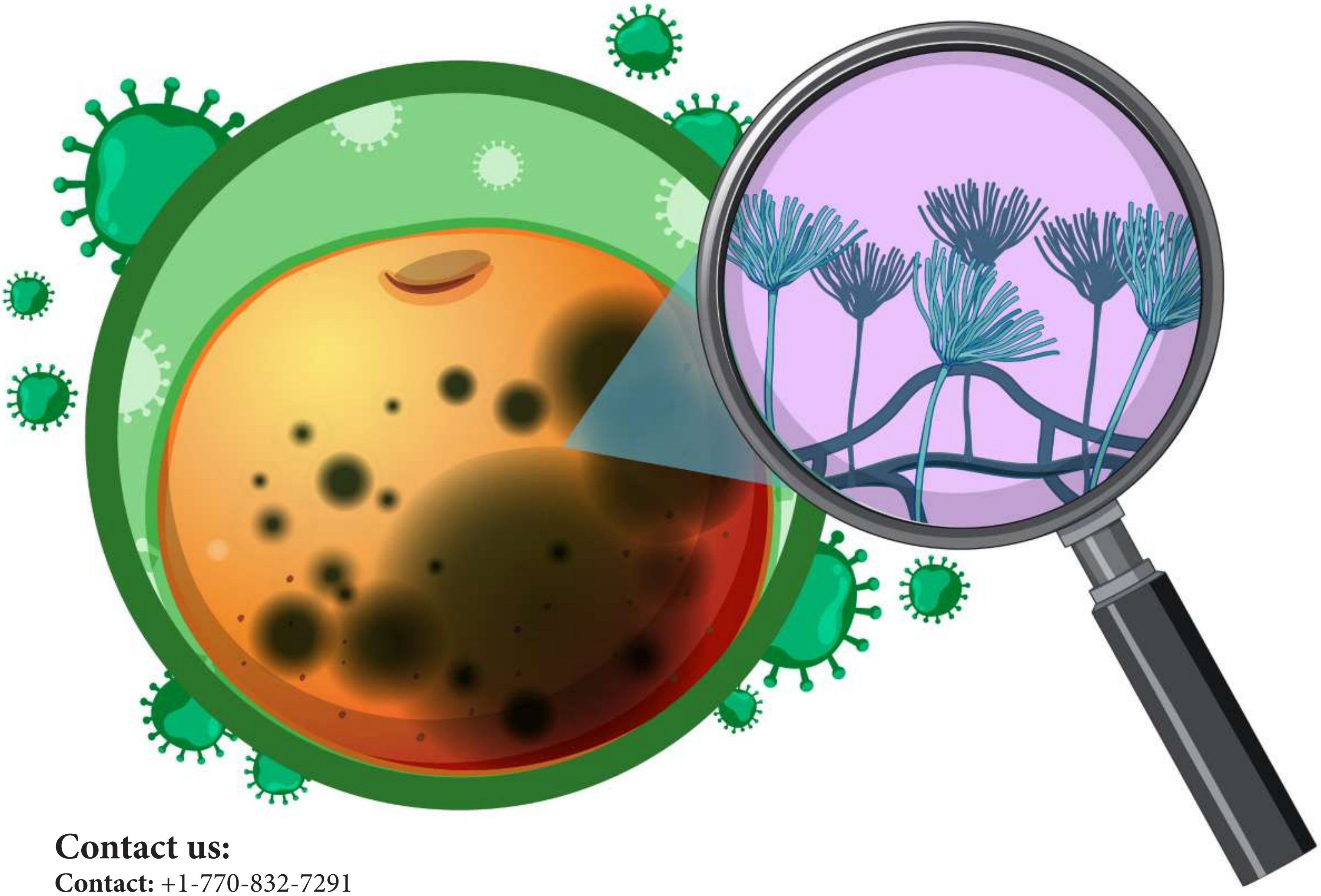
SCI SYNOPSIS

*Joint Event*

# $4^{th}$ International Conference on
# Infectious Diseases
# &
# Microbiology

October 20-21, 2025 | Dubai, UAE



**Contact us:**
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**Scisynopsis LLC**
Atlanta, GA 30326
USA

# Speaker Representations

FRIEDRICH-LOEFFLER-INSTITUT
FLI
Bundesforschungsinstitut für Tiergesundheit
Federal Research Institute for Animal Health

Logo of Cheikh Anta Diop University - Dakar - Senegal

20TH HIT

HIT Harare Institute of Technology
success through innovation

GKIB
CITY CLINICAL INFECTIOUS DISEASES HOSPITAL
Minsk, st. Kropotkina, 76

SPRINGER NATURE

VAN YÜZÜNCÜ YIL ÜNİVERSİTESİ
1982

HOPITAL LA RABTA

UNIVERSITY OF BIRMINGHAM | DUBAI دبي

NIFST

UKRI
MRC Unit The Gambia
LONDON SCHOOL of HYGIENE &TROPICAL MEDICINE

Service de Maladies Infectieuses
SMI
Hôpital Farhat Hached Sousse

University of Missouri

FACULTÉ DE MÉDECINE DE SOUSSE

Hôpital Farhat Hached Sousse

Association for Social Development
Pakistan

HEALTH SERVICES ACADEMY
GOVT OF PAKISTAN

KING GEORGE'S MEDICAL UNIVERSITY, UTTAR PRADESH, LUCKNOW, INDIA
SINCERITY SERVICE SACRIFICE

UNIVERSITAS BUDAPESTINENSIS DE SEMMELWEIS NOMINATA
1769

HEIM PÁL
Országos Gyermekgyógyászati Intézet
1907

WAYNE STATE
School of Medicine

NAZARBAYEV UNIVERSITY

# Wifi Details

*Username: CSS_Banquet*
*Password not Required*

# Conference Programme

# Day 1

## 20th October

### Session Chairs

**Ashwaq Madani Al Nazawi,** Jazan University, Saudi Arabia
**Luidmila Anisko,** Minsk City Infectious Diseases Hospital, Belarus

# Conference Programme

## Day-1 | October 20, 2025

| | |
|---|---|
| **Meeting Hall : El Dhiyafa 3** | |
| **08:00 - 08:45** | **Registrations** |
| **08:45 - 09:00** | **Introduction** |
| **Keynote Presentations** | |
| **09:00 - 09:40** | **Shigeaki Ogibayashi, Chiba Institute of Technology, Japan** |
| **Title:** Mechanism-oriented Agent-based Modeling for Uncovering Causal Mechanisms in Social Phenomena: The Case of A Pandemic Model | |
| **09:40 - 10:20** | **Luidmila Anisko, Minsk City Infectious Diseases Hospital, Belarus** |
| **Title:** The New Hospital Ecosystem: COVID-19–Driven Dysbiosis and Multidrug-Resistant Pathogen Colonization | |
| **Networking & Refreshments 10:20 - 10:40 @ Pre Function Area** | |
| **10:40 - 11:20** | **Amira Awad Moawad, Friedrich-Loeffler-Institute, Germany** |
| **Title:** Antimicrobial Resistance – The Silent Pandemic | |
| **11:20 - 12:00** | **Lakshmikantha Hallakere Channaiah, University of Missouri, USA** |
| **Title:** An Overview of The Baking Validation Research: Regulations and Challenges | |
| **Oral Presentations** | |
| **Session Chair** | **Ashwaq Madani Al Nazawi, Jazan University, Saudi Arabia** |
| **Session Chair** | **Luidmila Anisko, Minsk City Infectious Diseases Hospital, Belarus** |
| **Sessions:** | Nosocomial Infections and Control \| Antimicrobial Resistance \| COVID-19 \| Vector-borne Diseases \| Infection Prevention and Control \| Clinical Microbiology \| Food Microbiology \| Bacteriology \| Microbiome |
| **12:00 - 12:25** | **Dániel Steve Bednárik, The Semmelweis University and Heim Pál National Pediatric Institute, Hungary** |
| **Title:** Comparative Effectiveness of Different Therapies for Clostridioides difficile Infection in Adults: A Systematic Review and Network Meta-analysis of Randomized Controlled Trials | |

| | |
|---|---|
| **12:25 - 12:50** | **Pravalika Sathyanarayana, Dayananda Sagar University, India** |
| **Title:** Management of Carbapenem-resistant Enterobacteriaceae Infections in ICU Settings: A Comprehensive Analysis | |
| **Group Photo (12:50 - 13:00)** | |
| **Lunch 13:00 - 14:00 @ New Season Restaurant** | |
| **14:00 - 14:25** | **Kadir AKAR, Van Yuzuncu Yil University, Turkey** |
| **Title:** Molecular Investigation of Bacterial Agents in Abortion Materials of Small Ruminants in Some Eastern Anatolian Provinces | |
| **14:25 - 14:50** | **Tina Plankar Srovin, University Medical Centre Ljubljana, Slovenia** |
| **Title:** Hemoperfusion with CytoSorb® in Pediatric Patients: Experiences from Slovenia | |
| **14:50 - 15:15** | **UAWL Perera, Teaching Hospital Rathnapura, Sri lanka** |
| **Title:** Symptoms and Life Quality Post COVID-19 Syndrome among COVID-19 Patients | |
| **15:15 - 15:40** | **Ashwaq Madani Al Nazawi, Jazan University, Saudi Arabia** |
| **Title:** Impact of Insecticide-treated Materials (ITMs) on *Aedes aegypti* Host Location Behavior in Saudi Arabia | |
| **15:40 - 16:05** | **Nida Khan, Association for Social Development, Pakistan** |
| **Title:** Integrating an AMS Intervention into The Primary Healthcare System in Pakistan | |
| **Network & Refreshments 16:05 - 16:30 @ Pre Function Area** | |
| **16:30 - 16:55** | **Rym Ayari, Infectious Diseases Department of Farhat Hached Hospital/Faculty of Medicine of Sousse, Tunisia** |
| **Title:** Seroprevalence and Risk Factors associated with Phleboviruses and Crimean–Congo Hemorrhagic Fever Virus among Blood Donors in Central Tunisia | |
| **16:55 - 17:20** | **Lakshmikantha Hallakere Channaiah, University of Missouri, USA** |
| **Title:** Thermal Inactivation of Salmonella during the Oatmeal Chocolate Chip Granola Bar Manufacturing Process | |
| **Day 1 Concludes followed by Certificate Distribution** | |

# Day 2

## 21st October

### Session Chairs

**Ashwaq Madani Al Nazawi,** Jazan University, Saudi Arabia
**Travers Kudzai Chirova,** Harare Institute of Technology, Zimbabwe

## Day-2 | October 21, 2025

## Meeting Hall : El Dhiyafa 3

### Keynote Presentations

**09:00 - 09:40** **Gilbert GLADY, EBMA, France**

**Title:** TH1/TH2 Paradigm: Is It Infection or Allergy, or Both?

**09:40 - 10:20** **Travers Kudzai Chirova, Harare Institute of Technology, Zimbabwe**

**Title:** Evaluation of The Synergistic Antimicrobial Effects of *Combretum apiculatum* Extract, Green Synthesized Silver Nanoparticles, and Amoxicillin against *Staphylococcus Aureus, Escherichia Coli, Klebsiella pneumoniae, and Pseudomonas aeruginosa*, with The Development of A Novel Wound Dressing Hydrogel

**10:20 - 11:00** **Chinedu Obiageli Ajogun, Nigerian Institute of Food Science and Technology, Nigeria**

**Title:** Effect of Different Concentrations of Table Salt on Physicochemical and Microbial Quality of Fermented Catfish (*Clarias gariepinus*)

**Network & Refreshments (11:00 - 11:10) @ Pre Function Area**

### Oral Presentations

**Session Chair** **Ashwaq Madani Al Nazawi, Jazan University, Saudi Arabia**

**Session Chair** **Travers Kudzai Chirova, Harare Institute of Technology, Zimbabwe**

**Sessions:** Nosocomial Infections and Control | Antimicrobial Resistance | Mycology | Food Microbiology | Virology | Food Microbiology | Industrial and Applied Microbiology | Medical Microbiology |Antibiotics and Resistance | Bacteriology

**11:10 - 11:35** **Deen Bandhu Prasad, King George Medical University, India**

**Title:** High and Rising Colonisation Burden among Critically Ill Patients -A Longitudinal Surveillance in A North Indian ICU

**11:35 - 12:00** **Tabitha Merium Sabu, Amala Institute of Medical Sciences, India**

**Title:** The Optimal Antifungal Prophylaxis Post Bone Marrow Transplant

**12:00 - 12:25** **Shaheer Ellahi Khan, Health Services Academy, Pakistan**

**Title:** Contextual Analysis of Antibiotic Prescribing Practices for Upper Respiratory Infections and Diarrhea in Rural Health Centers of Punjab, Pakistan

<table>
<tr><th colspan="2">Poster Presentations</th></tr>
<tr><td><b>Poster Judge</b></td><td><b>Ashwaq Madani Al Nazawi, Jazan University, Saudi Arabia</b></td></tr>
<tr><td><b>IDMP-01</b></td><td><b>Dariga Zhazykhbayeva, Nazarbayev University, Kazakhstan</b></td></tr>
<tr><td colspan="2"><b>Title:</b> Antimicrobial Resistance among Clinical Isolates: A Focus on MDR Uropathogens</td></tr>
<tr><td><b>IDMP-02</b></td><td><b>Zhanar Kosherova, Nazarbayev University, Kazakhstan</b></td></tr>
<tr><td colspan="2">Title: Antimicrobial Stewardship Systems in Post-Soviet Countries: A Systematic Review</td></tr>
<tr><td><b>IDMP-03</b></td><td><b>Roger Alberto Palomino Huarcaya, Universidad Nacional Mayor De San Marcos, Peru</b></td></tr>
<tr><td colspan="2"><b>Title:</b> Tolerance and Degradation Profiles of Monoaromatic Hydrocarbons in <i>Pseudomonas aeruginosa</i> Strains from Oil Contaminated Environments in Peru</td></tr>
<tr><td><b>IDMP-04</b></td><td><b>Kolenchukova Oksana, Krasnoyarsk State Agrarian University, Russia</b></td></tr>
<tr><td colspan="2"><b>Title:</b> Phagocyte Activity in Response to Significant Antibiotic-Resistant Bacteria</td></tr>
<tr><td><b>IDMP-05</b></td><td><b>Kolenchukova Oksana, Krasnoyarsk State Agrarian University, Russia</b></td></tr>
<tr><td colspan="2"><b>Title:</b> Antibiotic Resistance of Significant Intestinal Bacteria</td></tr>
<tr><td colspan="2"><b>Lunch 13:00 - 14:00 @ New Season Restaurant</b></td></tr>
<tr><td><b>14:00 - 14:25</b></td><td><b>Mohamed El-Hadidi, University of Birmingham Dubai, UAE</b></td></tr>
<tr><td colspan="2"><b>Title:</b> From The Breast to the Brain: Unveiling Microbial Signatures Shaping Cancer and Neurodegenerative Disease</td></tr>
<tr><td><b>14:25 - 14:50</b></td><td><b>Imen Chihaoui, Hôpital la Rabta, Tunisia</b></td></tr>
<tr><td colspan="2"><b>Title:</b> Insight of The Resistance Mechanism of <i>H. pylori</i> to Clarithromycin</td></tr>
<tr><td><b>14:50 - 15:15</b></td><td><b>Abdullah Ibrahim Al-Homoudi, Wayne State University School of Medicine, USA</b></td></tr>
<tr><td colspan="2"><b>Title:</b> Structure-guided Design of Potent and Selective Covalent Inhibitors of SARS-CoV-1 and SARS-CoV-2 Papain-like Proteases with Antiviral Activity</td></tr>
<tr><td><b>15:15 - 15:40</b></td><td><b>Jehan Zeb, Higher Education Department Khyber Pakhtunkhwa, Pakistan</b></td></tr>
<tr><td colspan="2"><b>Title:</b> Genetic Diversity of Tick-Borne Zoonotic Pathogens in Ixodid Ticks Collected from Small Ruminants in Northern and North-Western Pakistan</td></tr>
</table>

## e-Poster Presentation

**IDMEP** **Aissatou SECK, Cheikh Anta Diop University, Senegal**

**Title:** Physiopathological Aspects of SARS-CoV-2 (COVID-19) Infection on Hemorheological and Inflammatory Functions: About 140 Cases in Senegal

## Video Presentations

**IDMVP-01** **Matthew Pritchard, Royal Hobart Hospital, Australia**

**Title:** Efficacy of Active Immunoprophylaxis with Uromune Therapy for the Prevention of Recurrent Urinary Tract Infections in Men: A Single Centre Observational Study

**IDMVP-02** **Rachel Kim, Tenafly High School, USA**

**Title:** Multiple Myeloma and AIDS: A Statistical Study and the Racial Disparities

**IDMVP-03** **Rufei Ma, Guangdong Country Garden School, China**

**Title:** Evaluation of Flavonoid-Rich *Chrysanthemum indicum* Extract Reveals No Zone of Inhibition against *Malassezia furfur* in an *in vitro* Model

**IDMVP-04** **Mutlaq Al shammri, Saudi Ministry of Health, Saudi Arabia**

**Title:** Investigation of Factors Affecting the Aerosol Transmission of *Mycobaterium tuberculosis*

**IDMVP-05** **Mahrukh Ehsan, Dudley Group NHS Foundation Trust, United Kingdom**

**Title:** Identifying Critical Gaps in Mews Implementation: A Pan-Site Audit of Modified Early Obstetrics Warning System in Emergency Department

**IDMVP-06** **Nouran Magdy, Dar Al Uloom University-College of Medicine, Saudi Arabia**

**Title:** Molecular Mechanisms of Colistin Resistance among Multi-drug Resistant (MDR) *Klebsiella pneumoniae* and *Escherichia coli* Isolated from ICU Patients and their Susceptibility towards Eravacycline

**Networking & Refreshments 16:05 - 16:30 @ Pre Function Area**

**Day-2 Concludes by Certifications and Vote of Thanks to the participants**

Day 1

# Infectious Diseases
# &
# Microbiology

## Keynote presentations

# MECHANISM-ORIENTED AGENT-BASED MODELING FOR UNCOVERING CAUSAL MECHANISMS IN SOCIAL PHENOMENA: THE CASE OF A PANDEMIC MODEL

**Shigeaki Ogibayashi**
*Chiba Institute of Technology, Japan*

## Abstract:

Scientific understanding of social phenomena requires elucidating their causal mechanisms, much like in natural sciences. However, unlike natural systems governed by universal principles, social systems are driven by human behavior and interactions, making controlled experiments difficult and equation-based theories limited in scope. Agent-Based Modeling (ABM) has emerged as a promising method to address these challenges by simulating artificial societies composed of diverse decision-making agents.

