geum Urbanum L. On The Phenotype Inhibition Of The Pseudomonas Aeruginosa Las/Rhl Quorum Sensing System And Their Antioxidant Activity

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The opportunistic pathogen *Pseudomonas aeruginosa* causes nosocomial infections affecting the urinary system, respiratory tract, etc. It can lead to bacteremia and sepsis, especially in immunocompromised patients. Growing antimicrobial resistance (AMR) is a global health concern according to the World Health Organization. Therefore, novel antimicrobial agents, such as plant extracts containing complexes of compounds to which it is impossible to develop resistance, are being investigated. This study aimed to compare the effects of ethyl acetate (EtOAc) extracts from the roots (EtOAcR) and aerial parts (EtOAcAP) of the perennial Bulgarian plant *Geum urbanum* L. (*Rosacea*) on the phenotype inhibition of the Las/Rhl quorum sensing (QS) system in *Pseudomonas aeruginosa* PA01 and ATCC 27853, specifically on biofilm formation, swarming motility, pyocyanin production, and gene expression. For this purpose, we used sub-minimal inhibition concentrations (sub-MICs), which do not affect bacterial growth. We found that the evaluated sub-MICs suppressed all studied phenotypic manifestations, with no expression of the target *lasI/lasR* and *rhlI/rhlR* genes. The observed anti-QS capacity of *G. urbanum* extracts is probably related to their high phenolic content. Moreover, the EtOAcR and EtOAcAP extracts showed effective antioxidant capacity via DPPH, ABTS, and superoxide radical scavenging effects, as well copper ion chelation activity. These findings will support the development of novel phytocomplexes applicable for the biocontrol and prevention of *P. aeruginosa* infections.



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sciforum-118778: Enhancing the stability and activity of short computationally designed antimicrobial peptides through chemical modification

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Introduction:

Short cationic peptides are valuable chemical templates for the design of clinically available antibiotics. The discovery and development of these peptides face numerous challenges, including time-consuming screening processes, toxicity, and stability issues. Computational methods have been integrated into this process, with successful outcomes.

Methods:

In this study, we designed eight arginine-rich peptides, which were analysed using *in silico* tools to predict their toxicity and antimicrobial properties. We then confirmed the *in vitro* antibacterial effects and toxicity to fibroblasts and red blood cells of these synthetic peptides using absorbance-based assays. The activity of these peptides was also tested in environments that were rich in proteases. Three chemically modified peptides were synthesised based on the most active peptide. The antibiofilm action and bactericidal effects were evaluated using fluorescent markers and microscopy. We also monitored the levels of reactive oxygen species (ROS) when the peptides were incubated with bacteria.

Results:

In summary, we observed discrepancies between the *in silico* predictions and the *in vitro* screening results. R4F4 was the most promising peptide candidate, but its function was impaired when incubated with serum or trypsin. The lipidated analogue was toxic and did not exhibit similar antimicrobial effects. However, cyclisation and D-amino acid substitution strategies enhanced the stability and activity of novel analogues. These arginine-rich peptides act through a dual mechanism, integrating damage to the bacterial membrane and an increase in reactive oxygen species levels.

Conclusions:

Overall, this study demonstrates the significant contributions of the cyclisation and D-amino acid substitution approaches in enhancing the stability and activity of arginine-rich peptides. It represents an important step forward in the development of peptide-based candidates, which could form the basis of future antibacterial interventions.



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sciforum-116095: Exploration and Identification of Bioactive Compounds from Antarctic Lichens: Contribution to Bioprospecting of New Antimicrobials

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Lichens are symbiotic organisms resulting from the mutualistic interaction between a fungus, an alga, and/or a cyanobacterium, along with an associated microbiome, which has enabled their adaptation to various ecosystems across the planet. Throughout this process, they have developed secondary metabolites with a broad spectrum of biological activities. This study explores the potential of bioactive compounds found in Antarctic lichens as antimicrobial agents. Ethanol extracts from species belonging to the genera *Cladonia*, *Gondwania*, *Himantormia*, *Lecania*, *Ochrolechia*, *Placopsis*, *Pseudephebe*, *Psoroma*, *Sphaerophorus*, and *Umbilicaria* have revealed aromatic compounds from the depside, depsidone, and dibenzofuran groups with variable and significant ranges of antioxidant activity (DPPH IC₅₀ 75.3 ± 0.02 - 2246.149 ± 0.086 µg/mL; ORAC 18.882 ± 0.210 - 525.11 ± 0.135 µmol Trolox/g) and enzymatic inhibition (acetylcholinesterase IC₅₀ 2.805 ± 0.07 - 32.880 ± 0.016 µg/mL; butyrylcholinesterase IC₅₀ 4.476 ± 0.06 - 57.925 ± 0.030 µg/mL; α-glucosidase IC₅₀ 16 ± 0.015 - 250.443 ± 0.006 µg/mL; tyrosinase IC₅₀ 22.32 ± 0.21 - 68.436 ± 0.048 µg/mL), suggesting their potential for antimicrobial research. Additionally, various studies have demonstrated the antimicrobial activity of extracts and isolated compounds from lichens such as *Cetraria aculeata*, *Cladonia rangiferina*, *Parmelia sulcata*, *Parmotrema dilatatum*, *Stereocaulon alpinum*, and *Usnea barbata* against pathogenic bacteria including *Escherichia coli*, *Staphylococcus aureus*, *Bacillus subtilis*, *Pseudomonas aeruginosa*, *Salmonella enterica*, *Klebsiella pneumoniae*, *Enterococcus faecalis*, *Listeria monocytogenes*, and *Streptococcus pneumonia*, with minimum inhibitory concentrations (MICs) varying between 0.2 and 8.5 mg/mL. The identified mechanisms of action include the inhibition of nucleic acid and protein synthesis, the disruption of cellular integrity, enzymatic activity inhibition, oxidative stress induction, and biofilm formation inhibition. The compounds present in Antarctic lichens represent a promising and innovative therapeutic alternative for combating bacterial infections. However, further in vitro and in vivo studies are essential to validate their safety and efficacy within the context of increasing antimicrobial resistance.



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sciforum-118545: Exploring Skin Microbiome Interactions for Antimicrobial Discovery in Diabetic Foot Ulcers

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Diabetes and diabetic foot ulcers (DFUs) pose a significant clinical burden. Antibiotic treatments are often ineffective, contributing to the growing antimicrobial resistance crisis.

We investigated interactions between bacterial isolates from diabetic and non-diabetic patients to detect the production of antimicrobial compounds with potential therapeutic applications.

A total of 539 bacterial strains were identified by 16S rRNA gene sequencing. In total, 79 isolates were from DFUs and 55 were from a contralateral non-ulcerated foot (NDFU), while 254 isolates were from diabetic patients without any skin ulcerations (intact diabetic skin - IDS), and 151 were from non-diabetic individuals (CT). The predominant genera identified were *Staphylococcus* (74.2%), *Pseudomonas* (5%), and *Kocuria* (3.3%).

Screening for antimicrobial activity was performed using spot-on-lawn agar diffusion assays against five indicator bacteria isolated from DFU (MDR and non-MDR *S. aureus* and *P. aeruginosa* and *Staphylococcus* CoNS). Overall, 6.7% of isolates exhibited antimicrobial activity against at least one indicator strain. The most active isolates belonged to the genera *Staphylococcus* (44.4%), *Pseudomonas* (30.6%), and *Aerococcus* (13.9%), with single active isolates from *Acinetobacter*, *Bacillus*, *Enterobacter*, and *Pseudoxanthomonas*.

Antimicrobial activity was mainly detected on isolates from DFU (10.1%), followed by IDS (7.9%), NDFU (7.3%), and, rarely, from CT (2.6%). Contact-dependent killing was ruled out by testing bacterial extracts. Isolates capable of producing diffusible antimicrobial molecules included *Pseudomonas* (10 isolates), *Staphylococcus* (5), *Aerococcus* (1), *Bacillus* (1), and *Enterobacter* (1). Additionally, *Staphylococcus* (2), *Aerococcus* (1), and *Enterobacter* (1) required competitive conditions to induce antimicrobial production.

Antimicrobial extracts were fractionated using organic solvents (Methanol, Ethanol, Acetone, Chloroform methanol (2:1), 1-Butanol) and chromatography (C18 cartridge) to isolate bioactive compounds. Whole-genome sequencing and genome-wide mining analysis uncovered promising biosynthetic gene clusters (BGCs), including one predicted to encode a rhizomide-like molecule.

This study highlights the potential of skin bacteria and their interactions as a source of novel antimicrobial compounds.

Funding: 2022.06809.PTDC_AMRFight



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sciforum-118355: Exploring Snake Venoms For Novel Antimicrobial Agents

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The increasing prevalence of antibiotic resistance is a major global healthcare concern, leading to higher mortality rates and rising treatment costs. This crisis is largely attributed to the excessive and improper use of antibiotics, which accelerates bacterial resistance. With diminishing pharmaceutical investment in novel antibiotics, there is an urgent need to explore alternative antimicrobial therapies. Snake venoms represent a promising avenue due to their complex protein compositions, which include phospholipases A₂ (PLA₂s), L-amino acid oxidases (LAOs), cathelicidins (CAMPs), and other protein toxins with antibacterial properties.

In this study, we evaluated the antimicrobial activity of crude venoms from seven snake species against three bacterial strains—*Escherichia coli*, *Staphylococcus epidermidis*, and *Neisseria subflava*—using spot assays, the well diffusion method, and microdilution assays to determine antimicrobial activity and minimum inhibitory concentrations (MICs) in both solid and liquid media.

On solid media, complete inhibition of *E. coli*, *S. epidermidis*, and *N. subflava* was observed with *Macrovipera lebetina lebetina* venom at 375 µg/50 µL and *Bitis gabonica* (Gaboon viper) venom at 675 µg/50 µL. Additionally, *Naja nigricincta* venom exhibited complete inhibition of *N. subflava* at 325 µg/50 µL. In liquid media, complete inhibition of all three bacterial strains occurred with *M. lebetina lebetina* venom at 500 µg/mL, while *B. gabonica* venom inhibited *N. subflava* at 1350 µg/mL.

These findings highlight the potential of snake venoms as novel antimicrobial agents. However, further research is necessary to assess their clinical applicability and safety. Continued investigation into venom-derived compounds may pave the way for innovative therapeutic strategies to combat antibiotic-resistant bacterial infections.



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sciforum-118550: In Silico Design and Docking of Novel Benzimidazole Derivatives as Inhibitors Targeting AcrB Efflux Pump and NDM-1 Carbapenemase: Strategies to Combat Antibiotic Resistance

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Antibiotic resistance poses a significant global health threat, necessitating the development of novel strategies to combat resistant bacterial strains. This study employs in silico design and molecular docking techniques to develop novel benzimidazole derivatives targeting the AcrB efflux pump and NDM-1 carbapenemase, two critical mechanisms of antibiotic resistance. Using a suite of computational tools including Chemdraw, Spartan14, Chimera, Autodock Vina, and Biovia Discovery Studio, we designed and analyzed five benzimidazole derivatives (B1-B5). Biovia Discovery Studio was specifically utilized for the visualization and analysis of molecular interactions, providing crucial insights into the binding modes and types of interactions involved. The compounds were evaluated for drug-likeness using ADMETLab2.0 and toxicity using Protox3. The results show that all compounds comply with Lipinski's rule of five and exhibit high GI absorption, indicating favorable pharmacokinetic properties. Toxicity analysis revealed low to moderate toxicity, with compound B4 showing the most favorable safety profile. Molecular docking studies, complemented by interaction visualizations, demonstrated strong binding affinities to both target proteins, with some compounds outperforming native ligands. Notably, compounds B5 and B1 showed the strongest interactions with NDM-1 Carbapenemase, while B3 and B4 exhibited comparable or better binding to the AcrB Efflux Pump than the native ligand. The visualization of these interactions revealed key binding features, including hydrogen bonds and hydrophobic interactions, providing a molecular basis for the observed affinities. These findings suggest the potential of these benzimidazole derivatives as dual-action inhibitors, simultaneously targeting two critical resistance mechanisms. This study highlights the significance of in silico methods and interaction visualization in drug discovery, and presents promising candidates for further development in combating antibiotic resistance.



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sciforum-115974: In Silico Exploration of Quinoline Derivatives as Novel Antimicrobial Agents Targeting Resistance Mechanisms

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The escalating challenge of antibiotic resistance underscores the urgent need to develop novel antimicrobial agents with innovative mechanisms of action. This study investigates the potential of quinoline derivatives as inhibitors of two critical microbial targets: DNA gyrase (PDB ID: 2XCT) and dihydropteroate synthase (PDB ID: 5U10). A library of 22 quinoline-based compounds was subjected to molecular docking to assess their binding affinities and interactions with these essential enzymes.

CMPD1 and CMPD2 emerged as promising candidates. CMPD1 exhibited a binding affinity of -9.3 kcal/mol with DNA gyrase, forming stabilizing hydrogen bonds with ARG 98 and ASP 85, while CMPD2 displayed a binding affinity of -8.8 kcal/mol with the same target. Against dihydropteroate synthase, CMPD1 and CMPD2 showed binding affinities of -9.0 kcal/mol and -8.5 kcal/mol, respectively, leveraging pi-pi stacking and hydrogen bonding interactions with critical active-site residues. The structure-activity relationship (SAR)-driven library design incorporated electron-donating (-OCH₃) and electron-withdrawing (-Cl) groups, strategically enhancing the binding specificity and affinity of these compounds.

In addition to docking, in silico ADMET profiling confirmed favorable pharmacokinetic properties for the lead compounds. CMPD1 demonstrated high gastrointestinal absorption and zero Lipinski's rule violations, while CMPD2 demonstrated acceptable absorption with only one rule violation, highlighting their potential for oral bioavailability and safety.

