PEERS ALLEY
MEDIA

Virtual Meeting

4TH WORLD CONGRESS ON

INFECTIOUS DISEASES AND ANTIMICROBIAL RESISTANCE

2026

26
27
JUNE

Peers Alley Media
701 West Georgia Street
Suite 1500 Vancouver
V7Y 1C6, Canada
+1 (506) 909 0537

SCIENTIFIC PROGRAM

DAY 01
FRIDAY

JUNE 26, 2026

BST (British Summer Time)

07:55-08:00	**Opening Ceremony**

Topics: Infectious Diseases and Global Health | Infection Prevention and Control | Virology and HIV/AIDS | Immunology and Clinical Microbiology | Public Health and Epidemiology | Influenza | Zoonotic Diseases | Contagious Diseases | Next-Generation Antibiotics | Vaccines and Immunization | Ophthalmological Infectious Diseases | COVID-19 | Blood-Borne Diseases | Clinical Trials

Distinguished Speaker Talks

08:00-08:20	Title: Artificial Intelligence in the Workplace Insights from the Perspective of Disability Management with a Focus on Early Intervention and Occupational Rehabilitation **Anne Rosken,** *ANED-HSG-PCU, Germany*
08:20-08:40	Title: Diagnosis of Diabetes using Artificial Intelligence Programs **Ammar Mohammed Zakariya,** *Al-Iraqia University, Iraq*
08:40-09:00	Title: Beyond Medicine: The Architectural Responsibility for Public Health and Climate Change Mitigation **Mai Mohamed Barakat,** *New Giza University, Egypt*
09:00-09:20	Title: Impact of Influenza Vaccination on Mortality and Major Cardiovascular Events in Adults with Cardiovascular Disease: A Systematic Review and Meta-Analysis of Randomized Controlled Trials **Khaled Khormi,** *Prince Sultan Military Medical City, Saudi Arabia*
09:20-09:40	Title: Canine Leishmaniasis in Algeria: A Retrospective Study **Razika BOUKERT,** *Saad Dahlab University, Algeria*

09:40-10:00	Title: Targeting Vitamins B1, B3 and B5 Metabolism Reduces *Streptococcus pneumoniae* Virulence in a Murine Influenza Co-Infection Model **Sai Yan Pyay Aung,** *Nanyang Technological University, Singapore*
REFRESHMENT BREAK 10:00-10:20	
10:20-10:40	Title: Molecular Characterization of Methicillin Resistant *Staphylococcus aureus* in West Bank-Palestine **Kifaya Azmi,** *Al-Quds University, Palestine*
10:40-11:00	Title: Comparative Outcomes of Anterior-Posterior Versus Posterior-Only Approaches for Lumbosacral Chordoma: A Meta-Analysis of Recurrence, Survival and Complications **Ashkan Azizi,** *Tehran University of Medical Science, Iran*
11:00-11:20	Title: Efficacy of Who Recommendation for Continued Breast Feeding and Maternal Cart for Prevention of Perinatal and Postnatal HIV Transmission in Zambia **Mary Shilalukey Ngoma,** *University of Zambia, Zambia*
11:20-11:40	Title: ESBL and Carbapenemase Producing *Enterobacteriaceae* in Bangladesh: Evidence from a One Health Meta-Analysis **Md Bashir Uddin,** *Sylhet Agricultural University, Bangladesh*
11:40-12:00	Title: Positivity Rate of *Aspergillus* spp. in Patients with Tuberculosis-like Symptoms in Yaoundé, Cameroon and Antifungal Resistance Profile **Solange MEYIN A Ebong,** *University of Yaoundé & Pasteur Center of Cameroon de Yaoundé Cameroon, Cameroon*
12:00-12:20	Title: Epidemiological Pattern of Lassa Fever Contacts in A Southwestern State of Nigeria, 2023 to 2025 **Adewale Moses Adejugbagbe,** *University of Ibadan, Nigeria*

12:20-12:40	Title: *In-silico* Design, Synthesis of Some Novel Chromen Derivatives and Evaluation of their Inhibitory Effect against SARS-Cov-2 in 3CL Protease Enzyme **Kalirajan Rajagopal,** *JSS Academy of Higher Education & Research, India*
LUNCH BREAK 12:40-13:10	
13:10-13:30	Title: Retrospective on Ticks in Domestic and Wild Animals for Sustainable Ectoparasite Management in Togo **Eyabana Mollong,** *Université de Lomé, Togo*
13:30-13:50	Title: Compound Vulnerability: Mitigating Neighborhood Inequality, Environmental Disaster and Health Inequity among the Poor **Carol Camp Yeakey,** *The Marshall S. Snow Professor of Arts & Sciences, School of Arts & Sciences, Professor of Public Health, Bursky School of Public Health, Washington University in St. Louis, USA*
13:50-14:10	Title: Incidence and Burden of Myocarditis in the Middle East and North Africa: A Secondary Analysis of Global Burden of Diseases Study 2019 **Fatemeh Nozari,** *Tehran University of Medical Sciences, Iran*
14:10-14:30	Title: Professional Nurses' Experiences Regarding Antiretroviral Adherence by Incarcerated Individuals Living with HIV and AIDS in Correctional Services **Mapholisa Ntavhanyeni,** *Sefako Makgatho Health Sciences University, South Africa*
14:30-14:50	Title: Anti-Tuberculosis Drug Resistance in a Pulmonary Tuberculosis Referral Health Facility in Etinan, Akwa Ibom State, Nigeria **Anne Ebri Asuquo,** *University of Calabar, Nigeria*
REFRESHMENT BREAK 14:50-15:10	
15:10-15:30	Title: Effects of Dietary L-glutamate, L-aspartate, and their Combination on Growth Performance, Diarrhea Severity, Intestinal Integrity, and Nutrient Digestibility of Weaned Piglets Challenged with *Enterotoxigenic escherichia coli* **Supatirada Wongchanla,** *University of California, USA*

15:30-15:50	Title: Investigating Pandemic Polarization with Agent-Based Models **David Knoke,** *University of Minnesota, USA*
15:50-16:10	Title: Stochastic Modelling of Co-Infection Dynamics: An Analysis of Dual Disease Transmission in Individuals **Sunil Maity,** *National Institute of Technology Patna, India & Texas Biomedical Research Institute, USA*
16:10-16:30	Title: Hidden Pathways of Resistance: How Environmental Fungicides Undermine Clinical Antifungals **Daniel Assis Santos,** *Federal University of Minas Gerais (UFMG), Brazil*
16:30-16:50	Title: *Lactiplantibacillus* sp. LH01 as an Adjuvant to Reduce Antibiotic use in Recurrent Urinary Tract Infections **Jesús Alonso Amezcua López,** *Universidad de Guadalajara, Mexico*
16:50-17:00 (Poster)	Title: Microbial Signatures Associated with HPV Infection: Differential Genus-Level Abundance in Cervicovaginal Microbiota Revealed by 16S rRNA Sequencing Analysis **Soudabeh Sabetian,** *Shiraz University of Medical Sciences, Iran*
17:00-17:10 (Poster)	Title: Liquid Chromatography–Mass Spectrometry Profiling, Antioxidant and Allelopathic Activities of Leaf Extracts from *Eucalyptus torquata* and *Eucalyptus campaspe* **Ferjani Dhaouadi,** *Centre National des Sciences et Technologies Nucléaires (CNSTN), Tunisia*
17:10-17:30	Title: Antimicrobial Potential of Zno-Zns and Activated Carbon Composite **Marta Beatriz Mediavilla Quintero,** *Central University of Venezuela, Venezuela & Antioquia University, Colombia*

NETWORKING

END OF DAY 1

SCIENTIFIC PROGRAM

DAY 02

SATURDAY

JUNE 27, 2026

BST - British Summer Time

07:35-07:40	**Introduction**

Topics: Infectious Diseases and Global Health | Infection Prevention and Control | Virology and HIV/AIDS | Immunology and Clinical Microbiology | Public Health and Epidemiology | Influenza | Zoonotic Diseases | Contagious Diseases | Next-Generation Antibiotics | Vaccines and Immunization | Ophthalmological Infectious Diseases | COVID-19 | Blood-Borne Diseases | Clinical Trials and Case Studies | Antiviral Drug Resistance