To overcome limitations in conventional ABM, we propose a “mechanism-oriented ABM” approach. This methodology adopts an entirely bottom-up structure, deliberately avoiding macro-level assumptions to construct models that faithfully reflect real-world social systems.

Models are classified into qualitative and quantitative types, with qualitative reproduction serving as a prerequisite for quantitative modeling. In qualitative modeling, hypotheses about agent behavior and attributes are tested through computer experiments to identify the model structure essential for reproducing observed phenomena. Once identified, the necessity of this structure is analyzed to understand the emergence mechanism within artificial societies. This approach enables systematic identification of causal mechanisms and is applicable not only to social systems but also to biological and pandemic phenomena. In a pandemic modeling example, the infection and recovery processes were simulated, incorporating medical knowledge about immunity. A key structural insight was that virus excretion is proportional to viral load, reflecting the immune-boosting effect of fever. However, due to individual differences in immunity, some individuals may experience uncontrolled viral replication in the body when the viral replication rate is extremely high. If such individuals move freely, the pandemic persists. Based on these findings, the study emphasizes two essential strategies for effective pandemic control: (1) individual-level monitoring and behavioral regulation based on body temperature trends, and (2) early isolation of severely infected individuals to curb transmission.

## Biography

Shigeaki Ogibayashi graduated from the Department of Physics at Tohoku University, Sendai, Japan, in 1969 and completed a master's degree in physics in 1971. Since then, he has been working in Nippon Steel Corporation as a research engineer in the field of metallurgy and solidification of steel, making significant contributions to R & D of many technologies, including oxide metallurgy and soft reduction in continuous casting. His belief in the research method is to attain the goal with minimum input, i.e. time, labor, and funds, through an effective combination of theoretical modeling, which he specializes in, and experimentation. In 1992, he got a Ph.D. at the School of Metallurgy at Tokyo University, a testament to his deep understanding and expertise in the field. In 1997, he retired from Nippon Steel and started his new career at the Chiba Institute of Technology as a professor in the Department of Management Information Science. In the first several years after beginning activities at Chiba Institute of Technology, he engaged in the administration field and research activities, organizing a new faculty of social systems science, a new course of graduate school, etc., in Chiba Institute of Technology. Since 2007, he has focused his research activities on modeling and simulation, especially agent-based modeling and simulation. He developed an agent-based model of an economic system that can calculate GDP in the same manner as in the real world. Namely, each agent records transactions using the double-bookkeeping method, closes its account, including the balance sheet at every period at the end of every time step, and the government aggregates the account data of all agents to calculate input-output table and GDP in the artificial social society. In 2014, he found a new principle of agent-based modeling. The causal mechanism of a social phenomenon can be clarified by a series of computer experiments in agent-based modeling that elucidate the set of behavioral rules, i.e., the model structure, that are indispensable to reproduce the desired phenomenon.  Since then, he has been focusing on validating this principle by applying it to various macroeconomic phenomena, such as business cycles and tax-cut effects.He retired from Chiba Institute of Technology in March 2017. However, he is continuing his research in agent-based modeling of social phenomenon, not only of macroeconomic phenomenon but also of bullying phenomenon as well as the Covid-19 pandemic. The model of the covid-19 pandemic features a micro model of the infection and recovery that incorporates the number of viral particles, innate immune cells, and antibodies, whose research articles are published in the form of proceedings CSS2020 by CSSSA and one of the chapters of the book entitled "Infectious Diseases, from prevention to control," e.d. Yvette S. Brewer, published by Nova Science Publishers, Inc.

# THE NEW HOSPITAL ECOSYSTEM: COVID-19-DRIVEN DYSBIOSIS AND MULTIDRUG-RESISTANT PATHOGEN COLONIZATION

**Luidmila Anisko**
*Minsk City Infectious Diseases Hospital, Belarus*

## Abstract:

**Background:** The COVID-19 pandemic precipitated an unprecedented reorganization of global healthcare, creating a unique environment for shifts in microbial ecology. This study aimed to comprehensively analyze the impact of the pandemic on the prevalence, distribution, and antimicrobial resistance (AMR) profiles of clinically significant microorganisms isolated from hospitalized patients.

**Methods:** A retrospective analysis was conducted on microbial culture data from a tertiary infectious diseases hospital in Minsk from 2019 (pre-pandemic) to 2022 (pandemic). Data included isolates from respiratory tracts, sterile sites (blood, cerebrospinal fluid), and the gastrointestinal tract. Antimicrobial susceptibility testing was performed according to standard guidelines.

**Results:** A significant restructuring of the respiratory microbiome was observed. The pre-pandemic leader, *Staphylococcus aureus* (32.2%), was supplanted by *Candida albicans* (29.5% in 2021). A marked rise in non-fermenting Gram-negative bacilli (NFGNB) like *Acinetobacter baumannii* (from 3.5% to 10.7% in 2020) and *Klebsiella pneumoniae* was noted, indicating a shift towards nosocomial flora. By 2022, a more even distribution among *Enterococcus faecalis, K. pneumoniae, S. aureus, and C. albicans* was seen.

I A dramatic increase (2.5-fold) in isolates from sterile sites was recorded in 2022 (n=713) vs. 2019 (n=280). A surge in *K. pneumoniae* and *Escherichia coli* was observed, alongside an increased proportion of *A. baumannii, Pseudomonas aeruginosa, and Enterococcus faecium*, confirming the systemic dissemination of resilient hospital-adapted pathogens.

**Gastrointestinal Tract Changes:** While overall isolation of traditional enteric pathogens (e.g., *Salmonella* spp.) decreased due to enhanced hygiene measures, the gut reservoir became a niche for typically nosocomial pathogens. *A. baumannii and P. aeruginosa*, previously rarely isolated, were detected from the start of the pandemic, with their presence increasing by 2022.

**Antimicrobial Resistance Escalation:** The pandemic exacerbated AMR trends. *A. baumannii* exhibited near-total (≈100%) resistance to carbapenems. Methicillin-resistant and even linezolid-resistant *S. aureus* strains emerged in 2021. *K. pneumoniae* showed rising resistance, including to colistin. Post-COVID, a concerning emergence of resistance to last-line agents (linezolid, tigecycline, vancomycin) was noted in Enterococcus spp.

**Conclusion:** The COVID-19 pandemic catalyzed a profound dysbiosis within the hospital ecosystem, characterized by the colonization of patients by multidrug-resistant, nosocomial Gram-negative pathogens across

multiple body sites, and a sharp escalation in resistance to last-resort antibiotics. This study highlights the unintended consequences of a healthcare crisis on microbial ecology and underscores the critical need for integrated antimicrobial stewardship and robust infection control measures to mitigate long-term threats from multidrug-resistant organisms.

## Biography

Luidmila Anisko MD is a laboratory head of Minsk City Infectious Clinic, PhD, associate professor, Department of Infectious Diseases, Belarusian State Medical University. L.Anisko has expertise in laboratory diagnostics and passion in improving the health. Now L.Anisko is a doctoral student and chief specialist in laboratory diagnostics in Minsk. She has demonstrated outstanding talents in both teaching as well as clinical practice spheres. She has a good experience in laboratory diagnostics of infectious diseases. Her scientific interests include: investigation the problems of COVID-19 infection; develop the best diagnosis criteria and create the algorhythm for diagnosis of COVID-19 infection. She introduced standardized PCR-based diagnostics for infections in Belarus. Oversaw nationwide training programs for infectious disease specialists in clinical epidemiology and laboratory safety. Coordinates the activities of the laboratory service of Minsk

# ANTIMICROBIAL RESISTANCE – THE SILENT PANDEMIC

**Amira Moawad**
*Friedrich-Loeffler-Institute, Germany*

## Abstract:

Antimicrobial resistance (AMR) represents a critical global health crisis, driven by interconnected factors such as population growth, climate change, land use, and the misuse of antibiotics across human, animal, and environmental sectors. The emergence of AMR has prompted global efforts to develop new guidelines and strategies aimed at mitigating its spread and impact. These guidelines are evolving, with both global organizations and individual countries establishing frameworks to address this critical public health threat. This global health threat requires innovative diagnostic approaches to detect, identify, and understand resistant pathogens effectively. Advanced diagnostic techniques are revolutionizing how we identify and combat AMR. Alternative treatment therapies for resistant pathogens are no longer an option. These therapies work through different mechanisms to fight resistant pathogens. The future likely involves combining multiple alternative therapies with traditional antibiotics when appropriate. No single solution will address all aspects of antimicrobial resistance. Addressing AMR requires cross-sectoral action, sustainable innovation, and equitable access to interventions to effectively combat the global threat of AMR.

## Biography

Amira Awad Moawad works as a Professor of Microbiology at the Animal Health Research Institute in Egypt and Friedrich-Loeffler Institute, the Federal Animal Health Research Institute in Germany. Since 2017 until now, she became a scientific researcher at Friedrich-Loeffler-Institut, Institute of Bacterial Infections and Zoonoses, Jena, Germany. She got two academic degrees. The first was PhD from Egypt and the second was Doctor Med. Vet. from Free University of Berlin, both are in the area of antimicrobial resistance in zoonotic pathogens between humans and animals. In 2016, she was granted from DAAD for Post doctor-Research in Germany. Since 2017 she has been involved in Veterinary medical research, coordinate international projects and training of veterinary practices in Friedrich Loeffler Institute. Starting from 2018 until now, she whas been involved in research projects with Friedrich-Loeffler-Institut and German Federal Foreign Office in the Frame of the German Biosecurity Programme. She is currently coordinating other project with Egypt in the frame of Biosafety and Biosecurity. She is an expert in the fields of Microbiology, Molecular biology, and Immunology. She has published several international publications in high ranked-Journals concerning the Emerging MDR-Pathogens (such as MRSA, *E. coli, Salmonella spp., Campylobacter Spp., Brucella Spp., Coxiella burnetii, Klebsiella pneumoniae, Burkholderia mallei*), Virulence determinants, and the mechanisms of multidrug resistance, and Food-borne pathogens, in addition to Epidemiological and Molecular diagnostic tools. She is concerned with the One Health approach, using the highly advanced tools of genome analysis and next-generation sequencing. She has given many talks and published many articles in several proceedings in different international scientific symposiums and conferences. She is a trainee at the One Health Training Program. She is a scientific reviewer at many international high ranked journals such as; Frontiers in Microbiology, BMC in Microbiology, Toxins, Molecules, Journal of Applied Microbiology, Plos One, Microorganisms, Antibiotics, European Journal of Medical Research, Diagnostics, Tropical medicine and infectious diseases, PeerJ Life and environment, International Journal of Environmental Research and Public Health, Qeios and Taylor&Francis peer reviewed journals. She works as an Associate Editor at BMC Microbiology. Besides, she serves as a guest Editor in Journal of Antibiotics. She is a member of Microbiology Society in London, German Research Platform for Zoonoses and Egyptian Knowledge Bank

# AN OVERVIEW OF THE BAKING VALIDATION RESEARCH: REGULATIONS AND CHALLENGES

**Lakshmikantha Hallakere Channaiah**
*University of Missouri, USA*

## Abstract:

For thousands of years, baked goods have been an essential part of the human diet and the global food industry. In the US, the baking industry is responsible for $42 billion in direct wages and has a total economic impact of more than $186 billion annually. However, like other food segments, microbiological spoilage has often been the major factor affecting the shelf life of bakery products resulting in foodborne illnesses in addition to significant economic losses to bakeries. Baked goods were responsible for 150 outbreaks and 3,506 illnesses reported in the United States between 2001 and 2010. Foodborne pathogens such as pathogenic *E. coli, Salmonella spp., Staphylococcus aureus, Listeria monocytogenes* can be introduced into bakery products through a wide variety of ingredients and other environmental factors. Insufficient process preventive controls such as baking could result in contaminated finished food products which could pose a risk to public health. Therefore, it is critical for bakers to implement a validated kill steps such as baking, cooking, roasting, boiling etc. to ensure the safety of the finished bakery products. The U.S. FDA's Food Safety Modernization Act (FSMA) signed into law in 2011, aims to enhance the U.S. food safety system by shifting the focus from addressing food safety failures than preventing them. The FSMA regulations clearly specifies that facilities subject to the preventive control requirements in 21 CFR part 117 must validate all preventive controls implemented by food facilities to effectively mitigate identified hazards as appropriate to the nature of the preventive control. Since the inception of baking validation research in 2013, more than 20 bakery products have been validated. Most baking validation research was performed against Salmonella, as it is one of the most dormant pathogens in low water activity foods under the worst-case scenario process conditions. Validation helps in manufacturing pathogen-free bakery products, complying with FSMA regulations, optimizing the baking process, and saving the food industry millions of dollars by avoiding recalls and other legal penalties due to foodborne illness outbreaks. Additional validation research is needed to better understand the survival of Salmonella, STEC and other foodborne pathogens in low water activity foods with high fat, salt, and sugar food matrices.

## Biography

Lakshmikantha Hallakere Channaiah with over With over 22 years of teaching and research experience, Dr. Channaiah's expertise spans food safety microbiology, process validation, microbial kinetics, molecular characterization of antibiotic-resistant bacteria, predictive lethality modeling, HACCP, and FDA-FSMA regulatory compliance. Lead a BSL-2 research lab focused on developing validated thermal intervention strategies to reduce foodborne pathogens to ensure safety. I serve as a process authority for the state of Missouri, sit on editorial boards of three leading food safety journals, and have authored 25+ peer-reviewed publications and two book chapters.