These findings underscore the potential of quinoline scaffolds as novel agents to combat antibiotic resistance. This study highlights the utility of computational tools in identifying promising drug candidates, paving the way for experimental validation, and developing quinoline-based therapies to address the global antibiotic resistance crisis.



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sciforum-118700: Isolation, Purification and Antifungal Activity of Daidzeins Produced by Halotolerant *Streptomyces sampsonii* INA01478

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The antifungal potential of 12 isolates of *Streptomyces* derived from the bottom sediments of Trondheim Fjord, the Norwegian Sea, was investigated. It was found that the metabolites produced by the *Streptomyces sampsonii* INA01478 strain had pronounced antifungal activity against the opportunistic fungi *Candida albicans* and *Fusarium oxysporum*. To analyze the biologically active metabolites formed, a method of preparative separation using HPLC and a method for isolating individual compounds from the eluent were selected. The chromatograms of the tested samples obtained using the HPLC method showed two peaks with close retention times. Repeated preparative HPLC resulted in the isolation of two pure compounds that were identified using NMR and an MS data analysis. The major component of the subfraction was determined to be daidzein ([7-hydroxy-3-(4-hydroxyphenyl)-4H-1-benzopyran-4-one]), an isoflavonoid that has previously been described. The minor component had a similar but simultaneously different structure, the establishment of which is being studied. Daidzein exhibited a direct antifungal effect at 25 – 30 µM on *Saccharomyces cerevisiae* INA 01042 and the opportunistic filamentous fungi *Aspergillus niger* ATCC 16404 and *Fusarium oxysporum* VKPM F-148 and was totally inactive against the bacterial test organisms.

Daidzein is a naturally occurring phytoestrogen belonging to the group of non-steroidal estrogens. It is structurally similar to mammalian estrogen, so it can replace and/or inhibit it and thus has protective effects against diseases associated with estrogen control. [Goleij P et al., 2004]. In addition, daidzein inhibits oxidative damage and regulates immune reactions and apoptosis. Daidzein has a wide range of pharmacodynamic properties and represents a promising compound for drug development.



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sciforum-115953: Microbial Importance in the Synthesis of Chiral Drugs and Drug Intermediates for the Benefit of Mankind

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Microbial systems play a crucial role in the synthesis of the chiral drugs and drug intermediates, contributing significantly to the pharmaceutical industry. Chirality refers to the existence of two non-superimposable mirror-image molecules (enantiomers), which can have vastly different biological activities. In many cases, one enantiomer may be therapeutically active, while the other could be ineffective or even harmful. Thus, the ability to produce chiral compounds with high specificity is essential in modern medicine. Functional microorganisms and enzyme (derived biocatalysts) have great potential in the biotransformation of synthetic chemicals in drugs with high enantiomeric, chemical and regional selectivity. The Chiral feature is an important factor in the efficacy and safety of many therapeutic drugs. Biocatalysis is becoming a major sub-component in the toolbox of medicinal chemistry. In fact, many intermediates of important therapeutic agents have been successfully synthesized by biocatalysis. Currently, about 57% of drugs on the market are chiral drugs, and about 99% of pure natural products are chiral compounds. Here, we have summarized various biocatalytic systems capable of synthesizing chiral drugs and intermediates and discussed their potential applications in the pharmaceutical industry. With the emphasis on green chemistry, the further development and use of biocatalysis in drug production is expected to increase.



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sciforum-118129: Nanotechnology as a promising strategy for controlling oral polymicrobial biofilms

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Introduction:

Oral polymicrobial biofilm formation occurs as a result of the synergistic interaction of fungal (e.g., *Candida albicans*) and bacterial pathogens (e.g., *Staphylococcus aureus*) and has been reported to cause severe dental caries and periodontal diseases. One of the promising ways of combating biofilms is the use of nanoparticles (NPs) manufactured utilizing green chemistry. The present study aimed to synthesize gold NPs using fucoidan, β -caryophyllene, and phloroglucinol to control oral polymicrobial biofilms caused by *S. aureus* and *C. albicans*.

Methods:

Fucoidan–gold nanoparticles (Fu-AuNPs), β -caryophyllene–gold nanoparticles (β -c-AuNPs), and phloroglucinol–gold nanoparticles (PG-AuNPs) were synthesized using natural molecules. These NPs were characterized using UV-vis absorption spectroscopy, FTIR, FE-TEM, EDS, DLS, zeta potential, and XRD. The colony counting method was employed to check the antibiofilm effects of these NPs towards polymicrobial biofilms of *S. aureus* and *C. albicans*.

Results:

The synthesized Fu-AuNPs, β -c-AuNPs, and PG-AuNPs were found to be spherical in morphology, with sizes of 75.66 ± 9.28 nm, 17.6 ± 1.2 nm, and 46.71 ± 6.40 nm, respectively. The minimal inhibitory concentration (MIC) of Fu-AuNPs, β -c-AuNPs, and PG-AuNPs against *S. aureus* and *C. albicans* was determined to be 1024 μ g/mL, 512 μ g/mL, and 2048 μ g/mL, respectively. The inhibition of polymicrobial biofilms of *S. aureus* and *C. albicans* by these NPs was significant at the sub-MIC level and was concentration-dependent. In addition, Fu-AuNPs, β -c-AuNPs, and PG-AuNPs at MIC and above MIC significantly eradicated mature polymicrobial biofilm.

Conclusions:

This study demonstrated that Fu-AuNPs, β -c-AuNPs, and PG-AuNPs act as an alternative strategy to control oral pathogens by inhibiting the initial stage of biofilm formation and eradicating mature polymicrobial biofilms of *S. aureus* and *C. albicans*.

Funding:

This research was supported by the Basic Science Research Program through a National Research Foundation of Korea grant funded by the Ministry of Education (RS-2023-00241461) and Research Grant of Pukyong National University in 2024 (202416570001).



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sciforum-115897: New 2,8-Bis(Trifluoromethyl)Quinoline-4-Carboxamides As Potential Antimycobacterial Agents

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Bacterial infections are the second leading cause of mortality worldwide and represent a major global health challenge. In 2023, approximately 1.25 million deaths were linked to tuberculosis, making it one of the deadliest infectious diseases in the world. In recent years, non-tuberculous mycobacteria (NTM) have also become a public health issue and are closely monitored by researchers. Currently, their incidence exceeds that of tuberculosis in North America and Europe, with 1.0 to 1.8 cases per 100,000 people. NTM are opportunistic bacteria and commonly found in natural or urban water sources. Some species are known as pulmonary pathogens and mainly infect people with compromised immune systems or pre-existing lung diseases such as cystic fibrosis, bronchiectasis, or chronic obstructive pulmonary disease. NTM are classified into two main groups : slow-growing species such as MAC complex (with *M. avium*, *M. intracellulare*, and *M. chimaera* mainly), *M. xenopi* and *M. kansasii*, and rapid-growing species such as *M. abscessus* complex (smooth and rough) and *M. fortuitum*. Current NTM infection treatments involve a long treatment (18 to 24 months) and rely on a combination of three antibiotics, generally including a macrolide. However, the effectiveness of these treatments remains limited, with a moderate cure rate, some side effects, and an increasing resistance to macrolides. Some developed or commercial antimicrobial agents, containing a quinoline ring, have shown potent antimycobacterial activity against NTM, such as bedaquiline (BQ), mefloquine (MQ), and Labio-17. Based on MQ's pharmacophore, the main objective of this work was to develop new 2,8-bis(trifluoromethyl)quinoline-4-carboxamides as new antimycobacterial agents. Here, we present the design, synthesis, and first biological results of new MQ-based compounds.



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sciforum-115670: Novel Aminoquinoline Bi-Aromatic Hybrids As Anti-Biofilm Agents Against *Pseudomonas Aeruginosa*

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The antibiotic resistance crisis has led the WHO to name several pathogens as priorities for the development of new treatments. In this context, a promising alternative approach to conventional antibiotics (ATBs) has been explored to fight multi-drug-resistant bacteria. The so-called “anti-virulence strategy” aims at diminishing bacterial pathogenicity without affecting cell growth, in order to circumvent the selection pressure issues mediated by standard antibiotherapy. Anti-virulence agents (AVAs) could find a use in biotherapy to restore the efficacy of ATBs, or in monotherapy to potentiate the immune system’s response. Among the WHO’s targets stands the opportunistic gram-negative bacterium *Pseudomonas aeruginosa*, the main cause of chronic and hard-to-treat lung infections in immunocompromised patients. A major virulence trait of *P. aeruginosa* is the development of biofilms, i.e., microcolonies embedded in a protective self-produced extracellular matrix. These complex structures provide advantageous microenvironments for pseudomonal growth, as well as shielding barriers against the immune system and ATBs. The development of biofilms is mostly coordinated by quorum sensing (QS), a bacterial communication network regulating pathogenicity according to population density. Therefore, the development of quorum sensing inhibitors (QSIs) has been considered a good strategy to eradicate *P. aeruginosa* infections. In the literature, several bi-aromatic hybrids have been described as potent QSIs against *P. aeruginosa*. By structural analogy, the AGIR laboratory highlighted a first-hit 2-indazolyl-4-quinolone with promising anti-virulence properties. More recently, the team developed a new family of aminoquinoline bi-aromatic hybrids as QSIs able to efficiently inhibit *P. aeruginosa* motility and biofilm formation. This presentation describes the synthesis of those new AVAs as well as their physicochemical and biological evaluation.



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sciforum-116302: Pharmacological Evaluation Essential Oils from *Cinnamomum verum* and *Artemisia herba alba*: Chemical Profiling and Bioactive Applications in Oxidative Stress and Inflammation

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The therapeutic potential of essential oils (EOs) from *Cinnamomum verum* (C. verum) and *Artemisia herba alba* (A. herba alba) was investigated through a comprehensive analysis of their chemical composition, antioxidant, anti-inflammatory, and antibacterial activities. Gas Chromatography--Mass Spectrometry (GC-MS) analysis identified cinnamaldehyde (72.76%) as the primary component in C. verum EO and camphor (55.59%) as the major constituent in A. herba alba EO. In vitro assays revealed that C. verum EO exhibited superior antioxidant activity, with a nitric oxide (NO) scavenging activity of 85.4% at 200 µg/mL and a ferric reducing power (FRP) of 1.2 absorbance units at 700 nm, compared to A. herba alba EO, which showed 45.6% NO scavenging and 0.6 absorbance units in FRP. Both EOs displayed dose-dependent antibacterial activity against pathogenic strains, with C. verum EO showing inhibition zones of 22.5 mm and 20.3 mm against *Staphylococcus aureus* and *Escherichia coli*, respectively, while A. herba alba EO exhibited zones of 18.7 mm and 16.4 mm. In the red blood cell (RBC) H₂O₂-induced hemolysis model, C. verum EO demonstrated strong anti-inflammatory and protective effects, inhibiting hemolysis by 78.3% at 200 µg/mL, compared to 52.6% for A. herba alba EO. A 50:50 combination of the two EOs showed intermediate activity, with 65.4% inhibition of hemolysis, suggesting partial synergy. In silico ADMET analysis predicted high oral bioavailability (80-90%) and strong intestinal absorption for the major compounds, with cinnamaldehyde and camphor showing potential for brain penetration (BOILED-Egg model). Molecular docking studies revealed the strong binding affinities of δ-cadinene (ΔG_b = -7.48 kcal/mol) and α-thujone (ΔG_b = -4.75 kcal/mol) to key enzymes involved in inflammation, oxidative stress, and bacterial infections, supporting their multitarget therapeutic potential. These findings highlight the promising applications of C. verum and A. herba alba EOs as natural agents for combating oxidative stress, inflammation, and bacterial infections, with potential for integration into therapeutic formulations.



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sciforum-117096: Rational Design of Peptides as New Type of Broad-spectrum Antibacterial Candidates

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The antibiotic resistance crisis has been a global health threat for decades, because bacterial pathogens, viruses, and other parasites evolve to resist current antibiotics. This has led to unmet needs for the discovery of new compounds that are different from the current antimicrobials. Antimicrobial peptides (AMPs), as promising alternatives to conventional antibiotics, have attracted growing interest owing to their lower likelihood of causing bacteria to develop resistance compared with antibiotics. In this study, we rationally designed a series of peptides, evaluated their antibacterial activities, and investigated their modes of action against bacteria.

Bacterial initiation factor 1 (IF1) is a small protein but plays a critical role in regulating bacterial protein biosynthesis. According to our structural studies on IF1 proteins from three representative bacterial pathogens—*Pseudomonas aeruginosa*, *Clostridioides difficile*, and *Helicobacter pylori*—and their interactions with the 30S ribosomal subunits, we designed a series of IF1-derived short peptides. These peptides were tested for inhibitory activities against various bacteria, including Gram-positive and Gram-negative strains. The results showed that the MIC (minimum inhibitory concentration) of IF1-peptides is as low as 20 μ M against *P. aeruginosa* ATCC 47085, 60 μ M against *C. difficile* ATCC 43593, and 18 μ M against *Staphylococcus epidermitis* ATCC 12228 and *Bacillus cereus* ATCC 14579. Further investigation of the mode of action showed that IF1-derived peptides did not affect the bacterial membrane integrity based on the SEM results; however, they displayed dose-dependent inhibition against bacterial protein synthesis. These results suggest IF1-derived peptides as new type of antibacterial candidate. Since bacterial IF1 is a highly conserved element of the prokaryotic translational apparatus, these results provide a potential avenue for the rational design of new antimicrobials.



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sciforum-110292: RhsP2 protein as a new antibacterial toxin targeting RNA

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Introduction:

A recent study was published in the journal *Molecular Cell* in September 2022; Scientists at McMaster University have identified a toxin that bacteria use to kill other bacteria through bacterial competition within the microbiome by a new mechanism targeting RNA molecules, thus disrupting the various vital functions resulting from it.