Distinguished Speaker Talks

07:40-08:00	Title: From Debt to Development: Evaluating the Effects of External Debt, Political Instability, and Inflation on Economic Growth in The Democratic Republic of Congo **Amini Jephté Byamungu,** *Zhejiang University of Science and Technology, China*
08:00-08:20	Title: Unmasking Melioidosis - A Journey through Diverse Presentations **Vaishnavi R,** *SRM Medical College Hospital and Research Centre, India*
08:20-08:40	Title: Towards Real-Time Precision Agriculture: Evaluating ViT-Base/16 and ViT-Base/32 Variants for High-Accuracy Plant Pathology Detection **Sajja Ratan Kumar,** *Anil Neerukonda Institute of Technology & Sciences(ANITS), India*
08:40-09:00	Title: Biosynthesis of Silver Nanoparticles and their Applications as Next-Generation Antibiotics **G. Narasimha,** *Sri Venkateswara University, India*

09:00-09:20	Title: Impact of Network Sparsity on Graph Based Classification in Biological Systems: Insights from Resting State Functional Connectivity in Autism **Kiran Raj V,** *Indian Institute of Information Technology Tiruchirappalli, India*
09:20-09:40	Title: From Mathematical Modeling to Public Health Action: Data-Driven Analysis and Control of HIV–COVID-19 Syndemic Dynamics **Anupam Priyadarshi,** *Banaras Hindu University, India*
09:40-10:00	Title: AI-Driven Early Warning Systems for Childhood Diarrhea Outbreaks in India: A Prescriptive Modeling Approach **Monalisha Pattnaik,** *Sambalpur University, India*
REFRESHMENT BREAK 10:00-10:20	
10:20-10:40	Title: Nano Biosensors for Microbial Contaminants and their Impacts on Food Industry **Manas Kumar Dhal,** *University of Delhi, India*
10:40-11:00	Title: Intelligent AI-Driven Predictive Analytics for Real-Time Infectious Disease Surveillance and Early Outbreak Detection **Vimala Roselin J,** *Kristu Jayanti University, India*
11:00-11:20	Title: Deep Learning Techniques for Cervical Cancer Image Segmentation: Architectures, Challenges and Future Directions **S. Ravi,** *Pondicherry University, India*
11:20-11:40	Title: Therapeutic Activities of Transition Metal Complexes with a 3ES4PThiosemicarbazone Based Ligands **Kavita Sandip Gour,** *Priyadarshini Bhagwati College of Engineering, India*
11:40-11:50 (Poster)	Title: Breeding Habitat Distribution and Adult Insecticide Susceptibility of *Aedes* Mosquitoes in Selected NCR Districts of Delhi, India **Lalthazuali,** *Bhagwant University, India*

11:50-12:10	Title: Pandemics, Power and Prediction: What Colonial Bengal’s 1918 Influenza Pandemic Reveals about the Preparedness for Future Global Pandemics **Saumitra Basu,** *Indian National Science Academy(INSA), India*
12:10-12:30	Title: Multisource AI Diagnostics: Harmonizing Imaging and Omics for Improved Patient-Level Predictions **Rosy Sarmah,** *Tezpur University, India*
12:30-12:50	Title: Targeting Drug-Resistant Pathogens using *Daphne papyracea* Wall. ex G. Don: An *in vitro* Study of it’s Antimicrobial Potential **Priyanka Sharma,** *Himachal Pradesh University, India*
LUNCH BREAK 12:50-13:20	
13:20-13:40	Title: Clock and Clot: Impact of Processing Time on the Quality of Fresh Frozen Plasma – A Comparative Analysis of Coagulation Parameters **Shubhi Yadav,** *Balrampur Hospital, India*
13:40-14:00	Title: Design, *In silico* Targeting, and Characterization of Curcumin Prodrug Microspheres for Brain-Specific Delivery in Alzheimer’s Therapy **Shakuntala Santosh Chopade,** *Poona College of Pharmacy, India*
14:00-14:30	Title: Artificial Intelligence for Infectious Diseases Learning and Research: Microbiology Students’ Perceptions, Ethical Considerations and Challenges at the University of Port Harcourt **Sandra Eberechukwu Augustine & Comfort N. Owate,** *University of Port Harcourt, Nigeria*
14:30-14:50 Pre-Recording	Title: SIOOT Oxygen-Ozone Therapy against Multidrug Resistant Bacteria Perspectives and Future Remarks **Marianno Franzini,** *Scientific Society of Oxygen Ozone Therapy (SIOOT), Italy*

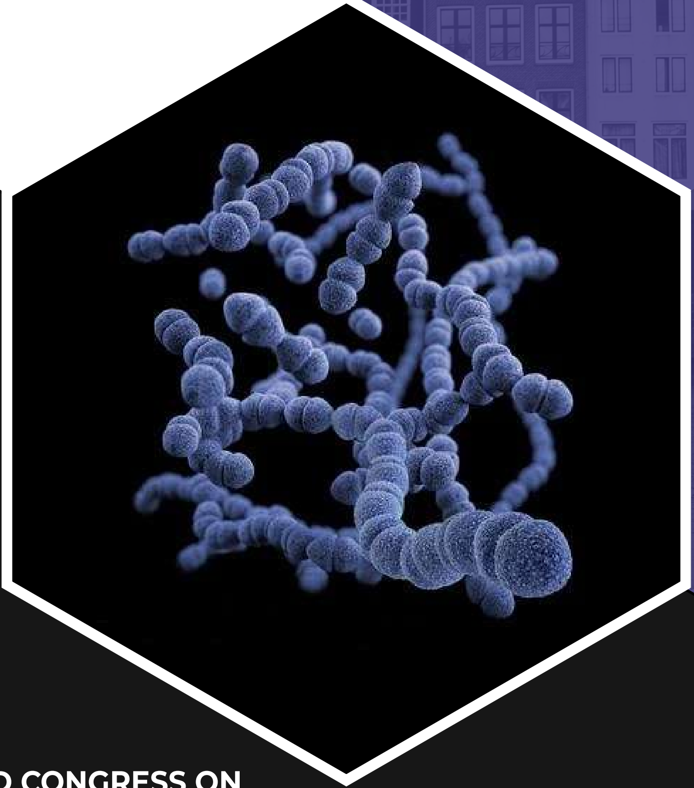
14:50-15:00 (Poster)	Title: Health and Safety Hazards and Associated Organisational and Social Support Factors for Deathcare Workers: A Global Scoping Review **Mary Aku Ogum,** *University of Cape Coast, Ghana*

NETWORKING

END OF DAY 2

PEERS ALLEY
MEDIA

DAY 01



4th WORLD CONGRESS ON

INFECTIOUS DISEASES AND ANTIMICROBIAL RESISTANCE

JUNE 26-27, 2026

SPEAKER TALKS

Artificial Intelligence in the Workplace Insights from the Perspective of Disability Management with a Focus on Early Intervention and Occupational Rehabilitation

Anne Rosken
ANED- HSG-PCU, Germany

Objectives and Focus of the Study: The objectives are to gain a clearer understanding of capabilities and options on the effectiveness of AI in Disability Management for disabled workers with a focus on early intervention and occupational rehabilitation.

Methodology: The starting point for the study comprised one overarching question about the dimensions of AI in the workplace. A structured document analyze and semi-structured expert interviews were used. The analyze strategy follows the principles of the method by Mayring.

Results of the Study: The results from the document analyze show a lot of difficulties and heterogeneous approaches by discussing and talking about AI solutions in the field of Disability Management in the workplace. There is no clear and homogen understanding what is best and what can/should be achieved in this context in present and in future. In this presentation the most important findings, the four main areas, will be presented and how to use AI in the workplace in a respectful way for people with and without disability.

Summary and Conclusion: In summary, it can be said that it is important to have intensive conversations and to carry out education across the entire area. In concrete terms, this means more exchange in each of the different areas and between them. A much more interdisciplinary approach is recommended so that the individual areas learn more from each other. Clear legal regulations with a flexible approach are crucial. This is immanent because AI and humans learn in an ongoing process. These developments should be incorporated into the design process. Legal regulations must respect this phenomenon and offer good opportunities to rework the paragraphs in line with the running learning approaches from theory and practice. In consequence, regulations must be flexibly adapted to these solutions.