Day 1

# Infectious Diseases
# &
# Microbiology

## Oral Presentations

# COMPARATIVE EFFECTIVENESS OF DIFFERENT THERAPIES FOR *CLOSTRIDIOIDES DIFFICILE* INFECTION IN ADULTS: A SYSTEMATIC REVIEW AND NETWORK META-ANALYSIS OF RANDOMIZED CONTROLLED TRIALS

**Dániel Steve Bednárik[1,2] ,Kincső Csepke Földvári-Nagy[1,3],Viktor Simond Anett Rancz[1], Noémi Gedea, Dániel Sándor Veres[1], Panagiotis Paraskevopoulos[1], Tamás Schnabel[4], Bálint Erőss[1,5], Péter Hegy[1,5], Katalin Lentia[1,6] and László Földvári-Nagy[1,6]**

*[1]Semmelweis University, Budapest, Hungary*
*[2]Heim Pál National Pediatric Institute, Hungary*
*[3]University of Warwick, United Kingdom*
*[4]Skien Hospital, Telemark Hospital Trust, Norway*
*[5]University of Pécs, Hungary*
*[6]Shared Last Authorship*

## Abstract:

**Background:** *Clostridioides difficile* infection (CDI) is one of the most common and serious causes of healthcare-associated diarrhea, with significant morbidity and mortality. The incidence of CDI is increasing worldwide, and it is therefore essential to carefully evaluate the efficacy of currently used therapies. The objective of this study was to clarify which is the most effective therapy available for CDI and which leads to the lowest risk of recurrence.

**Methods:** Potential therapies for the treatment and prevention of CDI were analyzed using a network meta-analysis of data from randomized controlled trials published up to 19 August 2024. Data collection was performed in MEDLINE, EMBASE and the Cochrane Central Register of Controlled Trials databases using a research protocol registered in PROSPERO (CRD4202222371210). The treatments were ranked according to P-score.

**Results:** It was assessed 73 RCTs with 28 interventions, involving 27,959 patients (49.2% female) in five networks. Fecal microbiota transplantation (FMT) was the most effective treatment in terms of the cure rate overall (P-score: 0.9952) and in recurrent cases (P-score: 0.9836). For recurrent cases, fidaxomicin (P-score: 0.67) showed significantly greater efficacy than vancomycin (P-score: 0.37) and tolevamer (P-score: 0.36), while for non-recurrent infections, ridinilazole, fidaxomicin, FMT and nitazoxanide were equally effective. For the prevention of recurrence, ridinilazole (P-score: 0.77) and fidaxomicin (P-score: 0.76) were the most effective. Probiotics were not effective in preventing CDI, with no significant difference between probiotics and placebo (even in old age). There was no difference between oral and colonoscopic routes of administration of FMT.

**Conclusion:** The superiority of FMT in the treatment of CDI highlights the potential for increased use of FMT in clinical settings. Further research on optimizing FMT protocols and exploring its long- term safety and efficacy in larger samples is needed. The findings suggest that the preventive use of probiotics might be questioned.

## Biography

He graduated in 2020 from University of Szeged as a medical doctor. In September of the same year, he started his residency at Heim Pál National Pediatric Institute, as a pediatrician, meanwhile he is also working on his PhD with a special interest in infectiology and gastroenterology. His main research field is related to Clostridioides difficile infection. His most recent publication on the effectiveness of different therapies for *Clostridioides difficile* infection in adults was published in The Lancet Regional Health – Europe.

# MANAGEMENT OF CARBAPENEM-RESISTANT ENTEROBACTERIACEAE INFECTIONS IN ICU SETTINGS: A COMPREHENSIVE ANALYSIS

**Pravalika Sathyanarayana, Sharadadevi MannurY and Mahadevamma Lingaiah**
*Dayananda Sagar University, India*

## Abstract:

Carbapenem-resistant Enterobacteriaceae (CRE) have emerged as a critical threat in intensive care units (ICUs), with significant implications for patient outcomes and healthcare systems. This study aims to investigate the risk factors, clinical outcomes, management strategies and molecular characteristics with CRE in ICU settings.

**Objectives:** To assess the risk factors, clinical outcomes, antibiotic susceptibility patterns, molecular characteristics of CRE isolates, and management strategies used in ICU settings.

**Materials and Methods:** A total of 90 clinical samples were collected from ICU patients with suspected CRE infections. Comprehensive risk factor analysis was performed, and clinical outcomes were evaluated. Antibiotic susceptibility testing was conducted using phenotypic methods, while molecular characterization using RTPCR identified resistance genes and mechanisms. Management strategies employed in CRE treatment were reviewed, including the use of different antibiotic regimens. Correlations between risk factors, molecular profiles, clinical outcomes, and treatment strategies were analysed.

**Inclusion Criteria:** Adults of either gender above the age of 18 years admitted to the ICU with CRE infections including respiratory, urinary, blood stream infections, and abdominal infections. (Isolates- Blood, Urine, Pus, Sputum, Tissue).

**Exclusion Criteria:** Discharge within 5 days of ICU admission or transfer to other facilities.

**Results:** Among the 90 isolates, 65% were confirmed as metallo-beta-lactamase (MBL) producers. Key risk factors for CRE acquisition included prior carbapenem exposure, prolonged ICU stays, mechanical ventilation, and invasive device usage. Clinical outcomes indicated a high mortality rate (32%), prolonged hospital stays and increased complications in MBL producers. Phenotypic testing revealed multidrug resistance in most isolates (65%), while genotypic evaluation identified predominant carbapenemase genes, including blaNDM (45%) and blaOXA-48 (30%). Meropenem-based regimens were the most frequently used (54.4%), followed by ceftazidime-avibactam (27.7%) and polymyxins (17.7%). A strong correlation was observed between specific resistance genes, adverse clinical outcomes, significant risk factors, and treatment effectiveness. Patients treated with ceftazidime-avibactam demonstrated relatively better therapeutic responses compared to those managed with meropenem monotherapy or polymyxins.

**Conclusion:** This study indicated a high prevalence of MBL-producing CRE isolates, with significant risk factors including prior carbapenem use, prolonged ICU stays, and invasive procedures. Clinical outcomes highlight a high mortality rate. Notably, ceftazidime-avibactam demonstrated better therapeutic response, emphasizing the importance of targeted therapies for effective management of CRE infections.

## Biography

Pravalika Sathyanarayana earned her Doctor of Pharmacy (PharmD) degree from Rajiv Gandhi University of Health Sciences, India, in 2020. She began her career as an academician and researcher at T. John College of Pharmacy, where she contributed to both teaching and research initiatives. Currently, she is pursuing her PhD at Dayananda Sagar University, focusing on antimicrobial resistance, particularly in carbapenem-resistant infections. She has actively presented her research at national and international conferences, earning recognition, including the Best Oral Presenter Award at “DSU-Pharmacon 2024.” She has published several research and review articles in Scopus-indexed and SCI (E) journals.

# MOLECULAR INVESTIGATION OF BACTERIAL AGENTS IN ABORTION MATERIALS OF SMALL RUMINANTS IN SOME EASTERN ANATOLIAN PROVINCES

**Kadir AKAR**
*Van Yuzuncu Yil University, Turkey*

## Abstract:

Abortion cases in sheep farms cause significant economic losses and represent an important concern in terms of public health. Determining the prevalence of causative agents in a specific region is crucial for controlling and preventing related diseases. This study aimed to identify the presence and prevalence of potential bacterial pathogens in 32 abortion cases from sheep in the provinces of Iğdır (13 samples) and Ağrı (19 samples) collected in 2022. Tissue and swab samples (lung, liver, kidney, vaginal swab, nasal swab) were analyzed. The study focused on detecting bacterial agents known to cause abortions in small ruminants, including *Chlamydia spp, Chlamydophila abortus*, *Coxiella burnetii*, *Salmonella spp, S. abortus ovis*, *Listeria spp*, L. *monocytogenes, Campylobacter spp*, *Brucella spp,* and *B. melitensis*. Following DNA extraction from the collected samples, molecular analysis was conducted using the polymerase chain reaction (PCR) method to detect the presence of these pathogens. No bacterial agents were detected in 22 of the total samples. Among the 19 samples from Ağrı, 5 were found to be positive (2 *C. burnetii*, 3 *Campylobacter spp*.). In Iğdır, bacterial agents were identified in 7 out of 13 samples (1 *Brucella spp*. [confirmed as B. melitensis], 2 *C. burnetii*, 2 *Campylobacter spp*., and 2 *Salmonella spp*.). These findings reveal the distribution of bacterial agents in abortion cases from the examined provinces and provide valuable epidemiological data. Identifying the presence of these pathogens is important for developing strategies to combat abortion agents in the region. Nevertheless, further comprehensive studies are needed to determine the dominant pathogens in these provinces. The information obtained is expected to support local veterinarians in diagnostic and control efforts.

## Biography

Kadir AKAR born in 1987 in Adana/Seyhan, he completed his primary, secondary, and high school education in Adana before graduating from Selçuk University Faculty of Veterinary Medicine in 2011. He began his career as a civil servant in 2012 and pursued his doctoral studies at Selçuk University Health Sciences Institute, Department of Veterinary Microbiology, from 2014 to 2021. Between 2017 and 2022, he served at the Brucella Vaccines Production and Reference Diagnostic Laboratory within the Pendik Veterinary Control Institute. Since 2022, he has held the position of Assistant Professor in the Department of Microbiology at Van Yuzuncu Yil University Faculty of Veterinary Medicine. As an academic in the Department of Preclinical Sciences, his expertise centres on veterinary microbiology. Throughout his career, he has made significant contributions to numerous national and international research projects, establishing himself as a specialist in his field Khaidarov Saken has expertise in evaluation and a passion for improving health and wellbeing. His open and contextual evaluation model based on responsive constructivism creates new pathways for improving healthcare research. He has developed this model after years of experience in research, evaluation, teaching, and administration, both in hospitals and educational institutions

# HEMOPERFUSION WITH CYTOSORB® IN PEDIATRIC PATIENTS: EXPERIENCES FROM SLOVENIA

**Tina Plankar Srovin, E Rihar, P Fister, V Peršič, A Jerman, G Mlakar, N Bezeljak and M Pokorn**
*UMC Ljubljana, Slovenia*

## Abstract:

Cytokine storm is a dysregulated cytokine response associated with sepsis and other conditions that result in a hyper-inflammatory state. Extracorporeal cytokine adsorption has the potential to restore a balanced inflammatory response. Hemoperfusion with CytoSorb® (CS) appears a short-term mode of treatment of sepsis in both adults and children. We treated eight critically ill children with CS at the University Medical Centre Ljubljana with clinically manifested cytokine storm with good outcome in children over 10 kg. We conclude that the adsorption with CS remains a potential treatment for cytokine storm in critically ill children.

**Objective of the Study:** The aim of our case-series is to present our pediatric experience with CS.

**Materials and Methods:** We performed a retrospective analysis of all-eight children (age from 3 days to 6 years) treated with CS in the pediatric intensive care unit in University Medical Center Ljubljana, Slovenia, from September 2018 to February 2020.

**Results and Discussion:** Five patients age from 16 to 75 months survived, 3 were previously healthy, 2 had hematologic diseases. Three children died, 2 newborns and 1 infant, all weighted less than 10 kg and had chronic diseases (metabolic disease, leukemia and prematurity with multiple birth defects). All but two children (with severe graft versus host disease and fulminant liver failure) were treated with CS because of septic shock.

In our experience, cytokine adsorption with CS remains a potential adjunctive treatment for cytokine storm in critically ill children. The effect of age and weight on complications are unclear as are the initiation and duration of treatment and volumes used. Future work measuring interstitial IL-6 or other cytokines is needed to determine the effect of hemoadsorption on cytokine storm.

## Biography

Tina Plankar Srovin, MD, PhD is a pediatrician who works at the Department for Infectious diseases at University Medical Centre in Ljubljana, Slovenia, for 20 years. She is a head of consultants for pediatric infectology at UMC Ljubljana, her special interests are infections in critically ill and immunocompromised children. She is mentoring pediatric residents and medical students. Her mission is also to educate other doctors about increasing problem of antimicrobial resistance and to promote appropriate use of antimicrobials. Her PhD work was about risk factors for the emergence of resistant bacteria in the hospitals. Besides her everyday work at the infectious disease pediatric department, she is also an assistant at the Faculty of Medicine, Ljubljana.She is currently involved in 2 international European research projects, Perform and Pegasus, which already resulted in some important publications.

## SYMPTOMS AND LIFE QUALITY POST COVID-19 SYNDROME AMONG COVID-19 PATIENTS

**UAWL Perera[1] and Kumudini Jayasinghe[2]**
*[1]Base Hospital Elpitiya, Sri Lanka*
*[2]National Hospital Kandy, Sri Lanka*

### Abstract:

**Background:** Health care systems and societies being overloaded by long-term effects after SARS-CoV-2 infection. According to the UK's latest National Institute for Health and Care Excellence guidelines post-COVID-19 syndrome is when the symptoms persist beyond 12 weeks in the absence of an alternative diagnosis.

**Objectives:** To determine the prevalence, common symptoms, associated comorbidities /risk factors and quality of life among following symptomatic Covid 19 infections.

**Method:** Descriptive cross-sectional study, using 150 post covid patients done in post covid clinic of medical unit 1(M1) at National Hospital Kandy (NHK) Sri Lanka. Simple random sampling. Data collection was done by using interviewer administered data collection form. Data analyzed by SPSS 20.

**Inclusion Criteria:** Moderate to severe covid pneumonia and patients with major complications and uncontrolled comorbidities who have been treated as inward covid patients at National hospital Kandy. Covid 19 patients who have been treated at Intermediate care centers who need further assessment due to ongoing symptoms and those who are aged 18 years and above

**Exclusion criteria:** Psychiatric patients who lack capacity in history giving. Critically ill patients and who were given ICU care during hospital stay, as they can develop post-intensive care syndrome

**Results:** Out of 150 patients who had symptomatic covid 19 infections 79 (53%) were female. Mean age was 52y.Prevalence of post covid syndrome was 18%.out of 150 covid 19 patients 96 (64%) were completely vaccinated. Study showed that patients with ischemic heart disease, hypertension, and diabetes were more likely to develop post covid syndrome. Quality of life was adversely affected by post covid syndrome in 125 (83.3%) patients. Also 22 (14.7%) lost their occupation, 54 (36%) post covid patients needed rehospitalization. Chronic fatigue syndrome 27(18%), ischemic heart diseases17(11.3%) and Interstitial lung disease21(14%) and hyperglycemia 10(6.7%) were the commonly identified long term complications.

**Conclusion:** Covid 19 patients need long term follow up to detect development of post covid syndrome. Their quality of life gets adversely affected by post covid syndrome. Comprehensive rehabilitation services and special post covid clinics should be encouraged.

### Biography

UAWL Perera studied medicine at Sri Jayewardenepura university Sri Lanka. She graduated MBBS in 2009 and received MD-General Medicine from Sri Lanka in 2021.Also holds a Diploma in Elderly medicine. She completed MRCP part 1 and 2. She has published several audits and quality improvement projects in journals and presented a research paper in EFIC conference in Spain

# IMPACT OF INSECTICIDE-TREATED MATERIALS (ITMS) ON *AEDES AEGYPTI* HOST LOCATION BEHAVIOR IN SAUDI ARABIA

**Ashwaq Madani Al Nazawi**
*Jazan University, Saudi Arabia*

## Abstract:

Insecticide-treated materials offer a simple yet effective method to reduce domestic infestations of disease vectors. However, their use against *Ae. aegypti* is complicated by the development of insecticide resistance.

**Objective:** The study objective was to investigate the resistant and susceptible of *Ae. aegypti* strains exhibit behavioural differences during host-seeking at insecticide-treated netting.

**Methods:** Two experimental assays were developed based on host seeking and final stage of host feeding behaviours on three strains of *Ae. Aegypti* that involved new orleans (pyrethroid-susceptible), Jeddah and Makkah (pyrethroid-resistant). Individuals were exposed to insecticide-treated and untreated materials and their host feeding behaviour were assessed based on groups of 5 mosquitoes, attempting to reach and feed on human bait. Host-seeking behaviour was assessed using a wind tunnel, with individuals flying upwind and allowed to pass through holed material.

**Results:** Behavioural events were recorded over 10 and 20 min respectively and logged manually. A significant reduction in time spent resting, probing or bouncing was seen with treated compared to untreated materials. However, no difference was observed between resistant and susceptible strains. After contact with treated nets, all strains of mosquito were seen to favour resting at a distance from the treated surface. ln the wind tunnel, hole entry was seen to vary between mosquito strains, along with a significant reduction in the number of mosquitoes that passed through treated compared to untreated material ($P<0.0005$). This effect was significantly greater for the susceptible strain compared to the resistant strains at ($P<0.01$) with this also being reflected in post-exposure knock-down and mortality.