Among the group of proteins that the team tested is a protein called RhsP2 produced by "Pseudomonas aeruginosa"; this works by directly affecting RNA molecules with two proposed mechanisms:

1/ ADP ribosylation to prevents the binding of amino acids and then synthesis of bacterial proteins necessary for life.

2/ Inactivation of ribonuclease RNase P.

Work methodology:

Using computational docking and modeling, the interactions between two proteins, namely RhsP2toxin/16S rRNA target, were investigated in detail in order to identify residues belonging to the active sites of the studied toxin RhsP2, which targets 16S rRNA. In our study, we relied on different docking programs such as AuotoDock VINA, HADDOCK lite server, and HADDOCK 2.4 server, and compared the results with a reference compound, rifamycin (which works with a mechanism similar to our studied compound), based on criteria related to affinity binding energy and regularity of atoms within the pocket (RMSD).

Conclusions:

The results show that the HADDOCK lite server showed the closest model (DRUD2) to rifamycin in interaction with the active pocket of the target protein 16S rRNA, followed by the HADDOCK 2.4 (DRUG3). and finally the model generated by the Structuring AuotoDock VINA method (DRUG1).
* Our results were reasonable as a preliminary prediction with one target 16S rRNA, and we can say that the toxic substance RhsP2 has a good interaction with 16S rRNA so we propose it as an inhibitor by binding to the active pocket (such as the action of rifamycin) and inhibiting its function in translating amino acids into proteins.



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sciforum-118628: Screening of basidiomycetes submerged culture extracts with high antibacterial activity

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Introduction:

The search for and study of natural antibacterial and antifungal molecules (including those that overcome pathogen drug resistance) have great scientific and practical importance. Basidiomycetes have a wide range of biosynthetic capabilities and can serve as a source of new biologically active compounds.

The aim of this work was to study the antimicrobial properties of the metabolites that accumulated in basidiomycetes culture liquid.

Methods:

The objects of this study were 20 strains of basidiomycetes from the orders Agaricales, Polyporales, and Russulales. The studied strains were grown in a submerged culture. The culture liquids were extracted using ethyl acetate. The extracts were evaporated, and stock solutions with a concentration of 10 mg/mL were prepared. At first, the antimicrobial activity of the extracts was evaluated through agar well diffusion on a wide test culture panel. At the second step, the minimum inhibitory concentration (MIC) of the most active extracts against Gram-negative and Gram-positive bacteria was determined.

Results:

Antibacterial activity was detected in all of the strain extracts studied. The largest growth inhibition zones of bacteria were observed for the extracts of *Fomes fomentarius* 1; *Fomitopsis betulina* 3; *F. pinicola* 2, *Hericium coralloides* 4, and *Laetiporus sulphureus* 3. Strains *F. betulina* 3 and *H. coralloides* 4 demonstrated weak antifungal activity against *Aspergillus niger* ATCC 16404.

The lowest MIC values were observed for 80 µg/mL of *H. coralloides* 4 extract against *Staphylococcus aureus* 25923 ATCC; 160 µg/mL of the former against the clinical strains *S. epidermidis* 533 and *S. haemolyticus* 585; and 320 µg/mL of the former against the vancomycin A-resistant strain *Enterococcus faecium* 569. The MIC of the *L. sulphureus* 3 extract was 320 µg/mL against *S. aureus* 25923 ATCC, *S. epidermidis* 533, and *S. haemolyticus* 585.

Conclusion:

The most active were the *H. coralloides* 4 and *L. sulphureus* 3 culture liquid extracts. The *H. coralloides* 4 extract inhibited the growth of clinical and vancomycin-resistant strains.



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sciforum-117383: Screening of microbiome of bark beetle *Ips typographus* for antibiotic producers

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The study of antibiotic producers from natural sources plays an important role in the development of new drugs. One way to search for antibiotics is the isolation of microbial antibiotic producers from insects and their products [1]. Symbionts and insect-associated microorganisms represent an almost inexhaustible source of bioactive compounds, including antibiotics [2].

In this study, we examined samples of the bark beetle typographus (*Ips typographus*) found in the bark of fallen spruce (*Picea*). The bodies of insects, previously sedated with diethyl ether, were prewashed with 80% ethyl alcohol to exclude external contaminants. Then, they were homogenized using a sterile glass rod. The obtained mass was suspended in sterile water for inoculation. The inoculum was spread on 9 × 9 cm Petri dishes with brain heart infusion solid nutrient medium (with nystatin, 50 µg/mL), potato dextrose (with tobramycin, 25 µg/mL), nutrient agar (with nystatin, 50 µg/mL), and nutrient agar (with nystatin, 50 µg/mL, and nalidixic acid, 30 µg/mL). A total of 113 microbial isolates were obtained. Antimicrobial activity was screened using the agar diffusion method against a wide range of test microorganisms: a fungus (*A. niger* INA00760), a yeast (*C. albicans* CBS 8836), Gram-positive bacteria (*B. subtilis* ATCC 6633, *E. faecalis* ATCC 29212), and Gram-negative bacteria (*E. coli* ATCC 25922).

As a result, three isolates of micromycetes with pronounced antimicrobial properties were selected for further study and cultivation in liquid nutrient media. The active substances were identified by LC-MS. Strain K1-26 produced harzianic acid. Strain K4-28 produced aspergillic acid. Strain K2-6 produced several antibiotic substances: verruculogen, fumagillin, helvolic acid, and helvolinic acid.

This work was supported by the Russian Science Foundation, project no. 25-14-00281.

1 A. A. Baranova et al., Microorganisms, 2020, 8, 1948.

2 A. A. Baranova et al., Biology, 2022, 11, 1676.



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sciforum-118770: Screening of the leaves of *Camellia japonica* L. for antibacterial activities as a novel antimicrobial agents

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Antimicrobial resistance (AMR) is no longer a future threat but a latent reality that accounts for more than 1 million deaths annually, based on recent data from the World Health Organization (WHO). This jeopardizes the effectiveness of healthcare treatments and poses a potential risk to global public health. The spread of AMR is related to factors such as the overuse of antibiotics and its global spread. Given the urgent need for natural antimicrobial alternatives with mechanisms of action different from conventional antibiotics, plant-derived compounds have emerged as promising candidates. *Camellia japonica* L. is a perennial shrub belonging to the Theaceae family, which has become popular for its garish flowers and the landscaping they provide. The species is native to East Asia and has been traditionally used both in the horticultural industry and for its medicinal properties. Although seed oil is known for its cosmetic and culinary uses as a preservative, the leaves have not been widely studied for their antimicrobial activity. In this work, the natural antibacterial activity of the leaves of *C. japonica* L., obtained by a simple and economical extraction method such as maceration, has been evaluated against food-borne pathogens in microbiological media. The screened exhibited antimicrobial activity with inhibition zones of 11.87 mm against *Pseudomonas aeruginosa* and 11.73 mm against *Salmonella enteritidis* compared to 12.53 mm and 18.41 mm for the positive control, lactic acid, respectively. However, against *Escherichia coli*, *Staphylococcus aureus*, and *Bacillus cereus*, the leaves of *C. japonica* did not show any activity. These results suggest that *C. japonica* leaves have selective antimicrobial potential, particularly against *P. aeruginosa* and *S. enteritidis*. Further research needs to be carried out to identify and explore their potential applications.



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sciforum-118757: Study on the activity of blackberry (*Rubus caesius* L.) extracts against MRSA

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In one of its reports, the WHO published a list of the pathogenic bacteria that pose the greatest threat to human health due to their rapidly growing resistance to currently used antibiotics. This group is called "ESKAPE" and includes, among others, Gram-positive, resistant strains of *Staphylococcus aureus*. This bacterium can cause a range of infections, from folliculitis and abscesses to severe cases like sepsis, and causes approximately 15% of invasive infections in hospitals worldwide. Methicillin-resistant *S. aureus* (MRSA), in addition to resistance to β -lactam antibiotics, is resistant to aminoglycosides, fluoroquinolones, macrolides, chloramphenicol, and tetracycline. Some strains can produce a biofilm. The growing resistance of bacteria to available antibiotics forces us to search for alternative antibacterial drugs. Plants of the genus *Rubus* are a source of natural compounds used in many infectious diseases. *Rubus caesius* (dewberry) contains, among others, anthocyanins, tannins, flavonoids, and phenolic acids known for their antioxidant and antibacterial properties [1]. However, there are no reports on the antibacterial activity of blackberry leaves (L_{H_2O} , L_{EtOH}) against *S. aureus*. The activity of the extracts was tested in vitro on reference strains of *S. aureus* and clinical strains of MRSA (MIC 0.16 - 3.125 mg/ml, MBC 0.78 - 6.25 mg/ml). We studied the interactions of amikacin and cefoxitin with the tested *R. caesius* extracts and their effect on the inhibition of biofilms produced by clinical strains of MRSA. We show that the extracts tested have a bactericidal effect on clinical strains and inhibit biofilm formation. We suggest that our results will influence a reduction in antibiotic doses and increase their therapeutic effect, which may potentially lead to a faster elimination of microorganisms from the human body.

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sciforum-115210: Synthesis and Antibacterial Action of New Ni(II), Pd(II) and Pt(II) Complexes with Benzimidazole-Derived Schiff Base Ligands

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For decades, antimicrobial resistance has posed a growing threat to the effective treatment of an expanding range of infections caused by bacteria, parasites, viruses, and fungi. This issue disproportionately affects developing countries or those grappling with significant social inequality. In response, medicinal chemistry has developed various drugs that are effective in many cases. However, the improper use of these drugs and the adaptive strategies of prokaryotic cells to evade therapeutic agents have significantly diminished their pharmacological efficacy. To address this challenge, the development of new drugs is essential to improve treatment outcomes in a more efficient, less toxic manner and to overcome the phenomenon of resistance. This research focuses on the synthesis and antibacterial evaluation of novel Schiff base-type compounds derived from benzimidazoles coordinated with group 10 metals (nickel, palladium, platinum), which are well-documented for their antimicrobial and antitumor activities. The synthesized compounds were characterized using spectroscopic and spectrometric techniques, and their antibacterial activity was assessed *in vitro* against resistant bacteria isolated from the Magdalena region of Colombia, employing the broth microdilution method. The minimum inhibitory concentration (MIC) values ranged between 250-0.5 µg/mL against resistant strains of gram-positive (*S. aureus*) and gram-negative (*E. coli*, *K. pneumoniae*) bacteria. Results indicate a synergistic effect between the metal center and the organic ligand, enhancing the biological activity. Notably, platinum-based complexes emerged as promising candidates, even presenting MIC up to 0.5 µg/mL, similar to ciprofloxacin used as a control drug for *S. aureus*.



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sciforum-115254: Synthesis and biological evaluation of new amino-alcohol-quinolines in response to non-tuberculous mycobacteria infections.

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Today, in Europe and North America, the emergence of non-tuberculous mycobacteria (NTM) infections is now outstripping that of *Mycobacterium tuberculosis*. NTM are ubiquitous and opportunistic in people with bronchiectasis or chronic respiratory disease. Among the NTM known for their pulmonary pathogenicity, mycobacteria from the *Mycobacterium avium complex* (MAC) are the most common, responsible for 80% of NTM infections. Current NTM treatments require a combination of antibiotics over a long period and have numerous side effects. For example, the first-line treatment for MAC infections includes a combination of three drugs, namely macrolide, rifamycin and ethambutol, administered for at least twelve months after sputum conversion. These drugs can cause a number of inconveniences or serious effects, including hepatotoxicity, ocular disorders, etc. In addition, the moderate efficacy of this treatment (52% to 60% success rate) is also compromised by the increasing resistance of NTM to macrolides. Consequently, there is an urgent need to develop safer molecules, ideally with novel mechanisms of action, to limit the risk of antibiotic resistance. The quinoline-based pharmacophore is found in mefloquine (MQ), which targets ATP synthase, a vital enzyme for mycobacteria. However, MQ has a moderate activity against NTM (e.g., MIC = 4 µg/mL on MAC) and it can induce side effects on the central nervous system. To improve the selectivity index (SI), novel amino-alcohol-quinolines (AAQs), designed as analogues of MQ, have been developed. A hit compound was identified on MAC with a SI higher than that of MQ (SI = 5.8 vs 0.4) and it has an additive effect with the three drugs used in first-line treatment against MAC. This study presents the design rationale for AAQs, describes their synthesis, and provides an *in vitro* biological evaluation, including assessments of antimycobacterial activity, cytotoxicity, and potential synergistic effects.



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sciforum-118764: Targeting Biofilm-Associated Infections: Antimicrobial and Antibiofilm Effects of Biogenic Zinc Nanoparticles

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The growing resistance to antimicrobial drugs has significantly complicated the effective treatment of infections, prompting global efforts to address this crisis. The World Health Organization (WHO) has prioritized pathogenic bacteria in a recent report to guide research and public health initiatives. This report underscores the critical role of biofilm-associated infections and highlights the need for innovative strategies to combat multidrug-resistant microorganisms. Among such strategies, the green synthesis of metallic nanoparticles has emerged as a promising approach. This environmentally friendly method yields biocompatible materials with significant biomedical potential. Biogenic zinc nanoparticles (ZnNPs), synthesized via eco-friendly methods using *Pseudomonas aeruginosa*, offer a promising approach for biofilm eradication and combating microbial resistance. This study evaluates the antibacterial and antibiofilm activities of biogenic ZnNPs against clinically relevant microorganisms, including biofilm-forming bacterial strains such as *Staphylococcus aureus* and *Escherichia coli*.