Presenter:
Anne Rosken
ANED-HSG-PCU, Germany

Diagnosis of Diabetes using Artificial Intelligence Programs

Ammar Mohammed Zakariya[1] and **Huda Abbas Kanber**[2]
[1]Al-Iraqia University, Iraq
[2]University of Baghdad, Iraq

Scientific development has occupied a prominent place in the medical field, becoming an important part of diagnosing diseases and determining their levels with high accuracy, surpassing traditional methods that caused pain, contamination, and the possibility of error due to the nature of the devices used and the efficiency of the energy sources that operate them. In order to achieve high accuracy without errors, we adopted in this research a method based on an intelligent application through the use of one of the most important libraries of the Python program, which is the OpenCV library, which is based on image analysis. Here, we took two directions in this study.

The first direction is to prove that the person suffers from a disease condition, and the second is to identify the code for diabetes. Here, the study showed the validity of distinguishing between the person with diabetes, as the program identified three cases for us: the healthy ones, which represented 82% or higher, and the second for the sick, where the difference in the images showed less than the previous percentage of change, to 65%. These are the ones who suffer from diseases, and this was confirmed by the code that appeared parallel to the first test. Therefore, we were able to formulate an algorithm that would identify diabetes from the image.

Presenter:

Ammar Mohammed Zakariya
Al-Iraqia University, Iraq

Beyond Medicine: The Architectural Responsibility for Public Health and Climate Change Mitigation

Mai Barakat

Lecture Assistant, New Giza University, Egypt

Architecture carries a significant underestimated responsibility for human health and well-being one that extends beyond individual patients to entire communities. Architectural decisions directly influence the physical, psychological, and environmental conditions experienced by occupants. Choices related to finishing materials, ventilation, and spatial proportions can affect mental health, contribute to biological illnesses, and shape human behavior daily. Poor lighting, inadequate ventilation, and toxic or high-emission materials may lead to emotional instability, reduced productivity, chronic health problems, and broader environmental harm. This research therefore investigates how toxic finishing materials and insufficient ventilation impact occupants' mental and physical well-being. The study also explores sustainable development goals (SDGs), mainly goals 3, 11, 12, and 13 to maintain an efficient community and enhancement through air quality enhancement and Climate Change mitigation.

In the context of climate change, architectural responsibility becomes even more critical. Building materials and finishes contribute significantly to greenhouse gas emissions throughout their life cycle. Reducing harmful emissions particularly volatile organic compounds (VOCs), formaldehyde, and embodied carbon improves indoor environmental quality while also lowering a building's overall environmental footprint.

This research employs both quantitative and qualitative methodologies to evaluate architecture's influence on human well-being. The quantitative component examines and measures toxic or high-emission materials that may cause respiratory illnesses, physiological harm, or mood disorders through daily exposure. The qualitative component involves assessments and questionnaires directed to 7–13 individuals in a controlled workplace environment to evaluate how spatial design, materials, and comfort affect mental states, behavior, and overall health.

The expected findings aim to demonstrate that poorly designed or neglected architecture can become an inescapable, silent threat to human well-being. Ultimately, the responsibility borne by architects and interior designers may exceed that of physicians, as their decisions affect the collective mind and body of society while also influencing the planet's environmental future.

Presenter:
Mai Mohamed Barakat
New Giza University, Egypt

Impact of Influenza Vaccination on Mortality and Major Cardiovascular Events in Adults with Cardiovascular Disease: A Systematic Review and Meta-Analysis of Randomized Controlled Trials

Khaled Khormi[8], **Sitah Alotaibi**[1], **Mazen Bostaji**[2], **Anas Alharbi**[3], **Latifa Alaqeel**[4], **Ghaida Alsharif**[5], **Afaf Albalawi**[6], **Naif Aloufi**[7], **Wedad Almarhbi**[9], **Seham Abulkhair**[10], **Turki Alshaikh**[11] and **Abdullah Almaqhawi**[12]

[1]Faculty of Nursing, Princess Nourah Bint Abdulrahman University, Saudi Arabia
[2]Faculty of Medicine, Umm Al Qura University, Saudi Arabia
[3]Family Medicine Department, Ministry of National Guard Health Affairs, Saudi Arabia
[4]Faculty of Medicine, Imam Mohammad Ibn Saud Islamic University, Saudi Arabia
[5]Faculty of Medicine, University of Jeddah, Saudi Arabia
[6]Family Medicine Specialist, General Administration of Medical Services, Tabuk University, Saudi Arabia
[7]Faculty of Medicine, Qassim University, Saudi Arabia
[8]Prince Sultan Military Medical City, Saudi Arabia
[9]Faculty of Medicine, Umm Al Qura University, Saudi Arabia
[10]Microbiology, Faculty of Science, Jeddah University, Saudi Arabia
[11]King Abdullah Medical Complex, Saudi Arabia
[12]Department of Family and Community Medicine, College of Medicine, King Faisal University, Saudi Arabia

Cardiovascular disease (CVD) remains the leading global cause of morbidity and mortality, with acute cardiovascular events often triggered by infections such as influenza. Influenza vaccination has been proposed as a secondary preventive strategy in patients with established CVD; however, its impact on mortality and major cardiovascular outcomes remains uncertain.

This study aimed to evaluate the effectiveness of influenza vaccination in reducing mortality and major cardiovascular events in adults with established cardiovascular disease. A systematic review and meta-analysis of randomized controlled trials (RCTs) was conducted in accordance with PRISMA 2020 guidelines. Databases including PubMed, CENTRAL, and Google Scholar were systematically searched up to November 2025. Eligible studies included RCTs comparing influenza vaccination with placebo or standard care in adult patients with CVD. Data were pooled using a random-effects model to calculate odds ratios (ORs) with 95% confidence intervals (CIs).

Eight RCTs met the inclusion criteria. Influenza vaccination significantly reduced the composite outcome of all-cause mortality, myocardial infarction, and stent thrombosis (OR 0.71; 95% CI 0.57–0.90; p=0.004). A marked reduction in major adverse cardiovascular events (MACE) was also observed (OR 0.44; 95% CI 0.26–0.74; p=0.002). Cardiovascular mortality was significantly lower in the vaccinated group (OR 0.64; 95% CI 0.47–0.86; p=0.003). However, no statistically significant reduction was observed in all-cause mortality.

In conclusion, influenza vaccination demonstrates a significant cardioprotective effect in patients with established CVD, particularly in reducing cardiovascular events and mortality.

Presenter:
Khaled Khormi
Prince Sultan Military Medical City, Saudi Arabia

Canine Leishmaniasis in Algeria: A Retrospective Study

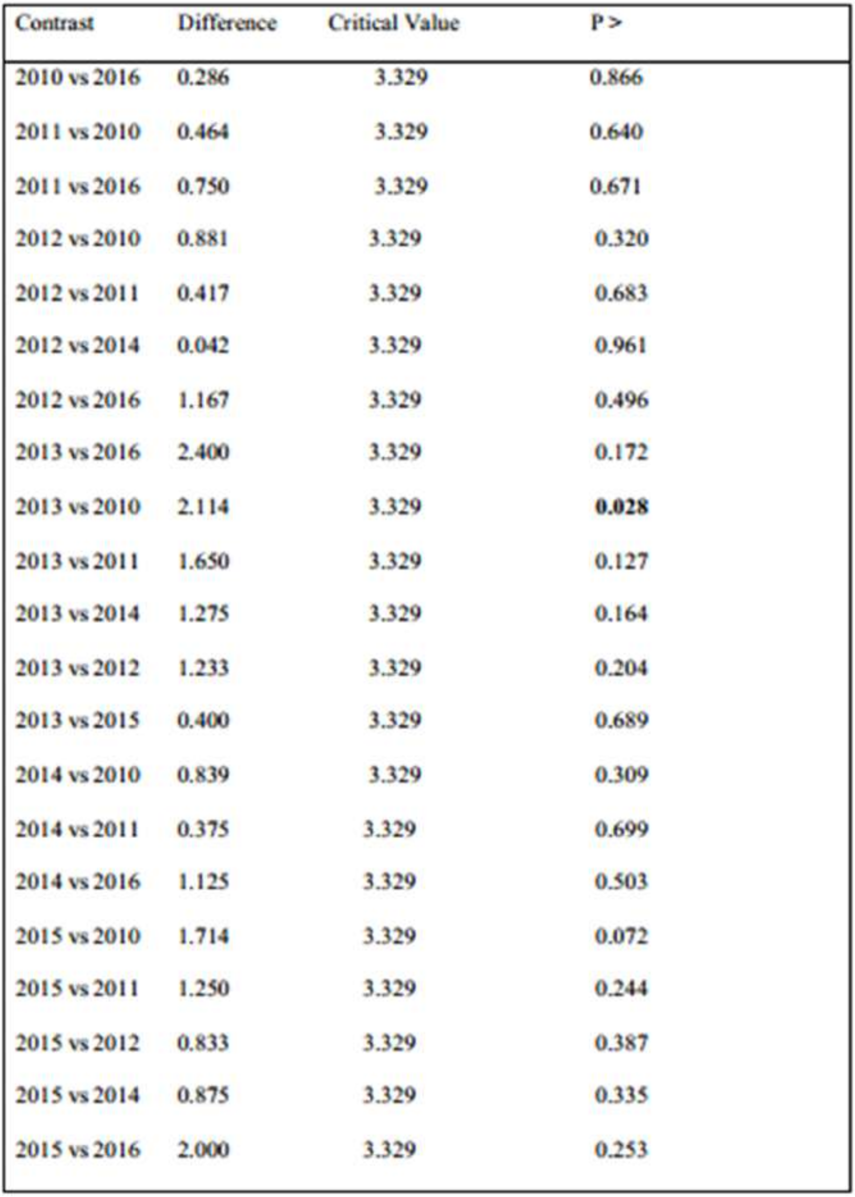
Razika Boukert[1], **Ali Bouali**[2], **Sara Boukert**[3], **Dalila Tarzaali**[1] and **Dahia Saidj**[1]