**Conclusion:**These results demonstrate how physiological resistance may enable mosquitoes to more easily pass through holed treated materials due to increased resilience to the insecticide rather than through altered behaviour, with patterns of behaviour being similar or not varying consistently between strains.

## Biography

Ashwaq is an Assistant professor in Public Health (Epidemiology program) at Jazan University, and an Expert in Molecular biology, innovation, and leadership. She served in the last 18 years as Technical Director at MoH, Jeddah vector surveillance and control, and Dengue advisory group, ISNTD consultant which includes expertise in insecticide resistance in mosquitoes and cross-resistance mechanisms. Dr. Ashwaq led and provide technical and scientific advice,and collaborate with other ministries and private partners locally and globally, on integrative resistance management, zoonotic disease control, and outbreak preparedness and response strategies in KSA and GCC. Dr. Ashwaq is a very dynamic and entrepreneur, Teamwork, Build relationships. Develop people, Inspire others, think critically, communication, lead change, scientifically multitalented, enjoyed multidisciplinary collaboration, effective communicator as a social media influencer in advocacy and promotion of better qualityy care delivery and women empowerment and resilience building against adversity. Dr. Ashwaq earned a Master degree (MSc) in Molecular Cell Biology at Nottingham Trent University and a Ph.D. in Tropical Medicine-Vector Biology in Liverpool School of Tropical Medicine. in addition, Master of the integrative government innovation system at Ajman university. Ashwaq is passionate for implementation and operational research, proficient in big data science and analytical tools, evidence synthesis and use in policy decision and anticipatory and resiliency actions as well as capacity building in tackling emerging diseases and threats to public health and improving social and economic livelihoods of the most vulnerable populations. She have gained a range of leadership, management, and risk assessment skills, productivity, research, and professionalism science with a strong proficiency in English and Arabic Languages.

# INTEGRATING AN AMS INTERVENTION INTO THE PRIMARY HEALTHCARE SYSTEM IN PAKISTAN

**Nida Khan**
*Association for Social Development, Pakistan*

## Abstract:

**Background:** Antimicrobial resistance (AMR) is a growing global health crisis, causing an estimated 4.95 million deaths in 2019, including 1.3 million directly attributed to AMR. The burden is particularly high in low- and middle-income countries (LMICs) due to weak health systems and unregulated antibiotic use. In Pakistan, antibiotic consumption rose by 65% between 2000 and 2015, reaching 1.3 billion defined daily doses.

Despite national initiatives, few interventions directly address antibiotic prescribing in rural primary care. Pakistan's health system lacks a structured model to promote rational antibiotic use for common infections. In Punjab-the most populous province-over 20% of outpatient visits at Rural Health Centres (RHCs) are for upper respiratory tract infections and diarrhoeal diseases. To address this gap, the Association for Social Development, in collaboration with the Health Services Academy and the Directorate General Health Services Punjab (DGHS), with support from ICARS, developed a contextualized intervention to improve antibiotic prescription and consumption practices at the primary healthcare level.

**Objectives:** The key objective was to develop an AMS intervention that can be integrated into the primary healthcare system in Punjab, Pakistan.

**Methods:** As a first step to ensuring the AMS intervention could successfully be integrated into the primary healthcare system in Pakistan, we conducted a thorough context analysis to understand the care delivery settings and practices. Then, we worked on the following three dimensions: a) care delivery-including implementation strategies and products, b) health system support-utilizing WHO building blocks for health system strengthening, and c) patient engagement and safety.

**Results:** To address the care delivery, for each listed AMR care delivery task, staff role distribution and requirements were defined. Implementation products (based on agreed care delivery strategies) e.g., desk-aide, staff training, and patient education tool, were developed. The implementation products were developed through a Core Expert Group, based on international guidance and contextual understanding, and a DGHS-led Technical Working Group (TWG) to review and guide the drafted strategies and products. All six WHO building blocks were addressed in the integrated care model components.

**Conclusion:** To integrate an AMS intervention into routine primary healthcare systems, equal attention needs to be given to care delivery and health systems considerations, the health department needs to be given the leadership and ownership of the development activity, a set of process abilities and professional credentials are required for developing a context-informed model of integrated care, and a range of expertise and meaningful stakeholders' engagement are required.

## Biography

Nida Khan is currently pursuing a DPhil in Evidence-Based Health Care at the University of Oxford. She holds an MS in Public Health and a graduate degree in Economics. Since 2011, she has served as Lead Professional in the Research, Monitoring, and Evaluation Unit at the Association for Social Development (ASD), Pakistan. Nida has extensive experience in developing, implementing, and evaluating integrated care models for various communicable diseases (including antimicrobial resistance (AMR), & TB/ DR-TB and hepatitis) and non-communicable diseases (such as diabetes, hypertension, lung health, maternal and child health, early child development and mental health). Her expertise spans pragmatic cluster randomized trials, process and economic evaluations, and community engagement strategies, particularly in low-resource public and private health settings. She has contributed to several studies and digital health innovations aimed at improving access, quality, and accountability in health service delivery. Nida has published widely in peer-reviewed journals and presented at national and international conferences. Her current research interests include the contextual adaptation of antimicrobial stewardship interventions, implementation science, and the use of digital tools to support patient-provider networks. She is particularly committed to generating evidence that informs policy and practice for more responsive and integrated primary healthcare in Pakistan.

# SEROPREVALENCE AND RISK FACTORS ASSOCIATED WITH PHLEBOVIRUSES AND CRIMEAN–CONGO HEMORRHAGIC FEVER VIRUS AMONG BLOOD DONORS IN CENTRAL TUNISIA

**Rym Ayari**
*Infectious Diseases Department of Farhat Hached Hospital/Faculty of Medicine of Sousse, Tunisia*

## Abstract:

The last few decades have been characterized by the global emergence of many new infectious diseases in the human population caused by arthropod-borne viruses (arboviruses) which have animal reservoirs. Little is known about the seroprevalence of arboviruses in North Africa, especially in Tunisia. From which, the aim of this study was to determine the prevalence of six viruses, from two families of the order *Bunyavirales*, in general population of central Tunisia. Sera collected from 377 asymptomatic blood donors were serologically assayed for Rift Valley fever virus (RVFV), Crimean–Congo hemorrhagic fever virus (CCHFV), and four sandfly-borne phleboviruses: Toscana virus (TOSV), sandfly fever Naples virus (SFNV), sandfly fever Sicilian virus (SFSV) and sandfly fever Cyprus virus (SFCV). Of the 377 subjects enrolled, 17.3% were IgG positive for at least one of the viruses tested. The most frequently detected antibodies were against TOSV (13.3%), followed by SFCV (2.9%), RVFV (1.9%), SFSV (1.3%), and SFNV (1.1%). Only one sample was IgG positive for CCHFV. Dual reactivity was observed in nine cases: SFSV + SFCV in three cases (0.8%) and TOSV + SFNV, TOSV + SFCV, and TOSV + RVFV in two cases (0.5%) each. 15.9% of donors were IgG positive against sandfly-borne phleboviruses. Among the 65 donors IgG positive for phleboviruses, 50.8% were from rural areas compared to 12.3% from urban areas ($p<0.001$); 92.3% had animals in living quarters ($p=0.009$); and 70.8% lived in the vicinity of stagnant water ($p=0.062$). Seroprevalence was significantly higher among donors living with chronic diseases ($p=0.039$). Furthermore, the seroprevalence of phleboviruses was higher in Kairouan, the central governorate, than in the two coastal governorates: Monastir and Sousse, with 33.4%, 24.2%, and 14.9%, respectively. The presence of antibodies in general population needs further investigation to better assess the extent of these viruses. Only TOSV was known to have an extensive circulation in Tunisia and in North Africa. Continued surveillance and interventions are necessary to detect the emergence of arboviruses and to prevent further transmission.

## Biography

Ayari Rym, PhD in microbiology, a researcher at Faculty of Medicine in Sousse, attached to clinical research in Infectious Diseases Department of Farhat Hached Hospital, assistant at Higher Institute of Nursing Sciences in Kairouan and former assistant at Faculty of Dental Medicine in Monastir. She has expertise in virology and a passion for improvement of research in some viral infectious diseases. After years in research and teaching, her works has been subject to several publications (Factors associated with fibrosis progression in chronic hepatitis B virus infection, Investigation of DNA sequences in basal core promoter, precore and core regions of hepatitis B virus from Tunisia shows a shift in genotype prevalence, Phylogenetic analysis of isolated HCV strains from Tunisian hemodialysis patients….) and many international communications (Relationship of WNV seroprevalence with ABO and D blood groups among blood donors: implication for transfusion safety, Study of Flavivirus infection in Tunisian blood donors, Arboviruses in aseptic meningitis in central Tunisia, Hepatitis Delta virus infection in central Tunisia

# THERMAL INACTIVATION OF SALMONELLA DURING THE OATMEAL CHOCOLATE CHIP GRANOLA BAR MANUFACTURING PROCESS

**Lakshmikantha Hallakere Channaiah**
*University of Missouri, USA*

## Abstract:

Salmonella is known to survive in low-moisture food products such as flour, oats, chocolate chips, milk powder, and spices for extended periods of time. Salmonella bacteria enter a dormant state in a dry food environment enhancing its survival as well as heat resistance. Outbreaks linked to contaminated oats highlight the importance of industry-wide interventions, such as validated thermal kill steps such as baking, toasting, and cooking. A study was conducted to assess the effectiveness of toasting old-fashioned oats as an effective kill-step in controlling Salmonella contamination originating from raw oats during oatmeal chocolate chip granola bar manufacturing process and assess the thermal resistance characteristics of (D- and z-values) of five serovar Salmonella cocktail in granola bars. The raw oats were inoculated with five serovar Salmonella cocktail (Typhimurium, Mbandaka, Agona, Newport and Senftenberg) and dried back to their original water activity level. The inoculated oats containing 11.14 ± 0.370 log CFU/g Salmonella population was toasted at 325°F/(162.7°C) for 12 minutes before mixing with other ingredients to manufacture oatmeal chocolate chip granola bars mimicking the commercial manufacturing process. Toasted oats and finished granola bars were enumerated using injury recovery media. While water activity varied during the process, the pH decreased significantly. The results indicated that toasting oats at 325°F/(162.7°C) for 12 minutes resulted in a reduction of 6.04 ± 0.22CFU/g in Salmonella population making it an effective kill step in controlling Salmonella. The D-values for 12 min toasted oats at 67, 70 and 73°C were 8.7 ± 1.02, 4.6 ± 0.99, and 1.4 ± 0.11 respectively and the z value was 7.7 ± 0.74. The results from this study help in optimizing food safety parameters during the manufacturing of chocolate chip granola bars thus protecting consumers from foodborne illness outbreaks.

## Biography

Lakshmikantha Hallakere Channaiah with over Gilbert GLADY With over 22 years of teaching and research experience, Dr. Channaiah's expertise spans food safety microbiology, process validation, microbial kinetics, molecular characterization of antibiotic-resistant bacteria, predictive lethality modeling, HACCP, and FDA-FSMA regulatory compliance. Lead a BSL-2 research lab focused on developing validated thermal intervention strategies to reduce foodborne pathogens to ensure safety. I serve as a process authority for the state of Missouri, sit on editorial boards of three leading food safety journals, and have authored 25+ peer-reviewed publications and two book chapters.

Day 2

# Infectious Diseases
# &
# Microbiology

Keynote Presentation

# TH1/TH2 PARADIGM: IS IT INFECTION OR ALLERGY, OR BOTH?

**Gilbert GLADY**
*European Bio Immune(G)ene Medecine Association, France*

## Abstract:

The ability of naïve CD4 T cells to differentiate into distinct cytokine-producing effector T helper (Th) cell subsets has been well appreciated over the last 35 years. The initial hypothesis set forth by Mosmann and Coffman in 1986 describes how T helper cells (Th cells) are polarized into two main types, Th1 and Th2, to orchestrate different immune responses against pathogens. So the Th subset primarily generated determines the class/subclass of immunity induced, and this in turn is important to clinical outcome in diverse medical situations, as seen in allergies, autoimmunity and in responses to infectious agents and cancer. An understanding of this mechanism is essential to the rational design of strategies to modulate immune responses for the benefit of the patient. Today it is widely agreed that Th1 cells promote a cellular immune response, involving cells like macrophages, to eliminate infected cells, and Th2 cells drive humoral immunity and are linked to allergic reactions. Actually the immune response tends to polarize towards either a Th1 or Th2 direction, a process that can be mutually suppressive. Finally, the roles of Th1 and Th2 cells are not fixed, but depend heavily on the specific context of the infection, the timing of cytokine release, and the location of immune activity. Some limitations of the paradigm have been described, as the discovery of other T helper cell subsets, However, in our clinical practice related to BI(G)MED, the TH1/TH2 differentiation remains very useful in guiding the therapeutic approach, as I will try to illustrate in my talk today.

## Biography:

Gilbert Glady graduated from Med School in 1977 and was then a resident in onco-hematology in the university clinic for several years. After a specialization in natural medicines in Paris, he returned to the Alsace region to work as a private practitioner. Through his work and encounters, he developed interest and expertise in immunology and immunogenetics, that leaded him to nanomedicine and nanobiotechnology. He thus became in 2010 the creator of the BI(G)MED method (Bio Immune (G)ene Medicine) and director of EBMA, the European association responsible for the communication and trainings in the field of BI(G)MED. He has participated in numerous international congresses in immuno-allergology, infectiology and oncology with posters and oral presentations, and is the author of several publications on nanobiotherapy in different journals.

# EVALUATION OF THE SYNERGISTIC ANTIMICROBIAL EFFECTS OF *COMBRETUM APICULATUM* EXTRACT, GREEN SYNTHESIZED SILVER NANOPARTICLES, AND AMOXICILLIN AGAINST *STAPHYLOCOCCUS AUREUS, ESCHERICHIA COLI, KLEBSIELLA PNEUMONIAE, AND PSEUDOMONAS AERUGINOSA*, WITH THE DEVELOPMENT OF A NOVEL WOUND DRESSING HYDROGEL

**Travers Kudzai Chirova**
*Harare Institute of Technology, Zimbabwe*

## Abstract:

Antibiotic resistance remains a significant global health concern, driving the need for alternative and more effective antimicrobial therapies. This research aimed to evaluate the synergistic antimicrobial effects of Combretum apiculatum acetone crude extract, green synthesized silver nanoparticles (AgNPs), and amoxicillin against selected pathogenic bacteria *Staphylococcus aureus*, *Escherichia coli, Klebsiella pneumoniae*, and *Pseudomonas aeruginosa*. The study also focused on the development of a wound dressing hydrogel incorporating the most effective combination. Fresh leaves of *C. apiculatum* and *Mangifera indica* were collected and subjected to maceration extraction using various solvents. Silver nanoparticles were synthesized using *M.indica* leaf extract through green synthesis, and characterized via UV-Vis and FTIR spectroscopy. Antimicrobial activities were tested individually and in combinations using the agar well diffusion method. The Minimum Inhibitory Concentrations (MICs) were determined, and synergistic effects were quantified using the Fractional Inhibitory Concentration Index (FICI) via checkerboard assays. Hydrogels were formulated using sodium alginate and calcium chloride and evaluated for antimicrobial activity in vitro.The results revealed that the combination of amoxicillin, *C. apiculatum* extract, and AgNPs exhibited a more potent synergistic effect against all test organisms than combinations with ciprofloxacin. The A+B+C treatment demonstrated FICI values indicative of synergism or additive interactions (≤1.0), particularly against *K. pneumoniae and P. aeruginosa*. The FTIR analysis confirmed the presence of phytochemical groups essential for nanoparticle stabilization. The formulated hydrogel exhibited antimicrobial zones of inhibition ranging from 4.5 mm to 12.6 mm, confirming its potential as a therapeutic agent. It is concluded that combining phytochemicals with nanoparticles and antibiotics may provide an effective strategy against multidrug-resistant pathogens. The study recommends further in vivo testing of the hydrogel formulation to establish its clinical applicability.