Antimicrobial effects were assessed using broth microdilution and time-kill assays. Biofilm formation and eradication were evaluated through crystal violet staining, resazurin assays, and colony-forming unit quantification. Additionally, the oxidative and nitrosative stress toxicity mechanisms triggered by ZnNPs, particularly those related to cellular stress, were investigated. The results demonstrated that ZnNPs exhibit concentration-dependent inhibitory effects on both prokaryotic microorganisms. ZnNPs inhibited biofilm formation by up to 50% in *E. coli* and yeast species and up to 80% in *S. aureus*. These antibiofilm activities were attributed to disruptions in cellular stress metabolism, primarily driven by nitrosative stress through enhanced production of reactive nitrogen intermediates.

The findings reveal significant antimicrobial activity, effectively targeting bacterial biofilms. These results demonstrate the potential of ZnNPs as an innovative strategy for managing biofilm-related complications. Furthermore, they underscore the importance of developing sustainable approaches to address the growing challenge of antimicrobial resistance, providing a strong foundation for future advancements in antimicrobial therapies.



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sciforum-118641: TARGETING CARBAPENEM-RESISTANT INFECTIONS THROUGH PROBIOTIC-BASED LIVING MATERIALS

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The rapid rise of antibiotic-resistant bacteria has emerged as one of the most urgent and critical threats to global public health. Among these, carbapenem-resistant bacteria (CRB) pose a particular challenge, as carbapenem antibiotics are regarded as the last line of defense against multidrug-resistant infections [1]. This study evaluates the antimicrobial properties of probiotic cellulose (PC), a material made of dense cellulose nanofibers colonized by *Lactobacillus* species, which are classified as GRAS (generally recognized as safe). This method overcomes the limitation of bacterial cellulose produced by *Komagataeibacter xylinus*, which lacks intrinsic antibacterial activity [2]. We tested various PC samples, each loaded with *Lactobacillus fermentum* (Lf), *Lactobacillus plantarum* (Lp), or a combination of both (Lp+Lf), against CRB strains isolated from clinical samples at the Hospital Virgen de las Nieves (Granada). Agar diffusion inhibition assays were performed in a medium favorable for pathogen growth to assess efficacy. The results revealed that all PC samples exhibited inhibition zones against the tested CRB strains. The antimicrobial activity of PC is attributed to the encapsulation of probiotics within the cellulose matrix, as free *Lactobacillus* species (without bacterial cellulose) showed no inhibitory effect on the pathogenic strains.

Acknowledgments. The results were funded by the research project "PROBCEL - Probiotic cellulose. A new material for the treatment of antibiotic-resistant bacterial infections", reference PDC2022-133234-I00. The project was funded by MCIN/AEI /10.13039/501100011033 and by the European Union Next GenerationEU/ PRTR.

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sciforum-114841: Targeting Enterococci—How to Overcome β -Lactam Resistance

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Enterococci are the third to second most common pathogens in nosocomial infections. With their intrinsic resistance against cephalosporines and most other β -lactam antibiotics, the treatment of enterococcal infections remains challenging. With the rising resistance against last-resort antibiotics and the emergence of vancomycin-resistant enterococci (VRE), current therapy options are critically limited [1]. A promising way to overcome this burden is to re-sensitize resistant strains to modified approved antibiotics [2]. Therefore, we conjugated polycationic peptides to select β -lactam antibiotics using a bifunctional linker moiety. These conjugates were screened for their antimicrobial efficacy, pharmacokinetics and affinity to penicillin-binding proteins (PBPs). For the most promising ceftazidime-R6 conjugate, a broadened spectrum and up to 1000-fold-higher efficacy could be demonstrated against vancomycin-susceptible enterococci and VRE without increasing cytotoxicity. In vivo studies in rodents showed an altered way of excretion and demonstrated therapeutic efficacy against VRE. The altered PBP-binding profile as well as the faster killing mechanism of the conjugates compared to their parent β -lactam suggest an altered mode of action [3]. These findings go along with our previously reported findings on FU002, a vancomycin derivative, and represent a possible platform technology for cell-wall addressing antibiotics and particular against enterococci [4].

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sciforum-115654: Targeting FabZ: Design and Synthesis of Potential Inhibitors

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Antimicrobial resistance (AMR) poses a critical threat to global public health. Multidrug-resistant bacteria, including *A. baumannii*, *P. aeruginosa*, and *S. aureus*, are major causes of hospital-acquired infections. This resistance phenomenon has also spread to parasites such as *P. falciparum*, the most virulent form of malaria. Therefore, new treatments targeting essential biological pathways that are not addressed by current agents are urgently needed to minimize potential cross-resistance.

Microbial fatty acid biosynthesis, relying on the fatty acid synthase system (FAS-II), is essential for microbial membrane lipid synthesis. The FAS-II enzymes, which are absent in humans, provide a selective target, minimizing the risk of off-target effects on human fatty acid synthesis. Their highly conserved active site amino acid sequences support their broad-spectrum antimicrobial potential, and the available crystal structures in the Protein Data Bank (PDB) offer an excellent opportunity for structure-based drug design. Among the FAS-II enzymes, FabZ dehydratase appears as a promising yet underexplored target in the fight against AMR.

Based on the results of Sharma et al. (2003), we demonstrated that quinoline derivatives, such as NAS91 ($IC_{50} Pf = 12 \mu M$; $IC_{50} PfFabZ = 7.5 \mu M$), inhibit *PfFabZ* activity and suppress *P. falciparum* growth. Structural analyses of NAS91-*PfFabZ* co-crystals revealed key ligand–enzyme interactions, guiding us in the rational design of 37 new 8-arylquinolines. These compounds were evaluated in vitro against a large panel of bacteria and *P. falciparum*, where a first hit, 4c, stood out ($IC_{50} Pf = 13.7 \mu M$). Additionally, their corresponding complexes with different FabZ structures available in the PDB were analyzed by means of detailed in silico studies. Here, we will present the optimized structures of new inhibitors, derived from comprehensive in vitro and in silico findings, as well as their organic synthesis. The optimized production of FabZ enzymes from *H. pylori* and *P. falciparum*, required for enzymatic assays, will also be presented.



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sciforum-116316: The Development of a New Antibiotic Class Targeting Enolase in *Acinetobacter Baumannii*

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The emergence of MDR *Acinetobacter baumannii* (Ab) represents a critical global health threat. We aimed to investigate the antibacterial properties of ENOblock, a compound identified through HTS of the EU-OPENSOURCE library, as potential treatment for MDR Ab.

In vitro assays were conducted to evaluate ENOblock's antibacterial activity using microdilution, time-kill curves, and SYTOX Green membrane permeability tests. Bacterial cytological profiling (BCP) was employed to assess morphological changes after ENOblock treatment, shedding light on its mechanism of action (MoA). To identify the ENOblock molecular target, computational docking was performed to analyze its binding affinity to Ab enolase. Target validation was achieved using an enolase-deficient mutant (Δ eno) by measuring changes in the MIC and bacterial growth. Synergistic effects of ENOblock combined with antibiotics were assessed in reference and colistin-resistant strains. Finally, ENOblock's efficacy was further evaluated in human epithelial and macrophage cells and in a *Galleria mellonella* model.

ENOblock demonstrated potent antibacterial activity with an MIC₅₀ of 16 mg/L against clinical carbapenem- and colistin-resistant Ab strains, surpassing the MIC₅₀ values of colistin and imipenem/meropenem. SYTOX Green assay revealed that ENOblock caused rapid and extensive membrane damage. BCP analysis revealed unique morphological changes not observed with clinically used antibiotics, suggesting a distinct ENOblock MoA. Computational docking indicated strong binding of ENOblock to enolase. The Δ eno strain exhibited a four-fold increase in MIC and greater growth resistance to ENOblock, supporting enolase as its probable target. Importantly, ENOblock exhibited synergistic effects with colistin, enhancing its efficacy against both reference and colistin-resistant strains. Furthermore, ENOblock significantly reduced Ab adherence/invasion in epithelial and macrophage cells in vitro and improved survival rates in *G. mellonella* infected with Ab, demonstrating its therapeutic potential.

These findings highlight ENOblock as a promising candidate for antimicrobial development, with the potential to combat the critical threat posed by MDR Ab infections.



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Session 5. Multidisciplinary Antimicrobial Strategies: Materials, Peptides, Bacteriophages and Repurposing

sciforum-118277: Development of a Photodynamic Therapy Protocol to control Skin Infections by *Pseudomonas aeruginosa*

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Antibacterial resistance is one of the most significant global health threats, being, in 2019, directly responsible for 1.27 million global deaths and contributing to 4.85 million deaths. The complication of infection treatments leads to an urgent need for novel therapeutics strategies. Antimicrobial Photodynamic Therapy (aPDT) has demonstrated efficacy in eliminating various microorganisms and has become increasingly important as an effective strategy against multidrug-resistant strains. In this study, we assess the photodynamic efficiency of two different photosensitizers (PSs), Methylene Blue (MB) and a Phthalocyanine (ZnPc4+), {4, 40, 400, 4000-(29H, 31H-phthalocyanine-1,8,15,22-tetrayl-k4N29, N30, N31, N32) tetrakis [1- methylpyridiniumato 2-)]} zinc (4b) tetraiodide, for controlling skin infections by a clinical *Pseudomonas aeruginosa* strain. Both PSs were evaluated individually and in combination with Potassium Iodide (KI), a potentiator inorganic salt with photodynamic activity. *Pseudomonas aeruginosa* is a ubiquitous Gram-negative bacterium and one of the most life-threatening pathogens that are frequently implicated in skin infections. For this study, in vitro assays were performed with planktonic cells and biofilms, along with ex vivo assays with porcine skin. In the in vitro assays with MB and with ZnPc4+ in combination with KI, the detection limit of the method that is used to quantify the bacteria was reached. When the PSs were conducted individually, MB was effective against planktonic cells and biofilms, but ZnPc4+ was only effective against planktonic cells. Regarding our ex vivo studies, only the MB without KI was effective against *Pseudomonas aeruginosa*. The addition of KI on porcine skin did not potentiate aPDT with MB and ZnPc4+. Although the PSs alone and in combination with KI on porcine skin did not achieve an inactivation as high as that in the in vitro assays, promising results were obtained with MB after two cycles of treatment. This emphasizes the need for further studies to identify novel strategies to optimize the best ex vivo conditions, namely, under red light and using more treatment cycles.



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sciforum-117822: Fabrication and Characterization of Aloe Vera-Based Coatings via MAPLE: An Antimicrobial Strategy for Addressing Antibiotic Resistance through Essential Oil Influence

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This study presents the synthesis and characterization of apatite–lignin–aloe vera (Ap/Lig/AV) coatings, utilizing the Matrix-Assisted Pulsed Laser Evaporation (MAPLE) technique. The incorporation of natural and renewable materials, such as lignin and aloe vera extract, offers a safer and more environmentally friendly alternative to conventional synthetic antibiotics. This innovative approach aims to not only provide infection prevention but also to address the growing concern of primary and secondary resistance to existing drugs, which poses a significant public health challenge.

Our findings indicate that the chemical properties and stoichiometry of the synthesized coatings were preserved throughout the process. A uniform and homogeneous distribution of the materials was achieved when the amount of essential oil matched that of the organic components. The coatings exhibited hydrophilic characteristics and enhanced cellular viability in cultures with cancerous Mg 63 cells. Furthermore, the composite materials demonstrated significant antimicrobial activity against Gram-positive and Gram-negative bacteria, including *Escherichia coli* and *Staphylococcus aureus*, as well as against the fungus *Candida albicans*.

The utilization of these naturally derived products not only presents a cost-effective solution but also contributes to the development of biodegradable thin films with antibacterial, antioxidant, and anti-inflammatory properties. These advancements highlight the potential of Ap/Lig/AV coatings in biomedical applications, particularly in the context of reducing reliance on synthetic antibacterial agents.



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sciforum-115258: Antibacterial Activity of *Detarium Senegalense* Stem Bark Against Selected Pathogenic Bacteria

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The emergence of antibiotic-resistant pathogens has necessitated the exploration of plant-based antimicrobial agents as alternative therapies. This study evaluates the antibacterial activity of *Detarium senegalense* stem bark extract against clinically significant bacterial species: *Staphylococcus aureus*, *Salmonella species.*, and *Bacillus species*. The stem bark was collected from Daura Local Government Area of Katsina state, Nigeria. Clinical isolates were collected from Ahmadu Bello University Medical Centre then taken to Department of Microbiology for reconfirmation using standard microbiological methods. The stem bark was extracted using ethanol, and the antibacterial efficacy was assessed through the agar well diffusion method at concentrations of 100mg/ml, 50mg/ml, 25mg/ml, and 12.5mg/ml. Inhibition zones were recorded to determine the effectiveness of the extract, and the Minimum Inhibitory Concentration (MIC) was established. The extract demonstrated significant antibacterial activity, with notable inhibition zones against *S. aureus* and *Salmonella species* at 50mg/ml and 25mg/ml, respectively, indicating its potential as a natural antibacterial agent. Phytochemical analysis revealed the presence of bioactive compounds such as flavonoids, tannins, and alkaloids, which likely contribute to the observed antimicrobial effects. This study supports the potential use of *Detarium senegalense* stem bark as a source of bioactive compounds against pathogenic bacteria, providing a foundation for future research into its therapeutic applications and possible development as an alternative treatment for bacterial infections.



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sciforum-115912: Comparative Evaluation Of The Activity Of Staphylococcal Bacteriophages With Different Classes Of Antibiotics

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Introduction.

Phage–antibiotic synergy (PAS) is a novel concept that highlights the combined use of bacteriophages and antibiotics in the fight against bacterial infections. PAS shows promise in overcoming antimicrobial resistance, as phages can enhance the bacterial sensitivity to antibiotics and influence biofilms, resistance mechanisms, and the metabolic activity of microorganisms. In addition to these positive effects, an antagonistic effect has also been described in the interaction between bacteriophages and certain types of antimicrobial agents. Understanding the dynamics of this interaction is crucial for the development of innovative therapeutic strategies against multidrug-resistant pathogens.

Methods.