[1]Institute of Veterinary Sciences, Saad Dahlab University, Algeria
[2]High National Veterinary School, Algeria
[3]Department of Biology, University Saad Dahleb Blida1, Algeria

The main objectives of our study were to highlight the annual incidence of Canine Leishmaniasis (CanL) in Algeria. A retrospective study was conducted on CanL in Algeria between 2010-2019, by means of a questionnaire survey of thirty (30) canine veterinarians practising in the North central region, Algiers. The retrospective study showed seventy-eight (78) cases of Canine Leishmaniasis (2010 and 2019), with an average of 13.73 per year. The highest mean was observed in 2013:3.400, [1.517-5.283] 95%, with a significant difference (p=0.028). The cross-sectional survey showed that 44.4% of Canine Leishmaniasis cases are prevalent in spring and summer. Weight loss was the most frequent clinical sign 88.9% and skin sampling was the most used diagnostic test to confirm this disease 66.9%. Our study provides a general view of the situation of this disease; particularly the number of cases and their geographical distribution in Algeria .Canine leishmaniasis (CanL) is a serious zoonosis. Strict measures must be put in place. Abstract should give clear indication of the objectives, scope, results, methods used, and conclusion of your work.

Algeria is the country most affected by canine leishmaniasis, with an important reported prevalence (36%) by Medkour et al.[18] and cutaneous leishmaniasis with annual incidence ranging between 132,300 to 202,600 between 2004-2008 in human beings [19]. In this context, we conducted a retrospective study on canine leishmaniasis in order to determine the number cases of CanL and the incidence in Algeria in the period from 2010 to 2016. Add A total of seventy-eight (78) Canine Leishmaniasis cases were recorded between 2010-2016 from the veterinary service of the Ministry of Agriculture and Rural Development. The highest positive cases of CanL were recorded in the north of the country between 2010-2016, with Bejaia and Tizi-Ouzou (23 and 19 cases respectively) cities as the most affected, as shown in Figure 1. A significant average during the year 2013 (P=0.028) in Table1.

Table 1. Incidence of CanL cases in Algeria (2010-2016)



Contrast	Difference	Critical Value	P >
2010 vs 2016	0.286	3.329	0.866
2011 vs 2010	0.464	3.329	0.640
2011 vs 2016	0.750	3.329	0.671
2012 vs 2010	0.881	3.329	0.320
2012 vs 2011	0.417	3.329	0.683
2012 vs 2014	0.042	3.329	0.961
2012 vs 2016	1.167	3.329	0.496
2013 vs 2016	2.400	3.329	0.172
2013 vs 2010	2.114	3.329	**0.028**
2013 vs 2011	1.650	3.329	0.127
2013 vs 2014	1.275	3.329	0.164
2013 vs 2012	1.233	3.329	0.204
2013 vs 2015	0.400	3.329	0.689
2014 vs 2010	0.839	3.329	0.309
2014 vs 2011	0.375	3.329	0.699
2014 vs 2016	1.125	3.329	0.503
2015 vs 2010	1.714	3.329	0.072
2015 vs 2011	1.250	3.329	0.244
2015 vs 2012	0.833	3.329	0.387
2015 vs 2014	0.875	3.329	0.335
2015 vs 2016	2.000	3.329	0.253

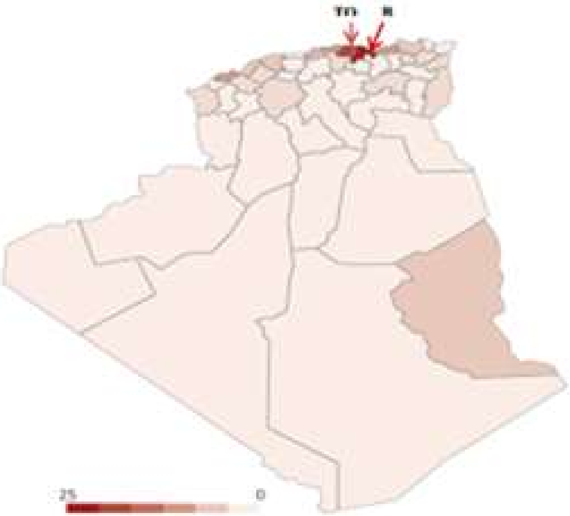


Figure1. Distribution of Canine Leishmaniasis in Algeria (2010-2016)

Presenter:
Razika BOUKERT
Saad Dahlab University, Algeria

Targeting Vitamins B1, B3 and B5 Metabolism Reduces *Streptococcus pneumoniae* Virulence in a Murine Influenza Co-Infection Model

Sai Yan Pyay Aung and **Kevin Pethe**
Lee Kong Chian School of Medicine, Nanyang Technological University, Singapore

Co-infection studies indicate that primary influenza infection promotes pneumococcal virulence by increasing capillary leakage of nutrients into the lower respiratory tract. This study investigates whether limiting the availability or uptake of auxotrophic B-vitamins can mitigate this nutrient-driven advantage and serve as a potential antimicrobial strategy. A two-pronged *in vivo* approach was used, combining inhibition of pneumococcal vitamin transporters with short-term dietary restriction of the corresponding host B-vitamins.

The well-characterised *Streptococcus pneumoniae* serotype 4 strain D39 was tested *in vitro* and in a murine influenza-pneumococcus co-infection model. A chemically defined minimal medium supporting robust pneumococcal growth was formulated, and auxotrophic requirements were determined using growth assays with single B-vitamin omissions, identifying vitamins B1, B3, and B5 as essential. Putative transporter genes were then deleted, mutants were confirmed by PCR, and dose-response growth curves across vitamin gradients were used to estimate half-maximal effective concentrations, allowing prioritisation of B1 and B5 transporter mutants for *in vivo* testing.

C57BL/6J mice were infected intranasally with influenza A virus and, 7 days later, challenged intratracheally with wild-type or mutant pneumococci, with selected groups receiving B-vitamin-restricted diets during the viral phase. Bacterial burdens in lung and blood were quantified 24 hours after bacterial challenge, and $\log_{10}$-transformed CFU were compared between groups.

B1 and B5 transporter deletion mutants showed reduced growth at low vitamin concentrations *in vitro* and lower pneumococcal burdens *in vivo* compared with wild-type. Short-term dietary depletion of vitamins B1, B3, and B5 similarly attenuated wild-type pneumococcal virulence in co-infected mice. In summary, genetic disruption of vitamin B1, B3, or B5 transport pathways increases dependence on exogenous vitamins and significantly reduces pneumococcal virulence *in vivo*. These findings highlight pneumococcal vitamin transporters and short-term modulation of host B-vitamin availability as complementary strategies that could inform the development of novel therapeutic and prophylactic approaches against pneumococcal infection.