## Biography:

Travers Chirova is a Lecturer in the Biotechnology department at the Harare Institute of Technology in Harare, Zimbabwe. His research has spread over a number of areas with most recent focusing on investigating for new antimicrobial compounds from both natural (plant) and synthetic materials, factoring in the assessment of these antimicrobial entities against antibiotic resistant strains of microbials. The passion being in ensuring improved health and management of infectious microbial agents to both humans and animals He has also researched on fermentation biotechnology areas with specific mention to citric acid production and its purification, only to mention a few. He has published several papers and a book chapter He earned degrees in Biotechnology (Btech Honors) from Chinhoyi University of Technology and a Master of Technologay Honors Degree in

Biotechnology from ITM University, Gwalior India. He has been Lecturing in University for over 7 years and has supervised many Bsc projects. He has published several papers and 1 book chapter. He has been part of delegates under the ministry of health and child welfare working on bio fortification policy documents and also part of members looking into antimicrobial resistance development and possible solutions to the problem. Also a member of the entre for Science & Technology of Non-Aligned and Other Developing Countries (NAM S&T Centre). Has peer reviewed papers for blind reviews for a number of journals.

# EFFECT OF DIFFERENT CONCENTRATION OF TABLE SALT ON PHYSCIOCHEMICAL AND MICROBIAL QUALITY OF FERMENTED CAT FISH *(CLARIAS GARIEPINUS)*

**Chinedu Obiageli Ajogun**
*Nigerian Institute of Food Science and Technology, Nigeria*

## Abstract:

Catfish *(Clarias gariepinus)* obtained from a local market in Port Harcourt, Rivers State, Nigeria was treated with different concentration of table salt (10%, 15% and 20% w/w) and allowed to ferment naturally and at ambient temperature (28 ± 2°C) for five days. Physicochemical and microbial analysis was carried out on the unfermented non-salted (control) and fermented salted samples of the catfish. Results obtained revealed that different concentration of the table salt produced significant effect on physicochemical quality; moisture content of the unfermented (control) cat fish was significantly higher (64.22%) than those of the various salt levels; 10% (60.33%), 15% (54.33) and 20% (52.13%); the higher the salt level the lower the moisture content (as a result of osmotic reduction). Fat and protein level was low through fermentation while ash content increased with increase in salt levels. Reduction in protein may be due to action of proteolytic enzymes. Microbiological analysis data showed significant decrease in total viable count from $4.30\times10^2$cfu/g in catfish treated with 10% salt concentration to $2.60\times10^2$ cfu/g in catfish treated with 20% salt concentration after 5 days fermentation. Similarly, there was a decrease in mold/yeast, Total coliform and *Staphylococcus aureus* after 10%, 15% and 20% salt treatment; increasing salt concentration in fermented catfish although promotes salt-tolerant microbes it however reduces water activity which is a key factor in preserving fish by inhibiting microbial growth thereby enhancing preservation and inhibiting spoilage and pathogenic microorganisms hence, it leaves the fermented product with a longer shelf life. Consumers are advised to use branded salts as they are subject to regulatory standards and quality control measures.

## Biography:

Chinedu Obiageli Ajogun, is a food scientist and Product development specialist. Highly motivated food scientist with expertise in food chemistry, microbiology, and product development. Proven track record of creating innovative, safe, and good food products. She has a patent on coconut wine which was one of the products produced during her PhD study. She is a member of The Nigerian Institute of Food Science and Technology (NIFST). Certified Food Scientist of Nigeria (CFSN). She is also a certified Lead Auditor ISO 22000:2018 Food Safety Management System. She obtained her B.Sc. in Food Science and Technology from University of Maiduguri Nigeria, M.Sc. in Food Microbiology University of Port-Harcourt Nigeria and PhD in Food Science and Technology Rivers State University Nigeria. She has published several papers which has been cited in various research sites. Her research interest is in food quality control and auditing, microbiology and food safety, food chemistry, food sustainability and affordability.

Day 2

# Infectious Diseases
# &
# Microbiology

## Oral Presentations

# HIGH AND RISING COLONISATION BURDEN AMONG CRITICALLY ILL PATIENTS-A LONGITUDINAL SURVEILLANCE IN A NORTH INDIAN ICU

**Deen Bandhu Prasad and Armin Ahmad**
*King George's Medical University, India*

## Abstract:

**Background:** Intensive care units (ICUs) represent critical epicentres for the emergence and dissemination of multidrug-resistant organisms (MDROs). Colonization-defined as the presence of microorganisms without overt clinical infection-creates a concealed reservoir that can precipitate ventilator-associated pneumonia, bloodstream infections, and other nosocomial complications once host defences are breached or invasive devices are introduced. Despite global recognition of this threat, data from North Indian tertiary care centres remain limited, particularly regarding multisite colonization dynamics over time and their relationship with subsequent infection risk.

**Objective:** This study aimed (1) to determine the incidence of bacterial colonization across multiple anatomical sites at ICU admission and (2) to characterize temporal changes in colonization patterns at 4-day intervals until discharge or death among critically ill patients in a 36-bed ICU at King George's Medical University (KGMU), Lucknow, North India.

**Methods:** In this prospective observational study, 100 consecutive adult ICU admissions were enrolled. Exclusion criteria included ICU stays under 48 hours or early mortality within six hours of admission. Demographic and clinical data-age, sex, comorbidities, APACHE II and SOFA scores, antibiotic exposures, and device use-were recorded. Under aseptic technique, swabs from five sites (axilla, endotracheal/tracheal tube, throat, nasal cavity, rectal/perianal area) were collected on Day 1 and every fourth day thereafter. Samples were plated on blood and MacConkey agar; organism identification and antimicrobial susceptibility testing were performed according to CLSI standards, with semi-quantitative growth classification (scanty, moderate, heavy) and categorization into pan-sensitive (PANS), multidrug-resistant (MDR), extensively drug resistant (XDR), or "did not culture" (DNC) groups.

**Results:** The cohort had a mean age of 42.8 ± 19.7 years; 58.3% were male. Median ICU length of stay was 7 days (IQR 3–15). At admission, overall colonization prevalence across all sites was 75.1%, rising modestly to 72.2% by Day 4 and 75.0% by Day 8, before a dip to 68.9% on Day 12 and a peak of 93.2% on Day 16. Site-specific colonization increases were notable: axillary colonization rose from 79.2% to 95.2%; endotracheal/tracheal tube colonization from 67.3% to 95%; throat from 75.2% to 95.2%; nasal from 70.3% to 90.5%; and rectal/perianal from 83.3% to 90.0%. Polymicrobial colonization became increasingly prevalent at all sites, peaking at 47.6% in the axilla and 40.5% in the rectal site by Day 16. Carbapenem-resistant Acinetobacter/Enterobacteriaceae (CRAB/CRE) colonization also rose, particularly in endotracheal sites (20% to 30%) and nasal sites (13.9% to 23.8%). Drug-resistance patterns demonstrated a shift toward MDR and XDR organisms over time. Notably, MDR prevalence at the rectal site climbed from 27.7% to 52.4% by Day 12, while XDR organisms persisted at 5–15% across several sites, underscoring the mounting resistance pressure.

**Conclusion:** Critically ill patients in this North Indian tertiary ICU exhibit a high burden of bacterial colonization at admission, which intensifies and diversifies with prolonged ICU stay. The progressive rise in MDROs-especially CRAB/CRE and XDR pathogens across multiple anatomical sites highlights the need for comprehensive, multisite surveillance to enable early decolonization and targeted antimicrobial adjustments. These findings support the implementation of region-adapted infection control bundles, including rigorous environmental hygiene, hand-hygiene enforcement, device-care protocols, and antimicrobial stewardship, to curb the silent but insidious threat of ICU colonization and its transition to invasive infection.

## Biography

Deen Bandhu Prasad is currently pursuing a DM in Critical Care Medicine at King George's Medical University (2022–present). He previously served as a Senior Resident in Medical Oncology at AIIMS, New Delhi (2018–2021). He holds a DNB in General Medicine (2013–2016) and has completed IDCCM from ISCCM (2016–2017), along with FCCS certification. Dr. Prasad has also contributed chapters to several recognized medical textbooks.

# THE OPTIMAL ANTIFUNGAL PROPHYLAXIS POST BONE MARROW TRANSPLANT

**Tabitha Merium Sabu**
*Amala Institute of Medical Sciences, India*

## Abstract:

Fungal infections are a obstacle for bone marrow transplantation. Appropriate antifungal prophylaxis is crucial. The risk of fungal infection varies with Haemopoietic Stem Cell Transplant (HSCT). Systemic reviews and metanalysis are needed to know the changes.

**Objective:** To find optimal antifungal for HSCT according to the type of transplant.

**Materials and Method:** Systemic review of literature on antifungal prophylaxis in HSCT

**Data extraction:** Pub Med and Cochrane databases.

**Inclusion Criteria:** Literature between 2015 and 2024 mentioning the fungal infection; comparing the efficiency of antifungal prophylaxis in HSCT.

**Exclusion Criteria:** Studies not mentioning HSCT type, antifungals or fungal infection

**Search Headings:** Stem Cell Transplant, fungal infection, Prophylaxis, Echinocandin, Azole, Polyenes.

**Results:** Initial search- 3743 articles. Eligible- 64studies. All eligible studies reviewed. Wong et al in metanalysis on 1617 patients (5 RCT) found lower invasive fungal infection (IFI); (RR, 0.43 [95% CI 0.28 to 0.66, p = 0.0001]) with Posaconazole compared with other antifungals. Zeng et al on Network meta-analysis (8513 patients) found Posaconazole superior to Amphotericin(OR, 4.97; 95% CrI, 1.73–11.35), Itraconazole (OR, 0.40; 95% CrI, 0.15–0.85) Fluconazole [odds ratio (OR), 0.30; 95% credible interval (CrI), 0.12–0.60]. Selby et al. compared intravenous Posaconazole and Voriconazole found less possible fungal infection with IV Posaconazole (p =0.0002, OR = 8.89, 95% CI 2.67–29.2).

**Conclusion:** There is an increase in mold infection. Risk of IFA is highest in post haploidentical and unrelated allogenic transplant. Prophylaxis with antifungals for mold is recommended for high risk transplants. Posaconazole is a optimal antifungal for these patients.

## Biography

Tabitha Merium Sabu is a Consultant in the Department of Infectious Diseases at Amala Institute of Medical Sciences, Thrissur. She holds MBBS, MD, DNB, MRCP(UK), MNAMS, and a Fellowship in Infectious Diseases and HIV from Tata Medical Centre, Homi Bhabha National Institute, Mumbai. She currently serves as the Clinical Lead for Antibiotic Stewardship, Convenor of the Hospital Infection Control Team, and Nodal Officer at the ART Centre. Passionate about improving patient care and infection control, Dr. Tabitha brings a focused and compassionate approach to her work. Her areas of interest include infections in immunocompromised and Post transplant infections. Outside of medicine, she enjoys cooking, reading, painting and cherishes her role as a mother to two children.

# CONTEXTUAL ANALYSIS OF ANTIBIOTIC PRESCRIBING PRACTICES FOR UPPER RESPIRATORY INFECTIONS AND DIARRHEA IN RURAL HEALTH CENTERS OF PUNJAB, PAKISTAN

**Shaheer Ellahi, Muhammad Ahmar Khan, Rabab Sakina, Mashal Amin, Faraf Zafar, Saad Alam, Erica Westwood, Wesal Zaman, Shahzad Khan and Muhammad Amir Khan**
*Health Services Academy, Pakistan*

## Abstract:

**Introduction:** Antimicrobial resistance is a major global health challenge, with LMICs bearing the greatest burden. In Punjab, where nearly 80% of primary care prescriptions include antibiotics, this study examines care practices and settings at rural health centers (RHCs) to inform interventions aimed at reducing inappropriate prescribing for upper respiratory tract infections and diarrheal diseases.

**Objective:** To understand the care settings and context at the RHCs for developing an antimicrobial stewardship intervention.

**Methods:** This study was conducted using a care-cascade framework. The mixed-methods design included: literature review; facility review (n=3); key informant interviews with healthcare providers (n=6) and patients (n=6); and focus group discussions with health managers (n=1), healthcare providers (n=2), patients (n=2), and patients with experience of using mobile healthcare applications (n=2). The data analyzed at each step informed the next step and was populated in the pre-defined care tasks considered as themes.

**Results and Discussion:** Using the care-cascade framework, four major care tasks were identified in URTI and diarrhea management at RHCs: (1) patient consultation and laboratory testing, (2) drug prescription, (3) drug dispensing, and (4) patient education and counselling. At the RHCs, no standard guidelines or diagnostic protocols were being followed, inadequate lab facilities, and very brief patient consultations. Antibiotic prescription was largely empirical, driven by doctors' clinical acumen and patient demands. Drug dispensing practices were inconsistent, involving dispensing partial courses without counselling. Patients were insufficiently counselled on disease management and antibiotic use. Stakeholders made context-specific recommendations for developing clinical protocols, patient counselling, and training both doctors and dispensers. They also informed the design and content of the digital tools for patient engagement.

**Conclusion:** This study highlights the complexity of antibiotic stewardship in rural health systems. Using a care-cascade framework, we identified key leverage points, emphasizing that stewardship must extend beyond clinical practice to become a health system priority.

## Biography

Shaheer Ellahi Khan is an Associate Professor at the Health Services Academy, Ministry of National Health Services Regulations & Coordination, Government of Pakistan. He holds a PhD in Medical Anthropology and has pursued advanced training in Postgraduate Research Skills & Positive Psychology from the University of Oxford, UK. He is also serving internationally as Adjunct Associate Professor at the Dalla Lana School of Public Health, University of Toronto, and as Guest Lecturer at the Nuffield Centre for International Health and Development, University of Leeds. At HSA, he leads as Program Coordinator for the BS in Public Health. His academic achievements include authorship of several books and numerous publications in national and international journals. Dr. Khan is a Member of the Faculty of Public Health (UK) through distinction at the Royal

Colleges of Physicians UK, and serves on the Editorial Board of PLOS ONE (Cambridge UK). He is also an Associate Fellow of the Higher Education Academy (UK), Affiliate Member of the Chartered Institute of Environmental Health (London), and Fellow of the Royal Anthropological Institute of Great Britain and Ireland. In addition to his academic contributions, Dr. Shaheer holds important national and international policy roles, including Technical Focal Person for Risk Communication and Community Engagement (RCCE) for the International Health Regulations (JEE 2023) and for the National Action Plan for Health Security (2024–2028). His leadership continues to advance public health education, health security, and research both in Pakistan and globally.

# FROM THE BREAST TO THE BRAIN: UNVEILING MICROBIAL SIGNATURES SHAPING CANCER AND NEURODEGENERATIVE DISEASE

**Mohamed El-Hadidi**
*The University of Birmingham Dubai, UAE*

## Abstract:

This talk is based on my recently published papers that explore the role of the microbiome in cancer and neurodegenerative disease through large-scale meta-analyses of breast and gut microbial communities.

The human microbiome is increasingly recognized as a key player in health and disease, extending its influence far beyond the gut. In this talk, I will present findings from two recent meta-analyses that reveal novel microbial signatures associated with triple-negative breast cancer (TNBC) and Parkinson's disease (PD), highlighting the microbiome's multifaceted role in disease progression.

Through the first comprehensive meta-analysis of the TNBC tissue microbiome, we identified a distinct microbial ecosystem enriched with butyrate-producing bacteria such as *Gemmiger formicilis* and *Anaerobutyricum soehngenii*, alongside the nitrogen-fixing *Azospirillum oryzae*. These species were linked to metabolic and inflammatory pathways that may contribute to TNBC aggressiveness and poor clinical outcomes.

In contrast, the PD meta-analysis consolidated over 1,000 fecal samples to uncover the enrichment of GABA-consuming and proinflammatory bacteria, notably *Evtepia gabavorous, Klebsiella variicola*, and *Streptococcus anginosus*. These species may influence neuroinflammation, α-synuclein aggregation, and neuronal excitability, underscoring the role of the gut–brain axis in neurodegeneration.

Together, these studies provide converging evidence that microbiome dysbiosis is a common thread linking cancer and neurodegenerative diseases, influencing cellular signaling, metabolism, and immune regulation. By integrating multi-cohort 16S rRNA data through standardized meta-analytic pipelines, our work lays the foundation for exploring microbiome-based biomarkers and therapeutic interventions across diverse disease contexts.