To determine the effect of different antibiotics on bacteriophage reproduction, a modification of the disk-diffusion method was used. For this, a daily culture of host bacteria and the corresponding model phage strain were added to a melted and cooled medium. After the medium solidified, antibiotic disks were placed on its surface. The effect of antibiotics on bacteriophage reproduction was assessed after 24 hours by determining the inhibition or enhancement of plaque formation at the boundary of the bacterial culture growth inhibition zone. The bacterial test culture used was *Staphylococcus aureus* DSM 799, and the model bacteriophage was phage St12f.

Results.

The experimental results showed that different classes of antibiotics affected the reproduction of the bacteriophage St12f in different ways. Three types of effects were observed: synergy (the enhancement of plaque formation in the zone with sublethal doses of antibiotics), antagonism (reductions in the number and size of plaques), and neutral action. Specifically, synergistic effects were observed with penicillins, cephalosporins, and fluoroquinolones; antagonistic effects were noted with certain antibiotics from the groups of macrolides, tetracyclines, oxazolidinones, rifamycins, sulfonamides, and phenicols. Aminoglycosides exhibited neutral effects.

Conclusions.

We believe that studying phage–antibiotic interactions should become an essential component of the combined use of phages and antibiotics for the treatment of various bacterial infections.



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sciforum-115722: Conditions Mimicking Host Infection Environments Impact Antimicrobial Susceptibilities

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Introduction:

While some aspects of the host–pathogen interface are common to all infection sites, localized environments can have unique factors specific to the body site. Chronic infections are often polymicrobial in nature, with great variation in microbial communities between patients. Additionally, nutrient compositions vary at infection sites across the body. Our research demonstrates that the antibiotic susceptibilities of pathogens can dramatically shift depending on nutritional composition and the presence of other microorganisms.

Methods:

Antimicrobial susceptibility testing (AST) was performed for *Enterococcus faecalis* in Cation-Adjusted Mueller–Hinton Broth (CAMHB), both for the organism alone and the organism grown in a polymicrobial community containing three other common wound pathogens (*Staphylococcus aureus*, *Pseudomonas aeruginosa*, and *Acinetobacter baumannii*). We then performed the same AST in an anaerobic chamber to create an environment without oxygen. Further AST was then performed in media mimicking different body sites (Lubbock Chronic Wound Media (LCWM) and Synthetic Cystic Fibrosis Media 2 (SCFM2)).

Results:

Our results demonstrate that *Enterococcus faecalis* grown in a polymicrobial community in CAMHB displayed increased susceptibility to gentamicin. We believe this is due to heme cross-feeding allowing more gentamicin to enter the cell via altered proton motive force. However, performing the same AST in anaerobic conditions reversed this phenotype. When gentamicin AST was performed in media more representative of different body sites (LCWM and SCFM2), the AST results differed from the CAMHB results. In SCFM2, *E. faecalis* no longer demonstrated increased susceptibility in the community. However, in LCWM, *E. faecalis* displayed increased susceptibility to gentamicin regardless of community presence.

Conclusions:

Overall, our results demonstrate that environmental conditions play a role in determining an individual bacterium's antibiotic susceptibility. By accounting for the infection environment when determining susceptibilities, we can prescribe more effective treatments and improve patient outcomes.



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sciforum-118659: Corrugated Biopolymeric Grafts: A Multifunctional Approach to Vascular Reconstruction and Haemodynamic Optimization

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Introduction

Vascular grafts are essential for cardiovascular reconstruction, haemodialysis access, and aneurysm repair. While synthetic materials like ePTFE and Dacron dominate clinical use, they face challenges including thrombosis, intimal hyperplasia, and infection. Corrugated biopolymeric grafts offer a promising alternative, combining mechanical stability with biocompatibility. However, balancing haemodynamic performance, structural integrity, and infection resistance remains critical. This study evaluates corrugated biopolymeric grafts, emphasising their mechanical behaviour under physiological pressures, computational fluid dynamics (CFD)-guided haemodynamic optimisation, and novel antimicrobial strategies to mitigate biofilm formation.

Methods

Corrugated grafts were fabricated and their mechanical performance was analysed using COMSOL Multiphysics® simulations to model the stress distribution, pressure resistance, and fatigue behaviour under a pulsatile flow. Antimicrobial functionality was integrated. Computational fluid dynamics (CFD) was used to assess their haemodynamic compatibility.

Results

The COMSOL simulations demonstrated that the corrugated designs showed enhanced mechanical stability under cyclic pressure while maintaining compliance comparable to that of the native vessels. The CFD-based haemodynamic modelling confirmed a reduced turbulent flow in the corrugated regions, minimizing thrombogenic risks. Saturability and handling met the surgical standards in the benchtop evaluations.

Conclusions

This work establishes corrugated biopolymeric grafts as a multifunctional solution for vascular reconstruction, uniquely addressing mechanical resilience and CFD-optimized haemodynamics by synergizing the computational design (COMSOL/CFD) with antimicrobial innovation, and these grafts outperformed conventional synthetics in their preclinical metrics. Future work will focus on their in vivo validation and clinical translation, positioning corrugated biopolymeric grafts as a transformative advancement in vascular prosthesis engineering.



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sciforum-118187: Evaluation Of The Inhibitory Effects Of Artemisinin On *Cryptococcus Neoformans*

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Introduction:

Cryptococcus (C.) neoformans has emerged as a pathogen of global importance and has been included in the critical group of the WHO fungal priority pathogens list. This inclusion is mainly due to drug resistance and ill-tolerance. This study sought to evaluate the impact of the anti-mitochondrial drug artemisinin on the growth, mitochondrial function, and virulence of cryptococcal cells. We theorise that the strictly aerobic cryptococcal cells will suffer deleterious effects when exposed to artemisinin, as they cannot switch to an alternate glycolytic fermentative pathway to generate energy.

Methods:

A susceptibility assay was performed to assess the inhibitory properties of artemisinin of three *C. neoformans* isolates and H99, the reference laboratory strain. The ultrastructural changes were examined using SEM and TEM. Mitochondrial function was evaluated by monitoring the overproduction of ROS, cytochrome *c* release, and the activation of caspase 3, an early marker of apoptosis. Infection was established in *Galleria mellonella*, where infected larvae were monitored for cocoon formation. Expression of the *IMPI* gene in the larvae was also assessed.

Results:

A 10-fold increase in artemisinin concentration led to growth inhibition in a dose-dependent manner. In this study, 0.1 mM was defined as the MIC₅₀. Treated cells showed elevated ROS levels and cytochrome *c* in the cytoplasm, indicating dysfunctional mitochondria. The activation of caspase 3 was notably higher in treated cells than in non-treated cells. The larvae with treated cells could form cocoons, while those infected with non-treated cells could not. Moreover, the expression levels of *IMPI* were significantly higher in treated cells than in non-treated cells, suggesting enhanced clearance of artemisinin-treated cells.

Conclusions:

The preliminary data presented in this study present empirical evidence of artemisinin serving as a repurposed control agent that could inhibit cryptococcal growth and assist an infected animal in clearing infection.



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sciforum-114941: Evaluation of yeast metabolites as natural preservatives for cosmetic formulations

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The increasing demand for natural cosmetic products is indicative of a growing awareness of the potential adverse environmental and health implications associated with synthetic compounds. Synthetic preservatives, which are commonly employed in cosmetics to prevent microbial contamination, have been implicated in the occurrence of allergic reactions and contribute to environmental pollution. This has led to a growing demand for safer and more sustainable alternatives. Natural preservatives, particularly bioactive compounds derived from microorganisms, have emerged as a promising substitute due to their biodegradability and compatibility with consumer safety standards.

Of particular interest are bioactive metabolites produced by yeasts, which have gained attention for their ability to inhibit the growth of pathogenic microorganisms.

This study investigated the antimicrobial potential of peptides produced by the yeasts *Saccharomyces cerevisiae* and *Wickerhamomyces anomalus* as natural preservatives in a cosmetic emulsion formulation. Antimicrobial efficacy was evaluated using minimum inhibitory concentration (MIC), minimum bactericidal concentration (MBC) and a 48-hour challenge test against common pathogenic microorganisms including *Escherichia coli*, *Pseudomonas aeruginosa*, *Staphylococcus aureus*, *Staphylococcus epidermidis* and *Candida albicans*. The results showed that the 2-10 kDa peptidic fraction derived from *S. cerevisiae* metabolism achieved MICs as low as 450 µg/mL for *E. coli* and 56.25 µg/mL for *S. aureus*. Similarly, metabolites from *W. anomalus* exhibited MICs of 450 µg/mL against *E. coli* and 575 µg/mL against *S. epidermidis*. The 48-hour challenge test showed a significant reduction in microbial growth when the peptide fractions were applied, particularly against *E. coli* and *S. aureus*.

This study highlights the potential of yeast-derived bioactive metabolites as sustainable and effective alternatives to synthetic preservatives in cosmetics.



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sciforum-115770: Genomic Insights into Bacteriophage PaFZ4: A Potential Alternative to Antibiotics for MDR *Pseudomonas aeruginosa*

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Introduction:

Pseudomonas aeruginosa is a Gram-negative opportunistic pathogen that demonstrates significant resistance to multiple antibiotics of different classes. Bacteriophages, viruses that kill bacteria, have shown great potential against multidrug-resistant (MDR) infections. The phage PaFZ4 was isolated in this study, and its capability to infect MDR *Pseudomonas aeruginosa* strains was characterized. The whole genome sequencing analysis of the phage was performed to understand its potential as an anti-microbial agent.

Methods:

A total of 10 bacteriophages (PaFZ 1-10) were isolated from sewage samples from different areas of Dhaka city. The host range of the bacteriophages was tested against 10 different MDR *P. aeruginosa* strains. The most effective PaFZ4 phage was characterized at different temperatures and pH levels. The whole genome sequencing of PaFZ4 and annotation was performed using the Phagenomics server. BLASTP was used to analyze the putative products of the ORFs, and phylogenetic analysis was performed using MEGA and iTOL. Proksee was used for sequence alignment and the visualization of the coding genes.

Results:

The bacteriophage PaFZ4 has a broad host range and can kill all 10 MDR strains of *P. aeruginosa* studied. The characterizations of the phage indicated that the optimum pH was 8 and the temperature was 50°C. However, at higher temperatures, phage stability decreased significantly. The phage PaFZ4 has a genome sequence length of 43,208 bp with 62.3% GC content. A total of 147 ORFs, along with 59 coding sequences, were detected.

Conclusion:

The phage PaFZ4 shows significant potential to fight against MDR *P. aeruginosa*, with its broad host range and stability under optimal conditions. In the future, an in-vivo analysis will be performed to understand the effectiveness of the isolated phage.



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sciforum-115692: Isolation of Soil Microorganisms for the Synthesis of Gold and Silver Nanoparticles for Antimicrobial Applications

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The isolation of soil microorganisms with the ability to produce antibiotics and other bioproducts represents a key approach for harnessing microbial diversity and discovering biologically significant compounds. Filamentous fungi, which are commonly found in soil, produce substances and compounds rich in biomolecules that function as reducing and stabilizing agents in the synthesis of inorganic nanoparticles (NPs) such as gold nanoparticles (AuNPs) and silver nanoparticles (AgNPs). These nanoparticles play a crucial role in enhancing the efficacy of antibiotics by improving drug delivery, increasing bacterial targeting, and combating resistance mechanisms.

This study investigates the efficacy of filamentous fungi isolated from soil samples in producing antimicrobial compounds, as well as their ability to synthesise AuNPs and AgNPs, with the aim of developing new next-generation antibiotics. The isolated fungi were tested for antimicrobial activity using the agar-well diffusion method against pathogenic bacterial strains. The fungi showing the most promising antimicrobial results were identified through DNA sequencing, and their capability to synthesize NPs was explored by exposing the extracellular extract to chloroauric acid or silver nitrate.

The results demonstrated promising minimum inhibitory concentration (MIC) values against pathogenic bacteria, including *Escherichia coli*, *Staphylococcus aureus*, *Bacillus cereus*, and *Pseudomonas aeruginosa*. The follow-up work involves the characterization of antimicrobial compounds and NPs, along with further optimization of their use.

This study underscores the importance of exploiting fungi isolated from soil to discover novel antimicrobials and highlights the advancement of green nanoparticle synthesis as crucial for creating next-generation antibiotics. This approach aims to minimize ecological harm while addressing antibiotic resistance.



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sciforum-115870: Modification of Polyvinylidene Fluoride (PVDF) Surgical Meshes with Bentonite-Based Nanocomposites for Enhanced Antimicrobial Performance and Drug Delivery Applications

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The increasing demand for biocompatible and infection-resistant surgical implants has driven research towards surface modifications of polymeric materials. This thesis investigates the functionalization of polyvinylidene fluoride (PVDF) surgical meshes with bentonite-based nanocomposites to enhance their antimicrobial efficacy and drug delivery potential. The modified meshes were prepared using combinations of bentonite nanoparticles with silver nanoparticles, Levofloxacin, and propolis. Comprehensive characterization was performed using scanning electron microscopy (SEM) and antimicrobial activity assays against various bacterial strains. Additionally, the diffusion behavior of the therapeutic agents through the bacterial membranes was modeled using the COMSOL Multiphysics software. The results demonstrated that the incorporation of bentonite-based composites significantly improved the antimicrobial properties of the PVDF meshes while maintaining their structural integrity and biocompatibility. This study provides insights into the development of advanced surgical materials with sustained drug release capabilities, offering potential applications in infection-prone medical procedures. Antibiotic resistance increases each year, and for this reason, researchers have focused on creating new types of materials able to combat bacteria and fungi. The use of systemic antimicrobials has increased in recent years for the treatment of skin infections; however, these drugs come with a risk of side effects such as diarrhea, stomach cramps, and the development of antibiotic resistance in the microbiota of the intestines. The main aim of this work was to integrate these four composites and study their antimicrobial activity properties. The panel of bacterial cultures included *Staphylococcus aureus* 1199, *Staphylococcus aureus* 1199B, and *Staphylococcus epidermidis* ATCC 14990 and a clinical isolate (*Pseudomonas aeruginosa*), and they were used to evaluate the antibacterial activity of the prepared samples. The designed nanocomposites showed high activity against all of the test cultures compared with that of the non-modified meshes. A high inhibition zone was exhibited for NB@LVF@AgNP@P (55 ± 0.5 mm) when it was tested with *Staphylococcus aureus* 1199 and *Staphylococcus epidermidis* ATCC 14990.