Presenter:
Sai Yan Pyay Aung
Nanyang Technological University, Singapore

Molecular Characterization of Methicillin Resistant *Staphylococcus aureus* in West Bank-Palestine

Kifaya Azmi

Associated Professor of Molecular Biology Head, Department of Biochemistry and Molecular Biology, Medical school/ Al-Quds University, Abu Dis-Jerusalem, Palestine

Background: Methicillin-resistant *Staphylococcus aureus* (MRSA) is a public health threat and a major cause of hospital-acquired and community-acquired infections. This study aimed to investigate the genetic diversity of MRSA isolates from 2015 to 2017 and to characterize the major MRSA clones and antibiogram trends in Palestine.

Methodology: Isolates were obtained from 112 patients admitted to different hospitals of West Bank and East Jerusalem, originating from different clinical sources. Antibiotic susceptibility patterns, staphylococcal chromosomal cassette *mec* (SCC*mec*) typing and *Staphylococcus aureus* protein A (*spa*) typing were determined. Also, a panel of toxin genes was studied, including: Panton-Valentine Leukocidin (PVL), ACME-*arc*A, Toxic Shock Syndrome Toxin-1 (TSST-1) and Exfoliative Toxin A (ETA).

Results: Of the 112 confirmed MRSA isolates, 100% were resistant to all β-lactam antibiotics. Resistance rates to other non- β-lactam classes were as the following: 18.8% were resistant to trimethoprim-sulfamethoxazole, 23.2% were resistant to gentamicin, 34.8% to clindamycin, 39.3% to ciprofloxacin, and 63.4% to erythromycin. All MRSA isolates were susceptible to vancomycin (100%). Of all isolates, 32 isolates (28.6%) were multidrug- resistant (MDR). The majority of the isolates were identified as SCC*mec* type IV (86.6%). The molecular typing identified 29 *spa* types representing 12 MLST-clonal complexes (CC). The most prevalent *spa* types were: *spa* type t386 (CC1)/(12.5%), *spa* type t044 (CC80)/(10.7%), *spa* type t008 (CC8)/(10.7%) and *spa* type t223 (CC22)/(9.8%). PVL toxin gene was detected in (29.5%) of all isolates, while ACME-*arc*A gene was present in 18.8 % of all isolates and 23.2% had the TSST-1 gene. The two most common *spa* types among the TSST-1positive isolates were the *spa* type t223 (CC22)/ (Gaza clone) and the *spa* type t021 (CC30). All isolates with the *spa* type t991 were ETA positive (*5.4%*). USA-300 clone (*spa* type t008, positive for PVL toxin gene and ACME-*arcA* genes) was found in nine isolates (8.0%).

Conclusions: Our results provide insights into the epidemiology of MRSA strains in Palestine. We report a high diversity of MRSA strains among hospitals in Palestine, with frequent SCC*mec* type IV carriage. The four prominent clones detected were: t386-IV/ CC1, the European clone (t044/CC80), Gaza clone (t223/CC22) and the USA-300 clone (t008/CC8),

Presenter:

Kifaya Azmi
Al-Quds University, Palestine

Comparative Outcomes of Anterior-Posterior Versus Posterior-Only Approaches for Lumbosacral Chordoma: A Meta-Analysis of Recurrence, Survival and Complications

Ashkan Azizi[1], **Seyed Amir Asef Agah**[1,2], **Farbod Yousefi**[3], **Mohammad Mehdi Hosseini**[4], **Moein Ghasemi**[1], **Hossein Kaviani Charati**[5], **Arash Mansoori Nia**[5], **Mohammad Hadi Akbarizadeh Mashkani**[6], **Neda Azarpey**[7] and **Behnam Amini**[1]

[1]School of Medicine, Tehran University of Medical Science, Iran
[2]Advanced Diagnostic and Interventional Radiology Research Center, Tehran University of Medical Sciences, Iran
[3]Department of Orthopedic Surgery, Mayo Clinic, USA
[4]Department of Otolaryngology, Head and Neck Surgery and Research Center, Amiralmomenin Hospital, Guilan University of Medical Sciences, Iran
[5]Faculty of Medicine, Islamic Azad University, Iran
[6]School of Medicine, University of Social Welfare and Rehabilitation, Iran
[7]Department of Radiology, Shahid Beheshti University, Iran

Objectives: To systematically evaluate the oncologic and functional outcomes, including postoperative complications, of combined anterior–posterior (AP) versus posterior-only (P) surgical approaches for the management of lumbosacral chordomas.

Scope: This study focuses on comparative surgical strategies for lumbosacral chordomas, assessing resection margins, local recurrence, survival, and postoperative complication profiles.

Methods Used: A systematic review and meta-analysis was conducted according to PRISMA guidelines, searching PubMed, Embase, and Scopus through July 2025. Comparative studies reporting resection margins, local recurrence, survival, and complications were included. Data were pooled using random-effects models to calculate odds ratios (OR) and incidence rate ratios (IRR).

Results: Ten retrospective studies comprising 134 patients (71 AP, 63 P) were included. The AP cohort contained a significantly higher proportion of complex, high-level (S1–S2) tumors ($p = 0.008$). There were no statistically significant differences in 3-, 5-, or 10-year overall survival between approaches.

However, the AP approach was associated with significantly higher odds of local recurrence (OR 3.50, 95% CI 1.63–7.55; p = 0.001) and a trend toward higher rates of contaminated margins (p = 0.059). Additionally, the AP approach demonstrated a significantly higher risk of total postoperative complications (IRR 2.27, 95% CI 1.42–3.64), including wound-related complications.

Conclusion: Posterior-only resection is associated with lower local recurrence rates and a more favorable safety profile compared to combined approaches. However, the higher recurrence rate in the AP cohort is likely attributable to confounding by indication, as AP strategies were preferentially utilized for extensive high-sacral lesions. Despite disparate recurrence rates, long-term survival remains comparable, suggesting that surgical selection should be individualized based on tumor topography, the necessity for ventral release, and the goal of minimizing postoperative complications.

Fig. 6 Forest plot of the meta-analysis for total complications rate. Comparison of the combined AP approach versus the posterior-only approach. The plot displays the Incidence Rate Ratio (IRR) for total complications across included studies. Unlike specific complication subtypes, the pooled analysis (random effects model) demonstrates a statistically significant higher rate of total complications in the AP group compared to the P group (IRR 2.27; 95% CI [1.42, 3.64]), with low heterogeneity (I^2 = 28.7%)

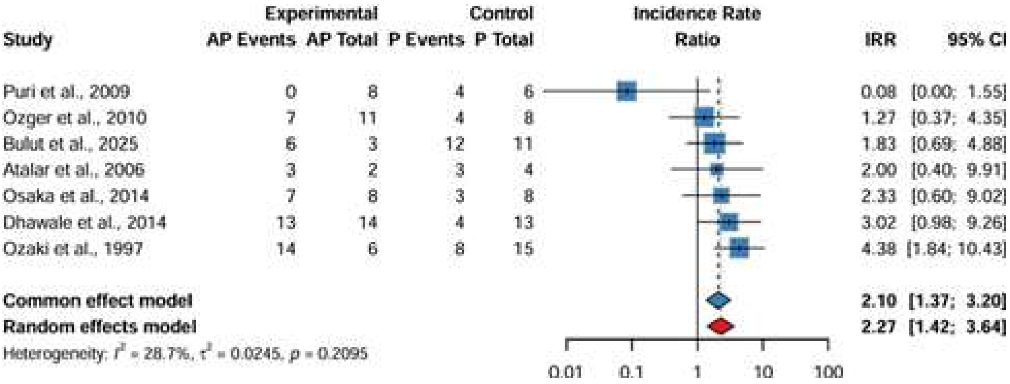
Table 4 Summary of meta-analysis for survival and recurrence outcomes (AP vs. P approach)

Outcome	No. of studies (k)	Pooled odds ratio (95% CI)	*p*-value	Heterogeneity (I^2)	Egger's test *p*-value
Overall Survival (OS)					
At 3 years	10	0.99 [0.42, 2.32]	0.979	18.0%	0.872
At 5 years	10	0.96 [0.40, 2.34]	0.935	18.0%	0.757
At 10 years	9	0.99 [0.34, 2.85]	0.986	0%	
At final follow-Up	10	1.22 [0.42, 3.55]	0.711	42.0%	0.905
Progression-free survival (PFS)					
At 3 years	7	0.77 [0.19, 3.11]	0.718	40.9%	Not available