## Biography

Mohamed El-Hadidi is an accomplished bioinformatician and academic leader, currently serving as Associate Professor and Director of the Bioinformatics MSc Program at the Department of Cancer and Genomic Sciences, School of Medical Sciences, College of Medicine and Health, University of Birmingham Dubai. With over 16 years of experience in computational biology and bioinformatics, and more than six years in biotechnology, Dr. El-Hadidi brings a unique interdisciplinary perspective shaped by international academic training and impactful research. He earned his Ph.D. in Bioinformatics from the University of Tübingen in Germany, and holds dual MSc degrees; in Biotechnology from Instituto Superior Técnico (IST) in Portugal, and in Computational and Systems Biology from Aalto University in Finland. Before joining the University of Birmingham Dubai, Dr. El-Hadidi was an Assistant Professor and Head of the Bioinformatics Research Group at Nile University in Egypt. There, he played a pivotal role in launching both the Bioinformatics Postgraduate Diploma and the Biomedical Informatics Undergraduate Program, demonstrating a strong commitment to education and capacity-building in the region. His research focuses on applied bioinformatics, including multi-omics integration, microbiome data analysis, and host–microbiome interactions, applied across medical and environmental domains. As a previous key member of the Scientific Committee of the Egyptian Genome Project, he has contributed to national efforts in large-scale genomic analysis and the advancement of precision medicine. Beyond academia, Dr. El-Hadidi has collaborated with various companies as a bioinformatics consultant, bridging the gap between research and real-world application. His work is widely published in high-impact journals and international conferences, reinforcing his standing as a thought leader in the field. With a rare blend of academic leadership, technical expertise, and industry insight, Dr. El-Hadidi continues to drive innovation in bioinformatics and inspire the next generation of scientists

# INSIGHT OF THE RESISTANCE MECHANISM OF *H.PYLORI* TO CLARITHROMYCIN

**Imen Chihaoui**
*Hôpital la Rabta, Tunisia*

## Abstract:

Helicobacter pylori *(H. pylori)* infection is closely associated with various gastric diseases, particularly gastric cancer. Our study aimed to evaluate the contribution of qPCR in identifying of *H. pylori* and detecting the most common resistance mechanism involved.

This is a retrospective study conducted from July 2023 to Mai 2025, covering patients tested for *H.pylori* at Rabta Hospital in Tunisia. Bacterial identification was carried out using biochemical, morphological and molecular tools: urease test, Gram staining test, culture and qPCR (Allplex™ *H.pylori* and ClariR Assay). Three mutations type in 23S rRNA gene conferring resistance to clarithromycin were also detected.

We collected 48 Biopsy gastric samples from 42 patients. The sex ratio M/F was 0.85. All diagnostic tests were positive in only 4% of cases. Culture showed low sensitivity, and became positive for only two cases (4.2%) and qPCR being positive in 23 patients (48%). Urease and Gram staining were positive in 16% and 14.6% of cases, respectively. QPCR identified *H. pylori* in 16 additional patients, but in one sample, morphological and biochemical methods being positive but the PCR was not valid. Resistance to clarithromycin was detected in 5 patients and A2142G and A2143G mutations seems to be responsible for clarithromycin resistance in three (60%) and four patients (80%) respectively. Two mutations were simultaneously detected in two patients. Our study highlighted the implication of qPCR in the diagnosis of *H. pylori* from clinical samples and to survey clarithromycin sensitivity. Clarithromycin should be used with precaution in order to avoid the emergence of resistant strains.

## Biography

Imen Chihaoui actually she is a PhD student in biological sciences. She focused on understanding psoriasis pathophysiology and its link with metabolic and cardiovascular comorbidities, analyzing clinical and biological data with biomarkers of inflammation, angiogenesis and matrix remodeling. She is currently an adjunct Instructor at the Maghreb Institute of Economic and Technological Sciences, teaching Biochemistry courses, and a Medical Biology Technician at Rabta Hospital, specializing in microbiological analyses, particularly bacterial resistance mechanisms and antibiotic susceptibility testing. Her experience is complemented by internships across various medical laboratory specialties, including Clinical Pharmacology, Immunology, Hematology, Toxicology and Parasitology-Mycology.

# STRUCTURE-GUIDED DESIGN OF POTENT AND SELECTIVE COVALENT INHIBITORS OF SARS-COV-1 AND SARS-COV-2 PAPAIN-LIKE PROTEASES WITH ANTIVIRAL ACTIVITY

**Abdullah Ibrahim Al-Homoudi**
*Wayne State University School of Medicine, USA*

## Abstract:

The papain-like protease (PLpro), one of two essential cysteine proteases in human coronaviruses, is indispensable for viral polyprotein processing and immune evasion through deubiquitination and deIS-Gylation of host proteins. This dual role makes PLpro an attractive antiviral target, either as a monother-apy or in combination with other direct-acting antivirals. Guided by structural insights, we designed and synthesized covalent inhibitors that exploit two key binding elements: Glu167 in the α-cleft (Site I), which mediates recognition of ubiquitin and ISG15, and the BL2 hydrophobic groove, which stabilizes inhibitor binding and shapes selectivity. The optimized inhibitors exhibited potent enzymatic inhibition ($IC_{50}$ = 25-100 nM), strong protein stabilization ($\Delta T_m > 20°C$), and submicromolar antiviral activity in SARS-CoV-2–infected A549-ACE2 cells ($EC_{50}$ = 130-350 nM), with no measurable cytotoxicity ($CC_{50} > 10$ μM). Lead compounds 8 (GL-612), 67 (GL-508), and 10 (GL-637) efficiently inactivated PLpro, with GL-637 achieving a kinact/KI > 18,000 $M^{-1}$ $s^{-1}$, and demonstrated selectivity by sparing host deubiquitinases USP7 and USP14 at concentrations up to 30 μM. Docking and mechanistic analyses revealed that cyclic amine-substituted benzamides reinforced electrostatic interactions with Glu167, while the (S)-3-fluoropyrrolidin-1-methyl-phenylthiophene scaffold anchored the BL2 groove, disrupting recognition of ubiquitin and ISG15 substrates. This dual engagement strategy improved covalent efficiency, strength-ened binding affinity, and translated into superior antiviral potency compared with benchmark compound 4. Collectively, these findings identify GL-612, GL-508, and GL-637 as first-in-class covalent PLpro in-hibitors that uniquely combine Glu167 engagement with BL2 groove occupancy, providing a strong foundation for broad-spectrum coronavirus therapeutic against current and emerging coronaviruses.

## Biography

Abdullah Al-Homoudi is a Postdoctoral Research Fellow at Wayne State University in Detroit, Michigan, jointly affiliated with the Department of Biochemistry, Microbiology, and Immunology at the School of Medicine and the Department of Pharmaceutical Sciences at the Eugene Applebaum College of Pharmacy and Health Sciences. He specializes in structure-guided drug discovery for antiviral therapeutics, focusing on the rational design of small-molecule inhibitors targeting viral proteases. His work combines molecular biology, protein engineering, biochemical and biophysical assay development, X-ray crystallography, and computational chemistry, including molecular modeling and AI-driven hit-to-lead optimization. He has authored and co-authored multiple peer-reviewed publications, deposited crystal structures, presented at international conferences, and contributed to patent-pending discoveries in COVID-19 therapeutic development. Beyond antivirals, his research interests also include anticancer therapeutics and ubiquitin proteases. In addition to his academic work, Dr. Al-Homoudi has gained practical clinical experience through roles in clinical informatics and hospital diagnostics, where he improved documentation accuracy, supported physician decision-making, and trained interdisciplinary teams. He has mentored graduate students, fostered interdisciplinary collaborations, and received awards for excellence in research and clinical practice. He maintains a strong interest in bridging translational research with patient-centered healthcare solutions and advancing patient care by translating complex science into practical healthcare applications.

# GENETIC DIVERSITY OF TICK-BORNE ZOONOTIC PATHOGENS IN IXODID TICKS COLLECTED FROM SMALL RUMINANTS IN NORTHERN AND NORTH-WESTERN PAKISTAN

**Jehan Zeb**
*Higher Education Department Khyber Pakhtunkhwa, Pakistan*

## Abstract:

Mapping tick distribution and pathogens in unexplored areas sheds light on their importance in zoonotic and veterinary contexts. In this study, we performed a comprehensive investigation of the genetic diversity of tick and tick-borne pathogens (TBPs) detection infesting/infecting small ruminants across northern Pakistan. We collected 1,587 ixodid ticks from 600 goats and sheep, an overall tick infestation rate of 50.2%. Notably, gender-based infestation rates were higher in female goats and sheep compared to their male counterparts. Age-wise analysis showed that the tick infestation rate was higher in older animals. This study identified 11 ixodid tick species within three genera: *Hyalomma, Haemaphysalis*, and *Rhipicephalus*, which were taxonomically classified using *16S rRNA* and cytochrome oxidase I *(cox1)* molecular markers. Sequence analysis indicated that reported ticks are similar to ixodid species found across various Asian and African countries. Tick-borne pathogens were detected by amplifying *16S rRNA* and citrate synthase *(gltA)* for bacterial pathogens and 18S rRNA for apicomplexan parasites. The present study reported a diverse array of TBPs in ticks from the study area, with *Rickettsia massiliae* (24.5%) and *Theleria ovis* (16.4%) as the most prevalent bacterial and apicomplexan pathogens. Phylogenetically, detected TBPs shared evolutionary relatedness with identical TBPs from old and new world countries. These findings highlight the presence of zoonotic TBPs in ixodid ticks from Pakistan. In addition, it also provides a foundation for future epidemiological research on ticks and TBPs, emphasizing their relevance in both zoonotic and veterinary contexts.

Day 2

# Infectious Diseases & Microbiology

E-Poster Presentations

# PHYSIOPATHOLOGICAL ASPECTS OF SARS-COV-2 (COVID-19) INFECTION ON HEMORHEOLOGICAL AND INFLAMMATORY FUNCTIONS: ABOUT 140 CASES IN SENEGAL

**Aissatou SECK**
*Cheikh Anta Diop University, Senegal*

## Abstract:

**Background:** COVID-19 infection is a highly contagious viral disease caused by SARS-CoV-2. It is associated with cardiovascular risk with microvascular lesions, coagulopathy, and venous thromboembolism (VTE), the mechanisms of which remain to be elucidated.

**Objective:** To assess the effects of SARS-CoV-2 infection on inflammatory hemorheological functions.

**Methods:** This was a cross-sectional, descriptive and analytical study carried out over a period of 9 months (January to October 2021). It involved a population of 140 patients hospitalized at the CTE of Fann Hospital in Dakar. The diagnosis of COVID-19 was made on the basis of the positivity of the antigenic RDT or RT-PCR. The biological variables identified and studied were: Prothrombin (PT) level, activated partial thromboplastin time (APTT), D-dimer, platelets, procalcitonin, fibrinogen and Creactive protein (CRP).

**Results:** The evaluation of pro-inflammatory parameters and thrombotic risk factors (TRF) showed elevated CRP and procalcitonin levels (98.43%, 39.58%, respectively). Increased D-dimer (78.1%) and fibrinogen (94.96%), thrombocytopenia (20.71%), prolonged TCA (3.33%), low TP (12.15%). Among the TRFs associated with inflammatory abnormalities, we found a decrease in TP correlated with the increase in procalcitonin ($p=0.04$) and a probable association between the increase in D-Dimer and that of procalcitonin ($p=0.052$). The increase in D-Dimer was significantly linked to the occurrence of death ($p=0.017$). Overall, there is a link between acute inflammation (procalcitonin) and coagulation disorders (TP, D-Dimers). Severe hypoxemia (found in 79.28% of cases) being a risk factor for thromboembolic complications, contributes to strengthening this link.

**Conclusion:** There is a "thrombo-inflammatory cycle" maintained by hypoxemia. Thus, premature control of the "links in this vicious circle" would help prevent the occurrence of hemorheological and cardiocirculatory complications.

## Biography

Aissatou SECK is a Doctor of Medicine with a PhD of Physiology and Human Pathology and a Researcher Professor at the Laboratory of Physiology and Functional Explorations in the Faculty of Medicine, Pharmacy, and Odontostomatology (FMPO) at Cheikh Anta Diop University (UCAD) in Dakar/Senegal. Professor Aissatou SECK has expertise in the health field, particularly in improving the health of mothers and children and disadvantaged populations. With many years of experience in research, teaching, and healthcare delivery, both in hospitals and higher education institutions, her areas of expertise have led to conclusive results that open new perspectives for a better understanding of the mechanisms involved in the onset and complications of certain diseases. This approach allows for better prevention and management of these pathologies, leading to improved healthcare. • Research areas: - Physiology and Functional Explorations – Pathophysiology of Communicable Diseases - Pathophysiology of Metabolic Diseases - Biology of Physic Exercise.

Day 2

# Infectious Diseases
# &
# Microbiology

## Poster Presentations

# ANTIMICROBIAL RESISTANCE AMONG CLINICAL ISOLATES: A FOCUS ON MDR UROPATHOGENS.

**Dariga Zhazykhbayeva[1], Zhanar Kosherova[1], Yerlan Suleimenov[2], Alexey Balas[2], Talgat Nurgeldiyev[2] and Yuliya Semenova[1]**
*[1]Nazarbayev University, Kazakhstan*
*[2]OLYMP Clinical Diagnostic Laboratories, Kazakhstan*

## Abstract:

Antimicrobial resistance (AMR) is a major threat to global health, particularly in developing countries where data on AMR remain scarce and largely unreported. In Kazakhstan, a Central Asian country, the invisible AMR is placing a burden and additional strain on health care systems by complicating treatment, increasing health care costs, and prolonging illness and recovery times. Urinary tract infections are among the most common bacterial infections that require antimicrobial therapy. The emergence of multidrug urinary pathogens has complicated the treatment of these infections. Understanding local resistance patterns is essential for treatment outcomes and the further prevention of resistant organisms. The pilot study was conducted at a major tertiary care hospital in Astana. Our primary objectives in this preliminary study were to identify the most frequently submitted clinical specimens for microbiological culture, to evaluate the prevalence of pathogens isolated from urine, and to assess patterns of non-susceptibility and multidrug resistance.

Retrospective tertiary hospital data were downloaded from the microbiology laboratory system operated by the clinical diagnostic laboratory “Olymp”. All samples were submitted for conventional microbiology culture assessment. Bacterial identification was performed via MALDI-TOF. Antibiotic susceptibility testing (AST) was carried out using standardized methods including serial microdilution for MIC determination and disk diffusion methods on Mueller- Hinton agar medium. The breakpoint definitions of the AST results were interpreted according to EUCAST standards.

In total 1164 specimens were submitted. The most common biomaterial was urine (33.9%, n=395). This was followed by respiratory tract (17.5%, n=204) and blood specimens (16.7%, n=194). Other miscellaneous biomaterials and wound samples, each accounted for 16% of the total, with 186 and 185 correspondingly. The chi squared test revealed significant gender-based differences in specimen distribution ($\chi^2 = 42.58$, df = 5, $p < 0.0001$) [**Table 1**]. Urine and miscellaneous specimens (eye, ear, feces, bile, drainage from various sites) were more common among females, whereas males submitted more blood, respiratory tract, and wound samples.

Among the 395 urine specimens, 90 (22.8%) yielded positive cultures. Gram-negative bacteria were isolated in 78% (n=70). Gram-positive bacteria accounted for only one-fifth of the urinary tract pathogens [**Table 2**]. *E. coli* was the predominant isolate (40%, n=36), followed by *Kl. pneumoniae* (16.7%, n=15). *Enterococcus sp.* (17%, n=15) and Enterobacterales sp. (9%, n=8). AST results for urinary isolates showed high resistance rates among *Kl. pneumoniae* to ceftriaxone, cefuroxime, and ciprofloxacin (66.7% each), whereas half of *E. coli* (56%) exhibited resistance to cephalosporins [**Figure 1**]. Almost a third of *Kl. pneumoniae* exhibited resistance to carbapenems. The analysis revealed multidrug resistance rate among the primary gram-negative bacteria, with *E. coli* demonstrating 38.9% and *Kl. pneumoniae* showing 46.7% resistance to three or more antibiotic

classes.