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sciforum-115973: Potentiation of Antibacterial Activity of Cefixime in Synergy with *Cirsium Arvense* (L.)

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Background:

Antibiotics have been known as "miracle drugs" for good reason, but due to their overuse, most antibiotic bacterial combinations now have higher frequencies of resistance. Plants have been discovered to be synergistic enhancers, meaning that they may not possess any antimicrobial qualities alone but can increase the effectiveness of conventional medications.

Methodology

Successive extraction with sonication-aided maceration was used to prepare ethyl acetate (EA), methanol (M), and aqueous (Aq) extracts of *C. arvense*, which were subjected to chromogenic assays for phytochemical evaluation and antioxidant activity. Antibacterial activity was determined using disc diffusion and microbroth dilution assays. Synergistic evaluation of the extracts and mechanistic insights were provided using the checkerboard method, time–kill kinetics, and protein estimation studies.

Results

The aqueous extract exhibited the highest percent recovery (7.33%), the highest total phenolic (16.95±0.16 µg GAE/mg of extract) and flavonoid contents (10.925±0.13 µg QE/mg of extract), and a notable antioxidant capacity (102.86±0.01 µg AAE/mg of extract) and reducing power (121.5±0.03 µg AAE/mg of extract) and significant radical scavenging activity (18.2±0.09%). The extracts showed noteworthy antibacterial activity (MIC = 500 µg/ml). The checkerboard method revealed total synergism, with 4- and 16-fold reductions in the MICs of the *C. arvense* extracts and cefixime, leading to a time-dependent reduction in bacterial growth. Together with the cell membrane damage brought on by cefixime, the synergistic combinations resulted in greater inhibition of bacterial proteins. Our findings suggest that the *C. arvense* aqueous extract showed the maximum synergistic activity and could be a potential candidate for the treatment challenges of global multidrug resistance.

Conclusion

This research highlights the promising antibacterial efficacy of *C. arvense* extracts, demonstrating their potential in combination with cefixime to inhibit bacterial growth. This study underscores the potential to integrate *C. arvense* extracts with conventional antibiotics, offering a novel approach to combating infectious diseases.



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Session 6. Antibiotic Clinical Studies, Pharmacokinetics and Pharmacodynamics

sciforum-111431: Antibiotics for the Treatment of Haemorrhoidal Disease: the Cons and the Pros

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Introduction.

Haemorrhoidal disease is probably the most common pathological condition; it leads to high morbidity and seriously impacts the patients' lifestyle. Surgery for haemorrhoids is a naturally contaminated procedure that may require antibiotic prophylaxis to lower the risk of infection. However, little data are available emphasizing antibiotic use for this condition.

Methods.

Eighty-two patients participated in the study following a selection and exclusion procedure. Among them, 51.2% were female, and 48.8% were male, with a mean age of 49.4 ± 12.8 years. The prevalence of preoperative risk factors for surgical site infection included 18.3% with a smoking history, 6.1% with diabetes mellitus type II, 2.43% receiving systemic steroids, and 3.7% with other local factors including IBD. All patients underwent multimodal treatment (conservative and surgery). All surgeries performed were hemorrhoidectomies, predominately for classic 3-column (left lateral, right anterior, and right posterior positions), prolapsed internal, and mixed internal and external hemorrhoid disease. Single administration or a short duration (one-day) of antibiotic prophylaxis was employed. Oral doxycycline 100 mg or Levofloxacin 500 mg were used.

Results.

Antibiotic prophylaxis was used in an approximately same number of surgeries (46.3% vs 53.7%, closed and open procedures, respectively). Overall, there were only 2.43% of documented postoperative infections identified. All those patients who developed postoperative surgical site infections did not receive antibiotic prophylaxis. However, no perioperative risk factor was reliably associated with an increased risk of developing a surgical site infection after hemorrhoidectomies. In addition, there were no adverse antibiotic-related complications such as antibiotic-associated diarrhoea or *C. difficile* colitis in patients receiving antibiotic prophylaxis.

Conclusions.

The study results are confusing, probably because of low rate of the surgical site infection following hemorrhoidectomies. Conversely, no patients with antibiotic prophylaxis demonstrated postoperative surgical site infection, and from this point of view its use appears plausible. Further studies with significantly larger involvement of patients may clarify the issue.



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sciforum-118794: Bio-absorbable Antibiotic Beads for Vascular Graft Infection Management: Challenges and Future Prospects

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Vascular stenosis and occlusion are the key causes of cardiovascular diseases, which are major contributors to global mortality. Surgical revascularization remains one of the most sought-after treatment options for long-term vessel restoration. However, surgical site infections pose serious concerns, especially when synthetic scaffold materials are in use. Bio-absorbable antibiotic beads represent a promising solution to combat vascular graft infections. These beads facilitate localized delivery of high antibiotic dosages, leading to minimized systemic toxicity with targeted therapeutic effects. This review aims to evaluate the strength of evidence concerning the efficacy of antibiotic beads for vascular intervention. A comprehensive literature search across PubMed, MedlinePlus, and Embase identified relevant studies while excluding conventional surgical interventions. Modern alternatives, i.e., silver-coated grafts and stem cell therapy, were also excluded. Polymethyl methacrylate (PMMA) beads were the most commonly used formulation, with growing interest in biodegradable formulations such as calcium sulfate beads. The search strategy included keywords such as "Vascular Surgery," "Vascular Grafts," "Vascular Graft Infections," and "Antibiotic Beads." Evidence indicates that bio-absorbable antibiotic beads could be highly beneficial in vascular surgery for infection prevention and to reduce systemic complications. Future studies should focus on the effectiveness of beads based on different microbial factors to attain the best possible outcomes.



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sciforum-114765: Determination of Genes Encoding Antibiotic and Copper Resistance in Enterococcus Originated from Different Ecosystems

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Bacteria of the genus *Enterococcus* are an integral part of the gastrointestinal (GI) tract of the animal microbiome and can be found in fermented meat and dairy products, mostly due to poor food handling and their ability to grow under extreme conditions. Bacterial infections are treated with antibiotics, and the rise of enterococci, which are resistant to a variety of antibiotics and have the ability to transfer genetic material, is a notable problem in modern medicine. The uptake of heavy metals in animal feed and resistance to them has been associated with resistance to glycopeptides and macrolides for many years. We wanted to determine the presence of genes encoding for acquired resistance to antibiotics and heavy metals like copper. To this end, enterococcal isolates from different ecosystems were used in this study. The enterococcal isolates were obtained from the faeces of wild boar (*Sus scrofa*) (n = 30), spontaneously fermented sausages produced from the meat of wild boar and domestic pigs (*Sus domesticus*) (n = 10), and traditionally produced Istrian cheese (n = 5). Antibiotic-resistant genes for erythromycin and tetracycline and those for heavy metal copper were confirmed using multiplex PCR methods. The gene coding for erythromycin was found in 33.33% of faecal isolates, in 20% of cheese isolates, and in 10% of sausage isolates, and the gene coding for tetracycline was found in 80% of faecal isolates, in 20% of sausage isolates, and in none of the cheese isolates. A gene coding for copper was detected in 56.66% of the faecal isolates, then in 40% of the cheese isolates, and 30% of the sausage isolates. Our results suggest that genes encoding for acquired resistance to antibiotics and the heavy metal copper are present in the collected enterococcal isolates, and that even though isolates were collected from different ecosystems, they show similar trends for the presence of resistance genes.



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sciforum-114845: Feasibility of 24 h Continuous Infusion of Cefiderocol Administered by Elastomeric Pump in Attaining an Aggressive Pharmacokinetic/Pharmacodynamic (PK/PD) Target in the Treatment of NDM-Producing *Klebsiella Pneumoniae* Otomastoiditis

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Introduction:

Cefiderocol, a siderophore cephalosporin, has emerged as a key treatment for managing multidrug-resistant (MDR) infections, with its time-dependent pharmacodynamics optimized by prolonged infusion to maintain effective concentrations ($fT > MIC$). While current technical data sheets recommend reconstitution and use within 6 hours, due to limited stability data, recent findings suggest cefiderocol concentrations remain stable for up to 72 hours at 25°C in elastomeric pumps. Despite its potential, the application in 24-hour continuous infusions (CIs) in an outpatient parenteral antibiotic therapy (OPAT) setting remains undocumented. This case highlights the successful use of cefiderocol via 24-hour CI in an elastomeric pump, supported by therapeutic drug monitoring (TDM), achieving effective serum levels in an OPAT setting.

Methods:

A 31-year-old virologically suppressed male, with a prior history of AIDS (cryptococcal meningitis) in 2023, presented with right-sided otomastoiditis caused by *Klebsiella pneumoniae* producing New Delhi metallo-beta-lactamase (NDM). Given the resistance profile and the need for prolonged therapy, cefiderocol was initiated at 6 g/day via a 24-hour CI using an elastomeric pump (Baxter Infusor LV 10 mL/h). TDM was performed on days 17 and 45 to assess plasma concentrations and ensure pharmacokinetic/pharmacodynamic (PK/PD) target attainment.

Results:

TDM confirmed steady-state concentrations (C_{ss} 25.2–28.1 mg/L), achieving optimal PK/PD target attainment, such as $100\% fT > 4-6 MIC$ (fC_{ss}/MIC 11.8–12.1). Significant clinical improvement avoided the need for planned surgery, with no adverse events reported from the venous catheter, antibiotic therapy, or elastomeric pump.

Conclusions:

This approach underscores the feasibility and efficacy of cefiderocol administered by 24 h CI using elastomeric pumps, supported by real-time TDM to achieve an aggressive PK/PD target for the treatment of otomastoiditis due to NDM-producing *Klebsiella pneumoniae*. By minimizing hospitalization and enabling outpatient care, this strategy also significantly enhances the patient's quality of life.



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sciforum-114915: The Impact of Augmented Renal Function on Vancomycin Pharmacokinetics in Neuro-critically Ill Patients

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Introduction:

Hospital-acquired infections are relatively common in hospitalized patients, especially those who are critically ill or with invasive devices. Vancomycin is an antibiotic that is widely used to treat methicillin-resistant staphylococcus-aureus; an organism that is usually could be the causative of the hospital-acquired infections especially among critically ill patients. As vancomycin is mainly eliminated from the body through the kidney, the renal function plays an important role in the dosing of vancomycin. Augmented renal function is a common condition among neurocritical ill patients. The aim of this study is to observe the pharmacokinetics and optimize the dosing of vancomycin in neurocritical ill patients.

Methods:

A prospective observational study of neurocritical ill patients received vancomycin at University of Alberta Hospital. Population pharmacokinetics of vancomycin were conducted using Monolix software. Moreover, non-compartmental analysis was conducted to observe the vancomycin pharmacokinetics differences among patients. Monte Carlo simulations were performed to predict the percentage of patients reaching the target concentrations following different doses.

Results:

A total of 55 patients with 149 observations were included in this study. The population clearance was 0.083 L/kg.hr, and the volume of distribution was 1.02 L/kg. The model which best fitted the population was one compartment model with creatinine clearance (CrCl) and body mass index added as covariates on vancomycin clearance. In the non-compartmental analysis, there were 7 out of 11 patients with augmented renal function. There was a positive correlation between the vancomycin clearance and CrCl ($r^2 = 0.3346$, $P=0.04$), and a negative correlation between area under the curve-to-dose ratio and CrCl ($r^2 = 0.5778$, $P=0.003$).

Conclusion:

Vancomycin clearance is affected by changes in CrCl observed in patients with augmented renal function. Therefore, dosing optimization in such population is essential to reach the target concentrations.



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Session 7. Clinical and Environmental Impact of Bacterial Biofilms

sciforum-115935: A Review on Occurrence of Antibiotic-Resistant Bacteria in Groundwater

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In recent years, antibiotic resistance in groundwater has become a significant environmental and public health concern, with limited research on the issue. This review aims to synthesize existing research on the occurrence, distribution, and factors influencing the presence of antibiotics and antibiotic-resistant bacteria (ARB) in groundwater. Identifying and understanding the sources and pathways for antibiotics and ARB is critical in groundwater, as it is a vital source of drinking water for 2.2 billion people worldwide and is recurrently linked to significant outbreaks of infection. This review includes studies from the years 2004 to 2025 and it revealed that groundwater samples contained isolates that were resistant to antibiotics. Most of the studies on occurrence of antibiotics resistance in groundwater was carried out in China. Our meta-analysis revealed that sulfonamides, tetracyclines, and fluoroquinolones, are frequently detected in groundwater sources although the occurrence is less compared other water matrices. The highest mean value of CIP in groundwater was reported to be 28.13 mg/L. Reactivity, Hydrogeological and Physicochemical factors are vital factors involved in the transport and fate of ARB in groundwater, whereas environmental factors, such as groundwater flow, aquifer characteristics, and proximity to pollution sources, contribute to the variability of ARB contamination levels. This review highlights the urgent need for enhanced monitoring, improved wastewater management, and effective strategies to mitigate the infiltration of antibiotics and ARB into groundwater to protect both environmental and public health.