At 5 years	8	1.11 [0.38, 3.26]	0.849	0%	Not available
At final follow-Up	9	0.70 [0.23, 2.15]	0.531	46.3%	Not available
Local recurrence					
At final follow-Up	10	3.50 [1.63, 7.55]	0.001	0%	0.362

This table shows the pooled results comparing the combined AP approach to the posterior-only approach, which is the reference group. An Odds Ratio (OR) > 1 suggests higher odds of the outcome with the AP approach. The only statistically significant finding is the increased odds of local recurrence with the AP approach

AP anterior-posterior, *CI* confidence interval, I^2 I-squared heterogeneity statistic, *k* number of studies, *OR* odds ratio, *OS* overall survival, *P* posterior, *PFS* progression-free survival



Presenter:

Ashkan Azizi

Tehran University of Medical Science, Iran

Efficacy of Who Recommendation for Continued Breast Feeding and Maternal cArt for Prevention of Perinatal and Postnatal HIV Transmission in Zambia

Mary Shilalukey Ngoma[1], **Amita Misir**[2] and **Michael Silverman**[3]

[1]Department of Paediatrics and Child Health
School of Medicine,University of Zambia, Zambia
[2]University of Toronto, Canada
[3]St Joseph Health Care, Canada

Introduction: The World Health Organization (WHO) guidelines recommend maternal combination antiretroviral therapy (cART) during pregnancy, throughout breastfeeding for 1 year and then cessation of breastfeeding to reduce transmission of HIV. We tested this.

Study site: Chelston, Lusaka, Zambia, 2008 to 2009

Objectives: to establish the Efficacy and safety of implementing the WHO recommendations for the reduction of Mother to Child Transmission of HIV and assess infant survival.

Scope: Studied 279 mothers and infants, demonstrating WHO recommendations in clinical practice in Zambia.

Methods: A prospective observational cohort study of 279 HIV-positive mothers, placed on zidovudine/3TC and lopinavir/ ritonavir tablets between 14 and 30 weeks gestation and continued indefinitely thereafter.

Women encouraged to exclusively breastfeed for six months, add complementary feed for the next six months and cease breastfeeding between 12 and 13 months.

Infants were followed for transmission to 18 months and for survival to 24 months.

Text message reminders, stipends , were provided to encourage adherence .

Results: Total MTCT was 9 of 219 live born infants (4.1%)

All breastfeeding transmissions (5/5) occurred after six months of age.

All mothers who transmitted after six months had a high six-month plasma viral load 1,000 copies/ml (p0.001).

Poor adherence to cART was associated with transmission (p 0.04).

Infant mortality was lower after six months of age (p 0.02).

The cumulative rate of infant HIV infection or death at 18 months was 29/226 (12.8%)

Age Categories 0-6 months	Age Categories 0-6 months	12 – 24 months
No transmission = safest period for the infant	Breast feeding transmission 5/5	29 /226 HIV infected or die
	Viral load mother >1000 copies P0.001	
	Poor adherence (p0.04)	
	Continued BF for lower IMR	

TOTAL = 9 of 219 Live births = 4.1, mother to child transmission (Below UNAIDS global target of 5%)

Breast feeding is mainstay for low income situation, no affordable alternate (2015)

MTCT lowest 0 -6 months, when EBF

Mother on cART reduces post partum transmission

Continuous BF props child survival

Conclusions: Maternal cART, good adherence and regular follow-up, may reduce MTCT to the UNAIDS target of 5%, supporting eradication of paediatric HIV. Continued breastfeeding prevents the rise in infant mortality after six months.

Presenter:
Mary Shilalukey Ngoma
School of Medicine, University of Zambia, Zambia

ESBL and Carbapenemase Producing *Enterobacteriaceae* in Bangladesh: Evidence from a One Health Meta-Analysis

Md. Bashir Uddin[2], **Md. Kaisar Rahman**[1], **Md. Shakil Mahmud Supto**[2], **Md. Rokibul Hasan Shanto**[2], **Shakil Ahmed**[3] and **Syed Sayeem Uddin Ahmed**[4,5]

[1]Zoonotic Disease Research Program, Institute of Epidemiology, Disease Control and Research (IEDCR), Bangladesh
[2]Department of Medicine, Sylhet Agricultural University, Bangladesh
[3]Department of Biology, University of Louisville, USA
[4]Department of Epidemiology and Public Health, Sylhet Agricultural University, Bangladesh
[5]Habiganj Agricultural University, Bangladesh

Antimicrobial resistance mediated by β-lactamase producing *Enterobacteriaceae* poses a major One Health threat in Bangladesh, where humans, animals, and the environment are closely interconnected. This systematic review and meta-analysis provides a comprehensive national-level synthesis of the prevalence, diversity, and distribution of β-lactamase genes across the One Health interface. Following PRISMA guidelines, 101 eligible studies published between 2011 and 2024 were included, comprising 46 human, 29 animal, 23 environmental, and 3 multidisciplinary investigations. Overall, 91 distinct β-lactamase genes were identified, demonstrating extensive genetic diversity and widespread dissemination. Extended-spectrum β-lactamase (ESBL) genes predominated across all sectors, with CTX-M type enzymes being the most prevalent. The pooled prevalence of ^{bla}CTX-M-15 among *Enterobacteriaceae* was 42.0% (95% CI: 26.1–59.8; $p < 0.0001$), with substantial heterogeneity ($I^2 = 94.5\%$). Environmental isolates exhibited the highest pooled prevalence (62.9%; 95% CI: 52.0–72.7; $p < 0.0001$), followed by human (47.8%; 95% CI: 25.6–70.9; $p < 0.0001$) and animal sources (12.9%; 95% CI: 2.2–49.1; $p < 0.0001$). In *Escherichia coli*, ^{bla}CTX-M-15 prevalence reached 59.3% (95% CI: 36.2–78.9; $p < 0.0001$), confirming its central role in resistance dissemination. The pooled prevalence of ^{bla}CTX-M-1 was 52.1% (95% CI: 29.3–74.0; $p < 0.0001$), while ^{bla}CTX-M-2 was comparatively low at 4.0% (95% CI: 2.5–6.4; $p = 0.183$) with moderate heterogeneity ($I^2 = 35.6\%$). Carbapenemase genes were widely detected, including ^{bla}NDM-1 (23.9%; 95% CI: 12.3–41.1; $p < 0.0001$), ^{bla}NDM-5 (21.3%; 95% CI: 6.2–52.4; $p < 0.0001$), and ^{bla}OXA-48 (15.0%; 95% CI: 5.5–34.5; $p < 0.0001$), predominantly in human and environmental isolates. Nine β-lactamase genes were shared across all One Health compartments, providing

strong evidence of cross-sector transmission. Collectively, these findings identify Bangladesh as a major reservoir of ESBL and carbapenemase genes and underscore the urgent need for integrated One Health surveillance, to curb further spread.

Presenter:
Md Bashir Uddin
Sylhet Agricultural University, Bangladesh

Positivity Rate of *Aspergillus* spp. in Patients with Tuberculosis-like Symptoms in Yaoundé, Cameroon and Antifungal Resistance Profile

Solange Meyin A Ebong[1,3], **Vigny Ndé Kengne**[1], **Moïse Ntah A Ayong**[2], **Loick Pradel Kojom Foko**[2,4], **Juliette Lauryn Nga Ambono**[1], **Ghislaine Metsina Ndzana**[1], **Mélanie Togonodji Baïdam**[1], **Oben Youguitcha**[2], **Olivier Ziem A Abah**[1,3], **Célestin Ayangma**[5] and **Francioli Koro Koro**[2]

[1]Department of Microbiology, Faculty of Science, University of Yaoundé, Cameroon
[2]Department of Biochemistry, Faculty of Science, University of Douala, Cameroon
[3]Department of Mycobacteriology, Pasteur Center of Cameroon de Yaoundé, Cameroon
[4]Center for Expertise and Research in Applied Biology (CEREBA), Cameroon
[5]Department of Bacteriology, Yaoundé No 1 Regional Military Hospital, Cameroon