This study demonstrates concerning levels of resistance among uropathogens isolated from clinical specimens. Of particular concern was the meropenem and multidrug resistance rate in *Kl. pneumoniae* isolates. The findings highlight the urgent need to strengthen AMR surveillance in Kazakhstan's health care system and to inform national antimicrobial stewardship policies. Further research is needed to comprehensively assess the current AMR situation in Kazakhstan, which would contribute valuable data to regional and global efforts to address AMR.

| **Specimens** | **Female** N=587 | **Male** N=577 | **Frequency (%)** N = 1164 |
|---|---|---|---|
| Blood | 74 (13%) | 120 (21%) | 194 (17%) |
| Urine | 215 (37%) | 180 (31%) | 395 (34%) |
| Respiratory tract specimens | 91 (16%) | 113 (20%) | 204 (18%) |
| Wound smear/exudate | 81 (14%) | 104 (18%) | 185 (16%) |
| Miscellaneous specimens | 126 (21%) | 60 (10%) | 186 (16%) |

$\chi^2 = 42.58$, df = 5, $p < 0.0001$

**Table 1**. Distribution of clinical specimens by gender in a tertiary hospital in Astana, Kazakstan

| **Microorganism types** | **Frequency (%)**<br>N = 90 |
|---|---|
| Gram-negative bacteria | 70 (78%) |
| Gram-positive bacteria | 19 (21%) |
| Yeast | 1 (1%) |
| | |
| **Isolates** | |
| *Acinetobacter baumannii* | 2 (2%) |
| *Candida albicans* | 1 (1%) |
| *Enterobacterales sp. (E.cloacae, Kl.oxytoca, Pr.mirabilis, S.marcescens)* | 15 (17%) |
| *Enterococcus sp (E.faecalis, E.faecium)* | 15 (17%) |
| *Escherichia coli* | 36 (40%) |
| *Klebsiella pneumoniae* | 15 (17%) |
| *Pseudomonas aeruginosa* | 9 (10%) |
| *Staphylococcus sp.(St. aureus, St.epidermidis)* | 3 (3%) |
| *Streptococcus agalactiae* | 1 (1%) |

**Table 2** Composition of microorganisms isolated from urine

| Antibiotics | *E.coli* | *Kl.pneumoni ae* | *Enterobacterales sp.* |
|---|---|---|---|
| Amoxicillin + Clavulanic 20 / 10 µg | 33% | 60% | 63% |
| Ceftriaxone | 56% | 67% | 25% |
| Cefuroxime | 56% | 67% | 63% |
| Ciprofloxacin | 39% | 67% | 25% |
| Gentamicin | 17% | 47% | 25% |
| Levofloxacin | 39% | 47% | 13% |
| Meropenem | 0% | 27% | 0% |
| Trimetoprim 1,25 µg + Sulfamethoxazole 23,75 µg | 44% | 40% | 25% |

**Figure 1** Antimicrobial resistance rates among urinary pathogens

# ANTIMICROBIAL STEWARDSHIP SYSTEMS IN POST-SOVIET COUNTRIES: A SYSTEMATIC REVIEW

**Zhanar Kosherova**
*Nazarbayev University, Kazakhstan*

## Abstract:

**Background:** Antimicrobial resistance (AMR) represents a critical global health threat requiring comprehensive surveillance and stewardship programs. Post-Soviet states face unique challenges in implementing antimicrobial stewardship (AMS) systems due to varying healthcare infrastructures and economic capacities. This is the first comprehensive assessment of AMS systems in post-Soviet states, establishing a crucial baseline for future monitoring and revealing that political commitment exists, but technical and financial capacity remain the primary barriers to effective implementation.

**Objective:** This systematic review evaluates the implementation status of antimicrobial AMS systems across 15 post-Soviet countries, analyzing their integration into national action plans, reporting to international networks, legislative frameworks, and optimisation of antimicrobial usage.

**Methods:** A comprehensive systematic review was conducted following PROSPERO registration (CRD42024626245). Data was gathered through systematic searches across multiple databases including PubMed, Google Scholar, Embase, CyberLeninka, and Scopus. Studies were selected based on specific inclusion criteria focusing on antimicrobial consumption monitoring and stewardship programs in human healthcare within the specified geographical areas and time periods. Additional documentation from official websites of both international and national health organizations was also incorporated into the literature review.

**Results:** Fourteen countries (93.3%) report antimicrobial consumption data to international networks, including the WHO AMC Network, GLASS, and ESAC-Net, with only Turkmenistan not participating. High-income countries (Estonia, Latvia, Lithuania) demonstrate the most comprehensive implementation, sharing data with both ESAC-Net and GLASS. The paradox of high international reporting rates despite low implementation capacity suggests countries may be prioritizing international compliance over domestic system strengthening, potentially indicating misaligned incentives in global health governance.

Upper-middle-income countries show varied implementation levels, while lower-middle-income countries face greater challenges. Only 40% of countries maintain foundational-level surveillance, with merely 20% achieving comprehensive monitoring systems.

## Biography

Zhanar holds a Master of Public Health degree from Nazarbayev University School of Medicine (2016–2018) and a Bachelor of Science in Biological Sciences from the same institution (2010–2015). She is now expanding her expertise as a PhD student in the Global Health program at Nazarbayev University, with a research focus on antibiotic consumption. From April 2021 to July 2023, Zhanar served as National Consultant on IPC and AMR at the WHO Country Office in Kazakhstan. In this role, she coordinated assessments, adapted WHO tools for local use, provided technical support, and played a key part in training and research at healthcare facilities. Her responsibilities also included reviewing institutional documents, organizing webinars, and advocacy at the national level. Previously, Zhanar contributed as a volunteer with the Regional Public Association Society of Infectious Diseases Physicians, helping with translation and research summaries (2017–2021). She was also an Expert in the Department of Science and Human Resources at the Ministry of Healthcare, where she aided in modernizing medical and nursing education (2015–2016).

# TOLERANCE AND DEGRADATION PROFILES OF MONOAROMATIC HYDROCARBONS IN PSEUDOMONAS AERUGINOSA STRAINS FROM OIL CONTAMINATED ENVIRONMENTS IN PERU

**Roger Alberto Palomino Huarcaya**
*Universidad Nacional Mayor De San Marcos, Peru*

**Abstract:**

**Background:** Monoromatic hydrocarbons such as benzene, toluene, ethylbenzene, and xylene (BTEX), are components of crude oil and refined petroleum products. They represent a serious environmental and public health risk due to their carcinogenicity and mutagenicity. Biotechnology has proven to be a cost-effective and highly efficient method to to remove these pollutants. Aerobic bacteria like *Pseudomonas, Bacillus, Acinetobacter*, and *Rhodococcus* have demonstrated degradative ability to eliminate these contaminants.

**Objective:** The objective was to evaluate tolerance and degradation abilities of *Pseudomonas aeruginosa* strains isolated from contaminated environments, through physiological and comparative genomics studies.

**Methods:** Sixty strains were grown in Bushnell Haas medium and mineral agar supplemented with 100 to 100 000 ppm of toluene, benzene, xylene, and ethylbenzene for tolerance assays. The degradative capacity was followed on 50 mL of Bushnell Haas medium by measuring the biomass at 620 nm. The comparative genomic were determined by gene topology and synteny for mla genes, this was performed a tblastx between the contigs of interest. For drawing we used the R package, genome. Oksana

**Results:** 27% of strains were tolerant to benzene, 41,66% to toluene, and 1,66% to xylene. The strains with the greatest tolerance were: benzene (PB25), toluene (IA3K2B), and xylene (IT5-B1). The strains with the greatest degradative capacity were IIT4B2 with 186,875 mg/L for benzene, IA3K2B with 2062.5 mg/L for toluene, and IT5-B1 with 10% for xylene. None of the strains exhibited tolerance or degradation ability to ethylbenzene. 6K-11 strain showed tolerance to toluene without degradative capacity. Comparative genomics for strains 6K-11, PB25, and 2K-1 determined the presence of mla genes responsible for tolerance, but not degradation genes.

**Conclusion:** The findings demonstrated differences between tolerant and degrading strains, reflecting variations both in physiological activity and structural genomics. It is necessary to study the genomic architecture to promote its application in environmental bioremediation processes.

## Biography

Roger Alberto Palomino Huarcaya, a graduate of the National University of San Marcos (UNMSM), holds a Master's degree in Molecular Biology. He has experience in the pharmaceutical and food industries, as well as laboratory management and performance audits, following good laboratory practices (GLP) and international regulations. He is a member of the Biotechnology for Bioremediation research group and a professor at the Microbiology and Microbial Biotechnology Laboratory (UNMSM). His main contribution to this line of research is related to the physiological and molecular characterization of microorganisms capable of degrading hydrocarbons. This research aims to develop the biotechnological tools necessary for the recovery of environments contaminated with these xenobiotic compounds

# PHAGOCYTE ACTIVITY IN RESPONSE TO SIGNIFICANT ANTIBIOTIC-RESISTANT BACTERIA

**Kolenchukova Oksana**
*Krasnoyarsk State Agrarian University, Russia*

## Abstract:

**Background:** The aim of the study was to determine the specific phagocytic activity of neutrophilic granulocytes when exposed to antibiotic-resistant and antibiotic-sensitive bacterial strains *Staphylococcus aureus, Pseudomonas aeruginosa and Klebsiella pneumoniae*

**Objective:** neutrophilic granulocytes of blood isolated from healthy people ($n=21$) and bacterial strains MRSA, MSSA, *P. aeruginosa* and *K.Pneumoniae* resistant and sensitive to antibiotics.

**Methods:** To detect MRSA, the Mueller-Hinton agar screening method containing 6.0 mg/ml of oxacillin was used. The determination of antibiotic resistance was carried out using the double disc method. The stained neutrophilic granulocytes were analyzed on an FC-500 flow cytofluorimeter in whole peripheral blood using FITC-labeled by bacteria. The phagocytic index (PhI) and phagocytic number (PhN) were determined. The reliability of differences between the indicators using the nonparametric Wilcoxon criterion.

**Results:** When studying the phagocytic activity of neutrophilic granulocytes in response to the effects of resistant and sensitive strains of *P. aeruginosa*, *S.aureus* and *K.pneumoniae* bacteria, a division into two subpopulations of cells with high and low light scattering rates was found. Thus, in response to MRSA, relative to MSSA, the PhI and PhN of actively phagocytizing cells are 6.2 and 7.6 times higher ($P<0.001$), respectively. At the same time, the PhI of weakly phagocytic cells is reduced by 1.7 times ($P<0.001$). In response to resistant strains of *K. Pneumoniae*, the PhI and PhN of actively phagocytizing neutrophilic granulocytes were 1.1-fold ($P<0.05$) and 1.6-fold ($P<0.05$) lower than those of sensitive phagocytic cells. There were no significant differences between the resistant and sensitive strains during induction by the bacterium *P. aeruginosa.*

**Conclusion:** Differences in the phagocytic response may be related to the features of the structure of bacteria, as a result of the acquisition of antibiotic resistance, the receptor apparatus changes due to modification of the cell wall.

## Biography

Oksana Aleksandrovna Kolenchukova, Doctor of Biological Sciences, Leading Researcher at the Scientific Research Institute of Medical Problems of the North, Federal Research Center KSC SB RAS, Head of the Department of Epizootology, Microbiology and Parasitology at Krasnoyarsk State Agrarian University, deals with the relationship between pathogen and macroorganism. Studies the immunological and microbiological foundations of such relationships in humans and animals. The field of research includes the state of the intestinal microbiome in various diseases. His research interests also include the study of the metabolic activity of bacteria and their virulent and persistent properties. Also antibiotic resistance. During his scientific work, 177 papers have been published, including 136 articles, materials from scientific conferences, monographs, patents and computer programs.

# ANTIBIOTIC RESISTANCE OF SIGNIFICANT INTESTINAL BACTERIA

**Kolenchukova Oksana**
*Krasnoyarsk State Agrarian University, Russia*

## Abstract:

**Background:** Determination of antibiotic resistance of significant microorganisms that are part of the intestinal microflora of cows.

**Objective:** Samples of fresh faeces of cows (n=40) from the Solyanskoe livestock farm were taken for bacteriological examination. Cattle were divided into 2 groups according to milk yield over 305 days of lactation into low-yielding (n=19) and high-yielding (n=20).

**Methods:** Samples were pre-diluted up to 10 times and the resulting 10-fold dilutions were seeded on Petri dishes with various selective, enriched and differential diagnostic media. Identification was performed on a mass spectrometer (MALDI-TOF Autof ms1000). Antibiotic resistance was determined as a result of disco-diffusion. The growth retardation zone on the ADAGIO apparatus was evaluated. Discs with tilmicosin; trimethoprim and salfamethoxazole; benzylpenicillin; tetracycline; azithromycin; ceftiofur; amoxicillin; florfenicol; ampicillin; tylosin; erythromycin; streptomycin, which are widely used in veterinary medicine, were used.

**Results:** Significant microorganisms in highly productive cows were *K.pneumoniae* (105 KOE/ml), *E. coli* Hly+ ($10^6$ KOE/ml), *P. mirabillis* ($10^5$ KOE/ml), *P. vulgaris* ($10^6$ KOE/ml), *S. saprophyticus* ($10^5$ KOE/ml). Significant microorganisms in low-yielding cows were *K.pneumoniae (*$10^6$ KOE/ml), *E. coli* ($10^5$ KOE/ml), *P. vulgaris* ($10^4$ KOE/ml), *S. saprophyticus* (103 KOE/ml). The study of the antibiotic resistance showed resistance of *K.pneumoniae* strains to tilmycosin, trimethoprim and salfamethoxazole and azithromycin and erythromycin. *E. coli* Hly+ strains were resistant to tilmycosin, trimethoprim and salfamethoxazole, benzylpenicillin, tylosin and erythromycin, and there were isolated cases of antibiotic resistance to tetracycline, azithromycin, ceftiofur and tylosin. *P. Mirabillis* and *P. Vulgaris* strains were resistant to tilmycosin, benzylpenicillin, tetracycline; azithromycin and erythromycin. There have been *P. Vulgaris* strains resistant to ceftiofur. *S.saprophyticus* strains showed resistance as trimethoprim and salfamethoxazole, benzylpenicillin, tetracycline, azithromycin, amoxicillin, ampicillin, and erythromycin.

**Conclusion:** The analysis of antibiotic resistance showed that significant microorganisms of intestinal microflora are the most resistant to antibiotics from the group of macrolides and beta-lactam antibiotics.

**Appreciation:** The research was carried out during a thematic task plan commissioned by the Ministry of Agriculture of the Russian Federation on the topic "Development of a procedure for diagnosing the state of the microbiota and measures to preserve or restore the normal microbiota of farm animals."

## Biography

Oksana Aleksandrovna Kolenchukova, Doctor of Biological Sciences, Leading Researcher at the Scientific Research Institute of Medical Problems of the North, Federal Research Center KSC SB RAS, Head of the Department of Epizootology, Microbiology and Parasitology at Krasnoyarsk State Agrarian University, deals with the relationship between pathogen and macroorganism. Studies the immunological and microbiological foundations of such relationships in humans and animals. The field of research includes the state of the intestinal microbiome in various diseases. His research interests also include the study of the metabolic activity of bacteria and their virulent and persistent properties. Also antibiotic resistance. During his scientific work, 177 papers have been published, including 136 articles, materials from scientific conferences, monographs, patents and computer programs.

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# EFFICACY OF ACTIVE IMMUNOPROPHYLAXIS WITH UROMUNE THERAPY FOR THE PREVENTION OF RECURRENT URINARY TRACT INFECTIONS IN MEN: A SINGLE CENTRE OBSERVATIONAL STUDY

**Matthew Pritchard**
*Royal Hobart Hospital, Australia*

## Abstract:

**Introduction:** Recurrent urinary tract infections are associated with significant morbidity for patients and place a huge burden on the healthcare system. Uromune is a polyvalent bacterial whole-cell-based sublingual vaccine used as an active immunoprophylaxis for patients suffering with recurrent urinary tract infections. It is equal percentages of selected strains of four bacterial species: *Escherichia coli, Klebsiella pneumoniae, Enterococcus faecalis and Proteus vulgaris*. Current literature regarding the efficacy of Uromune is largely focused on the female population with a lack of studies aimed at measuring the efficacy in men. This study aims to provide the first local Australian report on the efficacy of Uromune in males with recurrent urinary tract infections.

**Materials and Methods:** In this single centre, retrospective, observational study conducted in an Australian health setting we included male patients diagnosed with recurrent urinary tract infections and commenced on a three month course of Uromune therapy between August 2021 and December 2024. To analyse the efficacy of Uromune we recorded the rate of urinary tract infection recurrence through a positive urine culture in patients that completed the full course of therapy at 3, 6, 12 and 18 months follow up. The secondary outcomes were to identify predisposing comorbidities and which microorganisms were most frequently isolated on urine cultures.