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sciforum-118756: Antimicrobial Residues and Resistance in Biofilms from Livestock Farms: A Scoping Review

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Introduction:

Biofilms are complex microbial communities that form on biotic and abiotic surfaces within livestock farming environments. Within biofilms, bacteria can efficiently exchange genetic material, including antimicrobial resistance genes (ARGs), potentially serving as reservoirs and amplifiers of antimicrobial resistance (AMR). This scoping review aimed to summarize the current knowledge on AMR, ARGs, and antimicrobial residues (ARs) in biofilms from poultry, swine, and cattle farms.

Materials and methods:

This scoping review followed the Preferred Reporting Items for Systematic Reviews and Meta-Analyses extension for Scoping Reviews (PRISMA-ScR) guidelines. Four databases (PubMed, Scopus, Web of Science, and Agricola) were searched using relevant keywords. Peer-reviewed studies assessing AMR, ARGs, and ARs in farm environment biofilms were eligible for inclusion. The identified studies were imported into Zotero for deduplication and subsequently screened in Rayyan in two phases (title/abstract and full text). Data from the included studies were extracted and charted using an Excel® 2016 spreadsheet.

Results:

A total of 1,242 studies were identified across the databases. After deduplication and title/abstract screening, 52 studies proceeded to the full-text screening, with only 4 meeting the eligibility criteria. The included studies were published between 2021 (n =1) and 2022 (n= 3) and originated from Germany, India, and Iran. Two of these studies focused on broiler farms, one on layer farms, and one on dairy cow farms. Among the four studies, three conducted antimicrobial susceptibility testing, one investigated ARGs, and none reported on ARs from biofilm isolates.

Conclusion:

This scoping review reveals a significant gap in the scientific evidence regarding AMR, ARGs, and ARs in biofilms from livestock farms and emphasizes the need for further research to clarify their role in the spread of AMR in the livestock sector.



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sciforum-118616: Avian Pathogenic *Escherichia Coli* Biofilm Formation Ability At Different Temperatures (37°C And 42°C)

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Avian pathogenic *Escherichia coli* (APEC) is responsible for colibacillosis in poultry. *E. coli* can form biofilms, which facilitate horizontal gene transfer and contribute to the dissemination of antimicrobial resistance. This study aimed to assess the biofilm formation ability of APEC and the influence of temperature variations on this property.

Thirty-four APECs were isolated from diseased chickens (n = 27) and turkeys (n = 7). Biofilm production was assessed according to Laconi et al. (2023). Bacterial suspensions were incubated in microplates at 37°C and 42°C for 24 hours. The analysis was conducted in two biological replicates, each comprising three technical replicates. The optical density (O.D.) of samples (O.D.S) was calculated as the mean of the absorbance of replicates and compared with the mean O.D. of negative control (O.D.NC). The APECs were classified into four classes: non-(O.D.S ≤ O.D.NC); weak (O.D.NC < O.D.S ≤ 2 × O.D.NC); moderate (2 × O.D.NC < O.D.S ≤ 4 × O.D.NC); and strong (O.D.S > 4 × O.D.NC) biofilm producers.

At 37°C, 70.6% (24/34) of APECs were weak biofilm producers, 20.6% (7/34) were moderate, and 8.8% (3/34) were strong, with none classified as non-biofilm producers. The two different temperatures appear to have no significant effect on APEC's biofilm formation ability, although eight and three isolates exhibited reduced and enhanced biofilm formation ability, respectively, at 42°C compared to 37°C. A similar distribution of biofilm classes was observed between isolates from chickens and turkeys.

Despite being primarily weak biofilm producers, all isolates demonstrated the ability to form biofilms, potentially facilitating the exchange of resistance genes. Future investigations should focus on elucidating the genetic background underlying APEC biofilm-forming ability.

Acknowledgments: This study was co-funded by European Union Project 101136346

Laconi, A., Tolosi, R., Apostolakis, I., Piccirillo, A. (2023). Biofilm formation ability of ESBL/pAmpC-producing *Escherichia coli* isolated from the broiler production pyramid. *Antibiotics*, 12(1). <https://doi.org/10.3390/antibiotics12010155>



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sciforum-116134: Biofilm Formation and Antibiotic Resistance in *Pseudomonas Aeruginosa* Isolated From Blood and Cerebrospinal Fluid of Children

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Background:

Gram-negative bloodstream and central nervous system infections in children in intensive care units are among the most dangerous complications, leading to complications in therapy and often to fatal outcomes.

Aim:

We aimed to determine antibiotic resistance, the ability to form biofilms on abiotic surfaces, and biofilm formation genes.

Methods:

Antibiotic sensitivity was determined by a broth microdilution method; biofilms were grown in polystyrene plates, followed by fixation, staining, and elution, and biofilm formation genes were determined by PCR.

Results:

During the period from 2014 to 2023, we studied 34 isolates of *P. aeruginosa*, isolated from the blood and cerebrospinal fluid of children. Resistance to carbapenems was 76%, to aminoglycosides and fluoroquinolones it was 68%, to aztreonam it was 26%, and to protected cephalosporins it was 74%. All strains were sensitive to colistin. When determining the resistance phenotype, we identified 35% of multi-drug-resistant (MDR) isolates and 38% of extremely drug-resistant (XDR) isolates. When studying the ability to form biofilms, we determined that the majority formed high-intensity (47%) and moderate-intensity (32.5%) biofilms, while 20.5% of isolates formed low-intensity biofilms. It is noteworthy that isolates with moderate biofilm formation ability were mostly MDR (5/11), while isolates with high biofilm formation ability were more often XDR (8/16).

Genes responsible for biofilm formation, *pilA* and *pilB*, were identified in 12% and 41% of 34 isolates, respectively. Moreover, they were most often found in isolates with high and moderate biofilm-formation ability.

Conclusion:

We found widespread resistance to antibiotics, especially carbapenems and protected cephalosporins. The intensity of biofilm formation correlated with the resistance of isolates. Genes responsible for biofilm formation were more often found in isolates with high and moderate biofilm formation.



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sciforum-118774: Biofilm formation on the surface of medical devices: a growing concern for hospital-acquired infections

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Hospital-acquired infections (HAIs) are nosocomial infections or diseases that are contracted during medical care but were absent at admission. Usually resulting from biofilm development on device surfaces, these infections shield microorganisms and raise their resistance to antimicrobial therapies. Moreover, many infections are challenging to detect and treat, which raises morbidity, death, and medical expenses. On medical equipment, biofilms, which are dense microbial colonies surrounded by an extracellular matrix, have been reported to be a major cause of ongoing infections resistant to antibiotics and human immune responses. Up to 75% of all bacterial infections are associated with biofilms, which also significantly contribute to nosocomial infections, especially in intensive care units. Common device-associated infections include catheter-related bloodstream infections, urinary tract infections, and ventilator-associated pneumonia. Both bacterial and fungal pathogens cause these diseases; however, the multi-species biofilms of bacterial and fungal pathogens provide extra treatment difficulty. Common bacteria such as *Escherichia coli*, *Staphylococcus aureus*, and *Pseudomonas aeruginosa*, as well as fungal pathogens like *Candida albicans*, can form biofilms on various devices, including catheters, prosthetic joints, and ventilators. Most of the time, traditional treatment therapies fail. Therefore, device removal and long-term antibiotic treatment become necessary. The development of new strategies for prevention and treatment, including innovative anti-adhesive coatings and nanomaterial-based techniques targeting biofilm formation stages, the application of biofilm-active antibiotics, anti-quorum sensing agents, and biofilm dispersal agents has attracted attention in recent years. Here, we discuss the latest developments in relation to several strategies, such as antimicrobial coating, surface modification, nanostructured surface and nanomaterials, and the incorporation of regulatory molecules (natural and synthetic molecules) to prevent biofilms on the surface of biomedical devices.



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sciforum-114759: Effect of Methylparaben Disinfection By-products on the Chlorine Tolerance of Biofilms

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Chlorination is widely used as a tertiary treatment in water treatment plants to ensure the microbiological safety of drinking water (DW). However, this process inevitably leads to the formation of disinfection by-products (DBPs). In addition to microbial challenges, DW quality is also affected by emerging contaminants like parabens, which can react with chlorine to form parabens transformation products (PTPs). This study is the first to investigate the impact of PTPs derived from methylparaben (MP): mono-chlorinated MP (3-Cl-MP) and di-chlorinated MP (3,5-diCl-MP), on bacterial characteristics and tolerance to disinfection in 7-day-old dual-species biofilms of *Acinetobacter calcoaceticus* and *Stenotrophomonas maltophilia*. Exposure to 3-Cl-MP and 3,5-diCl-MP increased the number of viable but not culturable cells (VBNC) of *A. calcoaceticus* presented in dual-species biofilms by 3-fold and 5-fold, respectively. Exposure to 3-Cl-MP also resulted in a significant increase in the VBNC levels of the overall dual-species biofilms and a 10 µm increase in biofilm thickness. The polysaccharide content was higher for both 3-Cl-MP and 3,5-diCl-MP exposed biofilms in comparison to non-exposed ones. Interestingly, biofilms exposed to 3-Cl-MP showed increased susceptibility to chlorination, with higher log CFU reductions for *A. calcoaceticus* (1.26 ± 0.07), *S. maltophilia* (1.21 ± 0.14), and overall dual-species biofilms (1.17 ± 0.11). Similarly, increased reductions in total cells were obtained for 3-Cl-MP-exposed *A. calcoaceticus*, and for the overall dual-species biofilms after 3,5-diCl-MP exposure. A greater % of bacterial cells with damaged membranes was also obtained for both 3-Cl-MP and 3,5-diCl-MP-exposed biofilms. Although MP-derived PTPs did not increase bacterial tolerance to disinfection, 3,5-diCl-MP exposure increased the antibiotic tolerance of *S. maltophilia* to minocycline (MINO) and trimethoprim-sulfamethoxazole (TMP-SMX). These findings underscore the complex interactions between PTPs and biofilms, highlighting the potential implications for water treatment strategies, antimicrobial resistance and public health.



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sciforum-115909: Enterococcus Faecalis Biofilm: A Clinical And Environmental Hazard

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This review explores the biofilm architecture and drug resistance of *Enterococcus faecalis* in clinical and environmental settings. The biofilm in *E. faecalis* is a heterogeneous, three-dimensional, mushroom-like or multilayered structure, characteristically forming diplococci or short chains interspersed with water channels for nutrient exchange and waste removal. Exopolysaccharides, proteins, lipids, and extracellular DNA create a protective matrix. Persister cells within the biofilm contribute to antibiotic resistance and survival. The heterogeneous architecture of the *E. faecalis* biofilm contains both dense clusters and loosely packed regions that vary in thickness, ranging from 10 to 100 µm, depending on the environmental conditions. The pathogenicity of the *E. faecalis* biofilm is mediated through complex interactions between genes and virulence factors such as DNA release, cytolysin, pili, secreted antigen A, and microbial surface components that recognize adhesive matrix molecules, often involving a key protein called enterococcal surface protein (Esp). Clinically, it is implicated in a range of nosocomial infections, including urinary tract infections, endocarditis, and surgical wound infections. The biofilm serves as a nidus for bacterial dissemination and as a reservoir for antimicrobial resistance. The effectiveness of first-line antibiotics (ampicillin, vancomycin, and aminoglycosides) is diminished due to reduced penetration, altered metabolism, increased tolerance, and intrinsic and acquired resistance. Alternative strategies for biofilm disruption, such as combination therapy (ampicillin with aminoglycosides), as well as newer approaches, including antimicrobial peptides, quorum-sensing inhibitors, and biofilm-disrupting agents (DNase or dispersin B), are also being explored to improve treatment outcomes. Environmentally, *E. faecalis* biofilms contribute to contamination in water systems, food production facilities, and healthcare environments. They persist in harsh conditions, facilitating the spread of multidrug-resistant strains and increasing the risk of transmission to humans and animals. Therefore, understanding the biofilm architecture and drug resistance is essential for developing effective strategies to mitigate their clinical and environmental impact.



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sciforum-120922: High Risk of Pathogen and Antibiotic Resistance Transfer in Live Seafood Wet Markets

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The global demand for seafood necessitates robust food safety practices, particularly within traditional wet markets. This study investigated the microbiomes of live Japanese mantis shrimp (JMS) and their associated environments (water and biofilm) in local wet markets to assess the risk of pathogen and antibiotic resistance gene (ARG) transfer. Metagenomic analysis showed a significant link between microbiome composition and the type of sample (shrimp, biofilm, and water). While several known human pathogens were associated with shrimp samples, water and biofilm samples exhibited higher abundances of ARGs, suggesting a high risk of pathogen and ARG transfer from the market environment. Notably, this study focused on the diversity and characterization of poorly understood *Vibrio* species associated with JMS. The prevalence of β -lactam resistance genes in *Vibrio* isolates, combined with a comparative genomic analysis of several species, highlights this concern. Our study emphasizes the need to improve hygiene practices in wet markets to reduce foodborne illness risks and address antibiotic resistance. This work represents, to our knowledge, the first comparative genomic analysis of *Vibrio* species in the context of JMS and wet market seafood safety.



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sciforum-111517: Quorum Sensing and Antibiotic Resistance in Polymicrobial Infections

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Quorum sensing (QS) is a sophisticated bacterial communication system that regulates behaviors critical to pathogenicity, including biofilm formation, virulence, and antibiotic resistance. This review explores QS's pivotal role in polymicrobial infections, where interspecies interactions significantly enhance antibiotic resistance. It delves into the mechanisms of QS, focusing on acyl-homoserine lactones (AHLs) in Gram-negative bacteria and autoinducing peptides (AIPs) in Gram-positive bacteria, highlighting their contributions to biofilm-associated antibiotic resistance. The challenges presented by polymicrobial infections, such as those in cystic fibrosis lung infections, chronic wound infections, and medical device-associated infections, are analyzed in detail. Laboratory models, including flow cells, static biofilm systems, and mammalian models, are discussed as tools to study the interplay between QS and antibiotic resistance in controlled environments. Promising therapeutic approaches, particularly quorum sensing inhibitors (QSIs) like furanones, AHL analogs, and natural compounds such as flavonoids, are emphasized for their potential to disrupt bacterial communication, reduce virulence, and enhance antibiotic efficacy. Case studies demonstrating the efficacy of QSIs in both laboratory and clinical contexts are presented, underscoring their potential to combat recalcitrant infections. This review also considers the economic and healthcare burden posed by biofilm-induced antibiotic resistance, advocating for innovative strategies to mitigate this global challenge. By reviewing the complex interplay between QS and polymicrobial antibiotic resistance, this paper aims to advance therapeutic strategies and foster a deeper understanding of the mechanisms underpinning bacterial communication.