Pulmonary aspergillosis represents a significant public health concern resulting from the proliferation of *Aspergillus* species within the respiratory tract. This infection is frequently underdiagnosed in comparison to tuberculosis during the management of pulmonary infections, especially among individuals living with HIV. The objective of this study was to determine the positivity rate of *Aspergillus* spp. from sputum and bronchoalveolar lavage (BAL) samples of patients presenting with tuberculosis-like symptoms at Jamot Hospital in Yaoundé, Cameroon, and to evaluate their antifungal resistance profiles. A total of 114 samples (104 sputum and 10 bronchoalveolar lavage) were collected for mycological analysis. Data were verified, coded, and analyzed using StatView v5.0 and GraphPad v8.0.2 for Windows. Pearson's chi-square test of independence and multivariate logistic regression models were used to compare percentages, with $p < 0.05$ considered statistically significant. *Aspergillus* spp were detected in 12.3% of samples, with two species identified. *Aspergillus niger* was predominant (57%0), followed by *Aspergillus flavus* (29%). A. *niger* isolates tested (5) exhibited resistance to polyenes, with 80% resistant to amphotericin B and 40% to nystatin, and 20% resistant to the azole fluconazole. All *A. niger* isolates were susceptible to econazole and clotrimazole. Among the five A. *flavus* isolates tested, all demonstrat-

ed resistance to amphotericin B and fluconazole, 60% to nystatin, and 20% to clotrimazole. *Aspergillus* spp. is present in the respiratory tract but often overlooked, and can lead to a misdiagnosis of tuberculosis. Although the very small number of isolates tested, *Aspergillus* spp. could be also affected to the antimicrobial resistance observed in recent years.

Presenter:

Solange MEYIN A Ebong
University of Yaoundé & Pasteur Center of Cameroon de Yaoundé ,Cameroon

Epidemiological Pattern of Lassa Fever Contacts in A Southwestern State of Nigeria, 2023 to 2025

Adewale Moses Adejugbagbe[1], **Ayokunle Oluwafiyifunmi Orimolade**[2], **Olawumi Feyisike Johnson**[2] and **Stephen Fagbemi**[2]

[1]Department of Epidemiology and Medical Statistics, University of Ibadan, Nigeria
[2]Department of Public Health, Ondo State Ministry of Health, Nigeria

Background: Lassa fever, a viral hemorrhagic fever, continues to pose a significant public health challenge, particularly in West African Countries, including Nigeria. Ondo State, Nigeria, ranked the highest most affected state in the country with 2,679 suspected, 355 confirmed cases, and 49 deaths (13.8% CFR) in 2025. Most Lassa fever cases are asymptomatic, and effective contact tracing and follow-up are essential to detect cases early and reduce disease severity. We explore the epidemiological pattern of Lassa fever contact follow-up during outbreak response in Ondo State, Nigeria, to fill knowledge gaps about the interventions.

Methods: A retrospective secondary data analysis of Lassa fever contacts was conducted. Data on contact follow-up were retrieved from a Google Excel spreadsheet from January 2023 to October 2025. Key variables assessed include: date of contact tracing, date of last contact with the confirmed case, location, age, gender, symptomatic status, and follow-up outcome. Descriptive and analytical analyses were conducted, and statistical significance was set at $p < 0.05$.

Results: A total of 1,780 records were retrieved for analysis (29% data were excluded due to missing variables). A high proportion (870; 48.9%) of the contacts were located in the Akure South district. Majority (1,103; 62%) were females and within the age group 26-35 years (Mean: 30.6±15.3). Slightly above half (963; 54.1%) were followed up within 1-7 days of contact with a confirmed case. Thirty-three (1.9%) had symptoms, and 1021 (57.4%) did not complete the 21-day follow-up, with completion rates declining from March to September 2025. Significantly, high odds of completing follow-up were found among the males (AOR: 1.3, 95% CI 1.04-1.56) and those within 15-21 days of exposure to a confirmed case.

Figure 1: Trend of Lassa fever contacts follow-up completion rate in Ondo State Nigeria (January 2023 - September 2025)

Table 1: Association between completion of follow-up and key variables among Lassa fever contacts in Ondo State, Nigeria

Variables	Contacts completed follow-up		Total	P-value	Unadjusted Odds ratio	AOR (95% CI)
	Yes n (%)	**No n (%)**				
Age in years						
*≤ 35 years	482 (42.5)	653 (57.5)	1135	0.881	1.02	
> 35 years	277 (42.9)	368 (57.1)	645			
Gender						
*Female	453 (41.1)	650 (58.9)	1103	0.087	1.18	1.3 (1.04- 1.56)
Male	306 (45.2)	371 (54.8)	677			
Day of contact with confirmed cases and commencement of follow-up						
*≤ 14 days	440 (34.4)	839 (65.6)	1279	< 0.001	3.34	3.4 (2.74-4.24)
15- 21 days	319 (63.7)	182 (36.3)	501			
Symptomatic						
Yes	18 (54.5)	15 (45.5)	33	0.163	1.63	1.8 (0.87-3.66)
*No	741 (42.4)	1006 (57.6)	1747			

Conclusion: We found low Lassa fever contact follow-up, particularly during the rainy (spring-summer) season and among those with less than 2 weeks of exposure. Interventions targeting timely follow-up and contact engagement in self-monitoring, using digital tools as a supplement to traditional tracing, are recommended to reduce disease transmission.

Presenter:

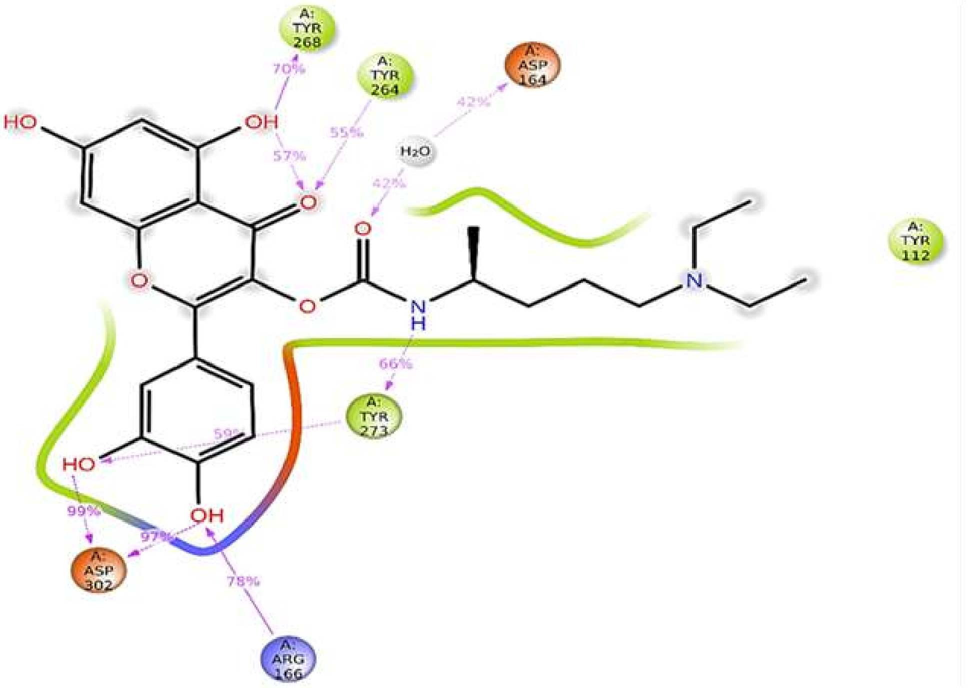
Adewale Moses Adejugbagbe
University of Ibadan, Nigeria

In-silico Design, Synthesis of Some Novel Chromen Derivatives and Evaluation of their Inhibitory Effect against SARS-Cov-2 in 3CL Protease Enzyme

Kalirajan Rajagopal and **Kannan R**

Department of Pharmaceutical Chemistry, JSS College of Pharmacy, JSS Academy of Higher Education & research, India

Since 2020, COVID-19 has created a major threat to human population across the globe. There are many mutations in SARS CoV-2 like Alpha, Beta, Delta and Omicron etc. A newly emerged SARS-CoV-2 variant B.1.1.529 has worried the health policy makers worldwide due to the presence of a large number of mutations in its genomic sequence, especially in the Mpro (Omicron) protein region. But still, we are not known about the effectiveness of vaccines and drugs against all the variants. In continuation of our research in SARS CoV-2, from the hits obtained from natural compounds by *in-silico* drug design, we have designed some novel Chromen derivatives by molecular hybridization approach. The final designed molecules were subjected to molecular docking studies by Glide module, MMGBSA binding free energy calculations by prime module and 100ns Molecular Dynamics simulation studies performed by Desmond module of Schrodinger suit-2021-4. The *in-silico* ADMET properties were predicted by using Qikprop tool which showed the favorable pharmacokinetic profile of the compounds. From the *in-silico* results, the significantly active molecules were synthesized and the final compounds are characterized by spectral studies. Finally *In-vitro* assay was carried out for all the derivatives and screened for their anti-SARS CoV-2 activity employing the 3CL Protease or Main Protease (Mpro) (B.1.1.529, Omicron Variant, P132H mutant) (SARS-CoV-2) assay Kit. The IC_{50} value of the test compounds were found between 45.28 μM and 203.5 μM compared to the standard inhibitor GC376 was 38.64 μM. The compounds K2 and Q2 shown significant activity against SARS-CoV-2 Omicron Variant.