**Results:** Forty eight patients (mean age of 57 years old) were included in the study. Two patients did not complete the course due to adverse side effects and six were lost to follow up. In the remaining cohort the urinary tract infection free rate was 62.5% (25/40) at 3 months, 50% (18/36) at 6 months, 46.2% (12/26) at 12 months and 34.6% (9/26) at 18 months. The most common microorganisms isolated in patients diagnosed with a recurrence after treatment were *Escherichia coli* (34.8%), *Klebsiella pneumoniae* (34.8%) and *Pseudomonas* (34.8%). Patients with a spinal cord injury had a 72.7% chance of a recurrence. Patients with a diagnosed bladder outlet obstruction (benign prostatic hyperplasia/urethral stricture) had a 40.9% chance of recurrence. All 5 of the patients with preexisting diabetes mellitus were diagnosed with a recurrence and one of the two patients immunosuppressed by medications had a recurrence.

**Conclusion:** Uromune therapy was associated with a good urinary tract infection free rate in all durations of follow up but particularly early on. Recurrence was often associated with an underlying predisposition, mostly spinal cord injury patients requiring intermittent self catheterisation or a suprapubic catheter. These findings support that Uromune therapy can be an effective option in managing recurrent urinary tract infections in men.

# MULTIPLE MYELOMA AND AIDS: A STATISTICAL STUDY AND THE RACIAL DISPARITIES

**Rachel Kim**
*Tenafly High School, USA*

## Abstract:

Multiple myeloma (MM) is an abnormality of plasma cells in the bone marrow, caused by several chromosomal translocations in chromosomes 13, 14, or 15. The etiology and risk factors are still unknown, but Black race is one of the risk factors accepted by clinical practitioners. While AIDS is also generally accepted as a risk factor, it is not yet an accepted factor. The data for incidence rates, mortality rates, and trend over time of myeloma was collected on the United States Cancer Statistics and its Data Visualizer database, and data for human immunodeficiency virus (HIV) and acquired immunodeficiency syndrome (AIDS) were collected from the Center for Disease Control National Center for HIV, Viral Hepatitis, STD, and Tuberculosis Prevention AtlasPlus. Graphs were made with the collected data, which inferred similar trends of MM incidence and AIDS incidence in the five racial categories: White, Black, American Indian/Native, Asian, and Hispanic. Such racial disparities are assumed to be caused by structural, socioeconomic, and cultural aspects of the Black communities, discouraging Black individuals from early screenings, diagnosis, and treatment of HIV/AIDS and even those of cancers, and the instilled racism, cultural mistrust, social obstacles, and limited access to healthcare/pre-exposure prophylaxis (PrEP) are the contributing factors to such community behaviors. Further studies and research on biomedical and genetic aspects are necessary, but current statistics suggest that there is an association between AIDS and multiple myeloma, intensifying the racial disparities among the diagnoses of the two conditions.

# EVALUATION OF FLAVONOID-RICH *CHRYSANTHEMUM INDICUM* EXTRACT REVEALS NO ZONE OF INHIBITION AGAINST *MALASSEZIA FURFUR* IN AN *IN VITRO* MODEL

**Rufei Ma**
*Guangdong Country Garden School, China*

## Abstract:

*Malassezia furfur* is a commensal, lipophilic yeast implicated in various dermatological conditions in humans and animals, including pityriasis versicolor and otitis. The emergence of resistance to conventional antifungals has spurred interest in alternative therapies, such as plant-derived extracts. This study investigated the in vitro efficacy of *Chrysanthemum indicum* extract, known for its flavonoid content, against *M. furfur* compared to ketoconazole. A disk diffusion assay was performed using plates inoculated with a suspension of *M. furfur* at $\sim 10^6$ CFU/mL. A 10:1 powdered *C. indicum* extract (standardized to >10% flavonoids) was dissolved in distilled water to create a 100 mg/mL stock solution (denoted as 100%), which was then serially diluted to 80%, 60%, 40%, and 20%. Sterile paper disks were impregnated with each concentration and placed on the agar alongside a ketoconazole control. After incubation at 32°C for 5 days, no zones of inhibition were observed for any concentration of the *C. indicum* extract. In contrast, ketoconazole produced a marked zone of inhibition. These results indicate that, under the tested conditions, *C. indicum* extract demonstrated no detectable antifungal activity against *M. furfur*, suggesting its constituents may not be effective against this specific yeast at the concentrations tested.

## Biography

Rufei Ma is a dedicated biologist with a passion for exploring innovative solutions in medical mycology. Her research focuses on evaluating natural compounds as potential alternatives to conventional antifungals. In a significant study, Ma investigated the *in vitro* efficacy of a flavonoid-rich *Chrysanthemum indicum* extract against the opportunistic yeast *Malassezia furfur*, a pathogen associated with various dermatological conditions. Utilizing a disk diffusion assay, Ma's work meticulously compared the extract to the standard antifungal ketoconazole. While the results demonstrated no detectable antifungal activity for the *C. indicum* extract at the tested concentrations, this rigorous null finding is a valuable contribution to the scientific community. It helps refine the search for effective plant-based therapies by highlighting the specificity of antifungal agents. Ma's commitment to evidence-based research underscores a deep desire to advance our understanding of infectious diseases and therapeutic development. Rufei Ma is young, dedicated biologists with an unwavering passion for advancing health and wellbeing. They form dynamic research to evaluate of Flavonoid-Rich Chrysanthemum indicum Extract Against *Malassezia furfur* in an *in vitro* Model. Through her collective, groundbreaking research, she has made significant contributions to *in vitro* efficacy of *Chrysanthemum indicum* extract, known for its flavonoid content, against M. furfur compared to ketoconazole. Her work has shed light on, these results indicate that, under the tested conditions, *C. indicum* extract demonstrated no detectable antifungal activity against *M. furfur*, suggesting its constituents may not be effective against this specific fungus at the concentrations tested. Her relentless pursuit of scientific discovery underscores a deep commitment to unraveling biological complexities and improving wellbeing at a fundamental level in infectious diseases.

# IDENTIFYING CRITICAL GAPS IN MEWS IMPLEMENTATION: A PAN-SITE AUDIT OF MODIFIED EARLY OBSTETRICS WARNING SYSTEM IN EMERGENCY DEPARTMENT

**Mahrukh Ehsan**
*Dudley Group NHS Foundation Trust, United Kingdom*

## Abstract:

This pan-site audit evaluated compliance with the Modified Early Obstetric Warning System (MEOWS) across two Emergency Departments (October-December 2024). Reviewing 60 obstetrics admissions (≥ 16 weeks gestation or ≤ 6 weeks postpartum), we found 50% MEOWS compliance (53.3% Peterborough City Hospital (PCH), 46.7% Hinchingbrooke Hospital (HH), falling short of the 100 % target. Staff reported paper MEOWS charts were easily misplaced during busy shifts, exacerbated by lack of Electronic Health Record (EHR) integration in Symphony. Delays were critical: 6/16 MEOWS at PCH completed>4 hours post-admission, while 3/14 at HH took>3.5 hours. Despite 100 % sepsis screening compliance when MEOWS was used,0% of the non-MEOWS cases received screening. Escalation failures were stark: 0% of red/yellow triggers at PCH prompted obstetric reviews (vs 100% at HH) and 40-50% of high-risk cases (suspected PE/SOB) lacked obstetric input despite meeting ED guideline 4.22 criteria. Recommendations included EHR-integrated MEOWS with real-time alerts, mandatory staff training on PE/DVT pathways and inclusion of<16 weeks pregnancies in MEOWS policies. These changes address systemic gaps highlighted by MBRRACE-identified risks, aiming to reduce maternal morbidity.

## Biography

Mahrukh Ehsan is a registrar in Obstetrics and Gynaecology at Peterborough City Hospital, with over three years of experience working in the NHS. She has a keen interest in improving patient safety and clinical outcomes, particularly in acute maternity care. This audit stemmed from her observations on the ground and a desire to strengthen early recognition of unwell women in Emergency Departments. She hopes the findings will contribute to more consistent use of MEOWS and better multidisciplinary collaboration across sites.

# INVESTIGATION OF FACTORS AFFECTING THE AEROSOL TRANSMISSION OF *MYCOBATERIUM TUBERCULOSIS*

**Mutlaq Al Shammri**
*Saudi Ministry of Health, Saudi Arabia*

## Abstract:

**Background:** Tuberculosis (TB) is the single greatest cause of death from any bacterial disease. Globally, more than one-quarter of the population harbour the agent of TB, *Mycobacterium tuberculosis* (Mtb) in their lungs, testament to its transmission success. Mtb transmits between individuals via aerosol droplets expelled from the respiratory system of those infected. Surprisingly, little is known of the properties of Mtb that promote of new infection. Understanding factors that impact Mtb entry into aerosol droplets, the physiological state of Mtb as it does so, and how it behaves and responds to changing physicochemical conditions therein following release (e.g. changes in temperature) might identify new opportunities to control TB.

**Objective of the Study:** To assess the survival pattern of *Mycobacterium tuberculosis* H37Rv in aerosols, and the pattern of H37Rv transcriptional changes on aerosolisation and survival stages during transmission.

**Materials and Methods:** Bacterial suspensions were prepared and nebulised using multi nebulisers for 5 min into a rotating drum. Aerosols samples were collected in distilled water (DW) or Guanidinium thiocyanate (GTC) at different time points over 2 hours for survival and transcriptional profile experiments, respectively. Survival of cells in aerosols was assessed and transcriptional changes samples were subject to RNA-sequencing analysis.

**Results:** Mtb H37Rv consistently showed>50% survival in aerosol for up to 2 hrs. Differentially expressed genes of Mtb H37Rv were detected at different stages during aerosolisation and due to the nebulisation process. However, no obvious transcriptional pattern of Mtb cells under the tested conditions was obtained. Investigation into the survival of Mtb and *M. bovis* BCG under different environmental conditions could provide better insight into the survival of these cells in aerosols.

**Conclusion:** While Mtb H37Rv showed the ability to survive in aerosols for at least 2 hrs, no obvious transcriptional pattern of tubercle bacillus under the tested conditions was obtained.

## Biography

Mutlaq Al Shammri is a consultant Medical Microbiologist and the head of the TB unit at King Salman Specialist Hospital in Hail. He completed his Ph.D. in Microbiology & immunity at the University of Leicester in the United Kingdom. Dr. Alshammri's main interest focuses on the transmission of tuberculosis area, where he spent his higher studies work experience. Dr. Alshammari also is a member of the tuberculosis development committee at the Saudi Ministry of Health.

# MOLECULAR MECHANISMS OF COLISTIN RESISTANCE AMONG MULTI-DRUG RESISTANT (MDR) *KLEBSIELLA PNEUMONIAE* AND *ESCHERICHIA COLI* ISOLATED FROM ICU PATIENTS AND THEIR SUSCEPTIBILITY TOWARDS ERAVACYCLINE

**Nouran Magdy**
*Dar Al Uloom University-college of Medicine, Saudi Arabia*

## Abstract:

The evolution of colistin-resistant strains is considered a great threat for patients admitted to intensive care unit (ICU). This study focused on screening the existence of mcr-1, mcr-2 and mutation in pmrA gene in *Klebsiella pneumoniae (K. pneumoniae)* and Escherichia coli *(E. coli)* isolates collected from patients admitted to ICU in Ain Shams University hospitals. Also, this study evaluated the susceptibility of colistin resistant microorganisms to eravacycline antibiotic.

**Methods:** Isolation and identification of *K. pneumonia* and *E. coli* were performed then antimicrobial susceptibility test and VITIC -2 compact system were used. Colistin susceptibility and minimum inhibitory concentrations were determined. The mcr-1, mcr-2 and pmrA genes were detected and then pmrA gene was sequenced. Eravacycline susceptibility against colistin resistant strains was determined via E-test.

**Results:** Colistin resistance appeared in 42.9% (36 out of 84) isolates. Mobilized colistin resistance (mcr-1) revealed in 94.4% (34 out of 36), Mcr-2 revealed in 27.8% (10 out of 36) and pmrA gene revealed in 61.1% (22 out of 36). Sequencing of pmrA gene in eight selected isolates revealed two-point mutation in all isolates. All colistin resistant strains showed sensitivity to eravacycline except two *K. pneumoniae isolates.*

**Conclusion:** This study revealed a high rate of mcr-1, mcr-2 and pmrA genes among MDR *K. pneumoniae* and *E. coli* isolated from ICU. Plasmid mediated mcr is a source of acquired resistance to colistin. So, there was a recommendation for broader surveillance of this resistance pattern. Eravacycline could be used for treatment of infections caused by colistin resistant *K. pneumonia* and *E. coli.*

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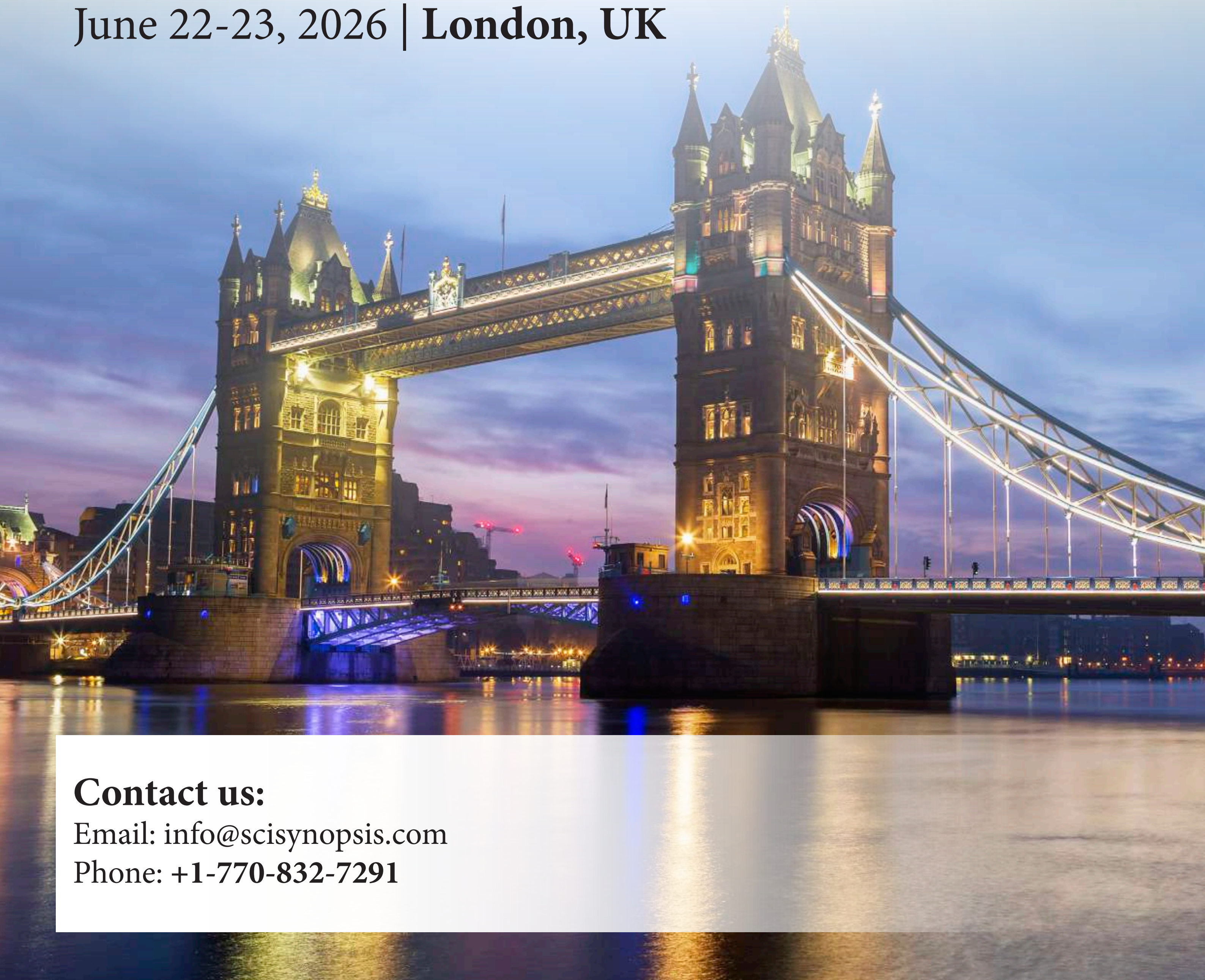

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