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Session 8. Artificial Intelligence Strategies to Tackle Antibiotic Resistance

sciforum-118697: AI-Driven Traffic Prediction Algorithm for Forecasting Antibiotic Resistance Trends in Hospitals

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Background:

The increasing burden of antimicrobial resistance (AMR) in hospitals necessitates proactive strategies for surveillance and intervention. Inspired by predictive models used in traffic forecasting, we propose a novel machine learning (ML)-based algorithm that integrates multiple hospital parameters—**antibiotic consumption patterns, resistance rates, patient admissions, and bed occupancy trends**—to predict AMR evolution and guide antimicrobial stewardship programs.

Methods:

The algorithm utilizes **long short-term memory (LSTM) networks and gradient boosting models (e.g., XGBoost)** to analyze temporal patterns in hospital antibiotic usage and AMR incidence. A dataset including **historical antibiograms, hospital admission rates, antibiotic prescribing data, and bed occupancy rates** was used for training. The model employs **autoregressive integrated moving average (ARIMA) and reinforcement learning techniques** to enhance predictive accuracy. Performance was assessed using mean absolute percentage error (MAPE) and root mean squared error (RMSE) against real-world AMR data from hospital surveillance reports.

Results:

The LSTM-based model demonstrated superior accuracy in predicting resistance trends, identifying early warning signals for **carbapenem-resistant Enterobacterales (CRE) and methicillin-resistant Staphylococcus aureus (MRSA)** outbreaks. The algorithm outperformed traditional statistical models, enabling real-time optimization of antibiotic prescriptions and resource allocation.

Conclusion:

AI-driven predictive analytics, originally developed for traffic modeling, can be repurposed for hospital AMR surveillance. Implementing such models in clinical workflows could improve infection control strategies and reduce resistance development. Future work should focus on real-time deployment and multi-hospital validation.



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sciforum-118693: AI-Enhanced Surveillance Systems for Early Detection of Emerging Resistance Trends

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Background:

The ability to detect emerging antibiotic resistance trends in real-time is critical for infection control and public health planning. Traditional surveillance systems rely on retrospective data analysis, which often leads to delayed interventions and ineffective containment strategies. Artificial intelligence (AI) and deep learning offer transformative solutions for real-time monitoring, predictive analytics, and early warning systems for antimicrobial resistance (AMR). By integrating hospital data, whole-genome sequencing (WGS), and electronic health records (EHRs), AI can provide timely insights into resistance evolution and guide targeted interventions.

Methods:

We developed an AI-powered epidemiological platform that utilizes **long short-term memory (LSTM) networks, convolutional neural networks (CNNs), and XGBoost models** to analyze vast datasets from microbiology labs, hospital antibiograms, antimicrobial consumption trends, and clinical outcomes. The model applies **natural language processing (NLP)** to extract key resistance patterns from EHRs and integrates **reinforcement learning algorithms** to optimize antibiotic prescribing strategies.

Results:

The AI-enhanced surveillance system successfully identified early warning signals for **carbapenem-resistant Enterobacterales (CRE), vancomycin-resistant Enterococci (VRE), and multidrug-resistant Pseudomonas aeruginosa** across multiple healthcare facilities. The predictive model enabled **proactive infection control measures**, reducing hospital-acquired infections by 20% and optimizing antibiotic stock management.

Conclusion:

AI-driven surveillance platforms offer a paradigm shift in AMR monitoring, enabling rapid detection and mitigation strategies. Future research should focus on **real-time AI model deployment, data standardization, and integration into hospital antimicrobial stewardship programs** to maximize clinical impact.



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sciforum-118786: Artificial Intelligence in Antibiotic Stewardship: Optimising Prescribing Processes and Overcoming Ethical Challenges

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The overuse and misuse of antibiotics increases antibiotic resistance (AMR), limiting treatment options and placing a major economic and clinical burden on healthcare systems (Ribers & Ulrich, 2019) (Price, 2016). According to WHO/ECDC's 2023 report, resistance to broad-spectrum beta-lactam antibiotics has reached critical levels in Europe. In the United States, more than 2.8 million resistant infections occur each year, and more than 35,000 people die. If no measures are taken, it is estimated that AMR-related deaths will reach 10 million annually by 2050. Against this threat, artificial intelligence (AI)-based clinical decision support systems (CDSSs) offer an innovative approach to optimise antibiotic prescribing processes. By analysing patient data, microbial profiles, and local antibiotic resistance patterns, personalised and targeted antibiotic recommendations can be provided (Ribers & Ulrich, 2019) (Tran et al., 2022). However, AI-assisted prescribing systems should not only improve the technical efficiency, but also comply with ethical principles. The utilitarian approach is proposed as the most appropriate ethical framework, as it aims to minimise the development of resistance while maximising patient benefit (Bolton et al., 2022). WHO launched the 'Antimicrobial Resistance (AMR) Call to Action' in 2021, accelerating the global response with the participation of 113 countries and 38 organisations. With the lessons of COVID-19, the WHO and the UN have identified AMR as a 'Silent Tsunami' and committed to take measures under the 2030 Agenda for Sustainable Development. As a result, AI-based strategies have great potential in combating antibiotic resistance (Pascucci et al., 2021). AI-powered systems can protect public health by reducing unnecessary antibiotic use. However, transparency, ethical standards, and regulatory frameworks are required for its successful implementation. Future research can contribute to sustainable antibiotic stewardship by improving the accuracy of AI models.



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sciforum-116763: GPT-Based Drug-to-Disease (DtD) Checker as a Tool for Optimizing Antibiotic Use and Reducing Resistance

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Background:

Inappropriate antibiotic prescribing is a major driver of antimicrobial resistance (AMR) and adverse drug effects. Traditional decision support systems often lack real-time adaptability and struggle to integrate complex patient-specific data. The advent of **GPT-based Drug-to-Disease (DtD) checkers** offers a novel AI-driven approach to assist clinicians in optimizing antibiotic therapy by ensuring accurate drug-disease matching, minimizing resistance risks, and preventing adverse effects.

Methods:

We propose an AI-powered **DtD checker based on a large language model (LLM) architecture**, trained on **clinical guidelines, antibiograms, pharmacokinetics, and patient-specific parameters** (e.g., renal function, comorbidities, and prior antibiotic exposure). The model leverages **natural language processing (NLP) and deep learning algorithms** to cross-reference antibiotic choices with patient characteristics, flagging inappropriate prescriptions and suggesting evidence-based alternatives. Its performance was validated against real-world antibiotic prescribing data in hospitalized patients.

Results:

The GPT-based DtD checker significantly reduced **inappropriate antibiotic prescriptions by 35%**, enhanced compliance with antimicrobial stewardship guidelines, and decreased the incidence of **drug-related adverse events by 25%**. Additionally, real-time integration with **electronic health records (EHRs)** improved clinical decision-making efficiency.

Conclusion:

AI-driven DtD checkers represent a transformative tool for antimicrobial stewardship, enhancing precision prescribing while mitigating AMR development. Future research should focus on **real-time deployment, clinician-AI interaction models, and broader validation in outpatient settings** to maximize patient safety and antibiotic effectiveness.



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sciforum-118795: Immersive Technologies in Healthcare: Virtual Reality's Role in Addressing Antibiotic Resistance

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Antibiotic resistance is an escalating global public health issue that requires innovative strategies for reduction. Virtual reality (VR) is being utilised as a cutting-edge technology for medical training, patient education, and drug development. In this study, we aimed to review the role of VR in combating antibiotic-resistant infections by improving antibiotic administration, infection control methods, and surgical plans for resistant infections. VR-based simulations provide medical professionals with authentic training environments to improve their clinical decision-making and avoid antibiotic abuse. VR-inspired health-tech helps model bacterial resistance and new drug candidates, optimizing the antibiotic detection process. The combination of virtual reality (VR) with artificial intelligence (AI) and big data analytics enables real-time diagnosis, personalized treatment planning, and precision medicine. Additionally, using VR in public health initiatives improves patients' compliance with infection control measures. It has great potential but also drawbacks, such as high cost, availability issues, and the need to validate interventions affected by VR. The current review provides a perspective on the latest advances, challenges, and future methods for the implementation of VR in the treatment of infectious diseases. The use of VR can change the way in which we fight antibiotic resistance and pave the way for improved and more sustainable health solutions around the world.



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sciforum-115006: MD simulation investigation of noncovalent interaction hotspots in the bacterial ribosome upon translocation as potential antibiotic targets

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The steady increase in antimicrobial resistance to existent antibiotics is a growing threat. The ribosome remains one of the most convenient targets for antibiotics due to its conservation, multiple copies of the rRNA genes, and universal central biochemical role. Multiple classes of ribosomal antibiotics bind to several conservative sites at or close to the crucial functional centers in this huge target. Antimicrobial resistance is provided by genes, inactivating or pumping these antibiotics out of the cell or modifying the binding sites, which are ancient products of evolution. A promising strategy to overcome evolutionarily acquired resistance is the identification of compounds with novel binding sites on the ribosome.

There are several reliable datasets about antibiotics affecting the ribosome translocation, a multistep stochastic movement that is catalysed by elongation factor G (EF-G), which transfers the ribosome from the A/A,P/P- to the P/P,E/E-state. For example, octapeptides argyrins trap the EF-G in the conformation corresponding to the pre-translocational state [1]. Even for aminoglycosides, trapping the ribosome in one of its intermediate states was recently considered to be the main mechanism of action [2]. Thus, there can be more than two sites in which drug binding can arrest the translocation process.

In order to identify another potential site for trapping ribosome translocation, we performed all-atom MD simulations of the pre- and post-translocational states of the 70S ribosome. In the obtained trajectories, our comparative and cross-correlation analyses revealed reproducible differences in non-covalent interactions (hydrogen bonds and stacking interactions) in elongation factor G and intersubunit bridges. A time series analysis of occurrences of these interactions detected "hotspots" of multiple concerted interactions that define one of the intermediate states of translocation.

All the MD simulations were performed using the Lomonosov-II supercomputer of Lomonosov Moscow State University's supercomputer center.

1. Proc Natl Acad Sci USA. 2022 119(19):e2114214119.
2. Nucleic Acids Res. 2021 49(12):6880–6892



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sciforum-118535: Use of Rational Design and Artificial Intelligence to Improve the Therapeutic Potential of Antimicrobial Peptides

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Antimicrobial peptides (AMPs) have emerged as promising alternatives to conventional antibiotics, addressing the growing concern of antibiotic resistance. Their efficacy primarily relies on two key properties: amphiphilicity and cationic charge, which promote targeted action on bacterial membranes. The Lynronne family, identified in the bovine rumen through metagenomic screening, already exhibits notable antimicrobial activity and low toxicity, making it a strong candidate for further development [1]. Our goal is to enhance the therapeutic potential of these AMPs using conventional and innovative strategies. Traditional approaches include substitutions with cationic amino acids and D/L enantiomeric modifications.

In parallel, we employed artificial intelligence techniques using the MRL (Molecular Reinforcement Learning) model for AMP design, based on the biophysical properties of the Lynronne family (cationic charge, hydrophobicity). The activity and toxicity of the designed peptides were first evaluated *in silico* using various prediction tools (MIC predictors and toxicity/hemolysis predictor). Their antimicrobial activity against diverse pathogens and their cytotoxicity on human cells were then measured, allowing comparison between predicted and measured activities. Their mechanism of action was studied via biophysical techniques, membrane permeabilization assays, and molecular dynamics simulations (GROMACS), confirming specific interactions with bacterial membranes and membranolytic effects. This study highlights how combining rational design strategies and AI can optimize Lynronne peptides, reinforcing their potential as alternatives to conventional antibiotics.



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sciforum-117007: Using Artificial Intelligence to Combat Antimicrobial Resistance: Advancements and Challenges

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Antimicrobial resistance (AMR) is a global public health concern that has developed at an alarming rate due to rapid genetic mutation, horizontal gene transfer, and the misuse of antibiotics. The current traditional methods used for the detection of ARGs and the development of new antibiotics are not only inefficient but also lack accuracy. AI and ML promise to address AMR through advanced computation techniques such as supervised learning, deep learning, reinforcement learning, and natural language processing. AI-based models use data from genomic sequences, microbiome profiles, and clinical records to predict the emergence of outbreaks of AMR, identify resistance determinants, and aid in drug discovery.

The transformer-based AI models show superior performance in analyzing genomic data, predicting bacterial resistance profiles, and unveiling the key ARG relationships. Furthermore, AI facilitates novel antibiotics through the modeling of the structure–activity relationship, Raman spectroscopy, and mass spectrometry. AI-based clinical decision support systems further optimize antibiotic prescription by reducing the misuse and development of resistance. However, in AMR research, AI faces the challenge of ethical issues and data privacy; the bias found in algorithms poses another significant concern. Future work on AI methods, especially combining pre-trained models of genomics, will enable the improved accuracy of predictions and implementation of precision medicine approaches for infection management. Indeed, with growing advancements in AI technology, this integration will provide the foundation on which the strategy of bacterial resistance control will thrive, preserving the efficacy of available antibiotics.



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