Presenter:

Kalirajan Rajagopal

JSS Academy of Higher Education & Research, India

Retrospective on Ticks in Domestic and Wild Animals for Sustainable Ectoparasite Management in Togo

Eyabana Mollong[1], **Boris Dodji Kasseney**[1], **Akpéni Rabiétou Bawa**[1], **Marius Lébri**[2], **Carine Marie-Magdeleine**[3], **Soudah Boma**[4], **Michel Naves**[3], **Jean-Christophe Bambou**[3] and **Yaovi Nuto**[1]
[1]Département de Zoologie Animale, Université de Lomé,Togo
[2]Centre de Recherche en Écologie, Université Nangui Abrogoua,Côte d'Ivoire
[3]INRAE, Petit-Bourg, France
[4]Institut Togolais de Recherche Agronomique (ITRA), Togo

Managing ectoparasites such as flies, tsetse flies, and ticks presents a major challenge within the One Health approach, particularly in light of climate change in tropical regions, which is leading to the redistribution and colonization of new agro-ecological areas by ticks. This article aims to explore and highlight the different tick species found on domestic and wild animals sharing the same ecological zones in Togo, in order to establish integrated management strategies to combat the resurgence of zoonoses and resistance to synthetic chemical acaricides. Indeed, this small tropical West African country serves as a transhumance corridor for the sub-region and could be a reservoir for ticks and associated diseases. Updating this metadata will allow for better framing and guiding future research on the natural resistance of cattle to tick attacks and the pathogens transmitted by these vectors. In this context, the phenotypic and genotypic characterization of ticks and resistant cattle breeds is inseparable, as natural resistance can depend on several factors, such as parasite load, parasite diversity, and the wildlife that may harbor the parasites. Therefore, genomic selection is essential to understanding the polygenic nature of tick resistance by leveraging complementary genomic tools, such as Marker-Assisted Selection (MAS). The adoption and integration of MAS and genomic tools could facilitate the development of cattle breeds resistant to ticks and their vector-borne diseases, which would benefit tropical and temperate regions due to the expansion of these ectoparasites linked to climate change. For effective tick management, it is essential to consider the specific challenges of each region/country and to have access to accurate data, given that tropical countries possess a wealth of genetic resources that can contribute to the sustainable management of livestock ticks on a global scale, particularly through certain integrated approaches already in place.

Presenter:
Eyabana Mollong
Université de Lomé, Togo

Compound Vulnerability: Mitigating Neighborhood Inequality, Environmental Disaster and Health Inequity among the Poor

Carol Camp Yeakey[1,2], **Allison S. Reed**[3] and **Bronwyn Nichols-Lodato**[3]

[1]The Marshall S. Snow Professor of Arts & Sciences, School of Arts & Sciences, USA
Professor of Public Health, Bursky School of Public Health, Washington University in St. Louis, USA
[2]School of Arts & Sciences, Washington University in St. Louis, USA

Mitigating disasters' health consequences is critical to promoting health equity, but few studies have analyzed the short- and long-term health effects of disasters on vulnerable marginalized populations. This study attempts to fill that void by examining low income, predominantly Black residents who experienced the recent devastating tornado in St. Louis, Missouri. The study goes beyond describing the destruction of the tornado to focus upon the yet unresolved human toll and impact on the health and well-being of the vulnerable population. This research is multi-purposive. First, it provides a case study analysis of the destructive results of the May 16, 2025, tornado in the city of St. Louis, in general, and the neighborhood of north St. Louis, in particular (Carmody MacDonald 2025; Kaur & Felton 2025). Three research questions emerge. First, after the storm, what has been governments' response on federal, state and local levels to the most vulnerable citizens in St. Louis, specifically on rebuilding poor neighborhoods of color? Second, given the fact that 'housing is health,' what are the multiple dimensions of housing insecurity that are exacerbated and remain unresolved, six months after the storm? Third, what anticipatory stressors and somatic anxieties have surfaced among the affected population (Jackson and Willias 2024)? Research has shown that anticipatory stress can have profound effects on both physical and mental well-being (Raker, et.al. 2020). A preliminary study of the north St. Louis neighborhood shows a predisposition to dis-ease as well as disease, as well as a reduced life span due to socioeconomic variables. Utilizing case study analysis, interviews, survey research, policy research analysis, and photovoice to analyze data, initial findings reveal blatant racial and class disparity in funding disaster response; marked anticipatory anxiety among residents; no therapeutic services provided residents suffering disaster relief; and governmental shift of all disaster response and financial responsibilities away from the federal government to states and locales themselves. A dis-

cussion of the foregoing, and their intended and unintended consequences, conclude this presentation, with particular emphasis on the social determinants of health and wellbeing among marginalized populations in America, given growing climate crises.

Presenter:
Carol Camp Yeakey
School of Arts & Sciences and Bursky School of Public Health, Washington University in St. Louis, USA

Incidence and Burden of Myocarditis in the Middle East and North Africa: A Secondary Analysis of Global Burden of Diseases Study 2019

Fateme Nozari[2], **Parvaneh Hamian Roumiani**[1] and **Mohammad Yaghoubi**[1]

[1]Cardiology Department, Azerbaijan Medical University, Azerbaijan
[2]Cardiology Department, Tehran University of Medical Sciences, Iran

Background Myocarditis poses significant challenges in diagnosis and management due to its diverse etiology and clinical manifestations. Despite advances in medical care, myocarditis remains a leading cause of heart failure and sudden cardiac death worldwide, necessitating comprehensive understanding of its regional burden. This study aims to assess the incidence and burden of myocarditis in the Middle East and North Africa (MENA) region. Methods Data were obtained from the Global Burden of Diseases Study 2019, utilizing standardized disease criteria and statistics collected by the Institute of Health Metrics and Evaluation (IHME). Global, regional, and national estimates of myocarditis mortality, incidence, and disability-adjusted life years (DALYs) were gathered for the period from 1990 to 2019. The Socio-demographic Index (SDI) was utilized as a measure of national development. Results The findings indicate a minor change in the age-standardized incidence rate (ASIR) of myocarditis over the three decades, while a notable decrease was observed in both the age-standardized mortality rate (ASMR) and agestandardized disability-adjusted rate (ASDR). Females exhibited higher ASMR and ASDR compared to males, despite similar ASIR trends. Country-level variations in myocarditis incidence were observed, with some nations experiencing increased rates, while others witnessed declines. Oman, Iraq, and Egypt had the highest ASMRs, whereas Bahrain, Jordan, and Turkey had the lowest. Conclusion This study underscores the need for targeted interventions to mitigate the burden of myocarditis in the MENA region. The observed disparities in incidence and mortality rates highlight the complex interplay between socio-demographic factors and disease outcomes, emphasizing the importance of comprehensive public health

Presenter:

Fatemeh Nozari
Tehran University of Medical Sciences, Iran

Professional Nurses' Experiences Regarding Antiretroviral Adherence by Incarcerated Individuals Living with HIV and AIDS in Correctional Services

Mapholisa Ntavhaneni[1], **Madumo M.M**[2], **Mudau T.S**[3] and **Mabunda N.F**[1]

[1]Nursing Science Department, School of Health Care Sciences, Sefako Makgatho Health Sciences University, South Africa
[2]Department of Development Studies, College of Human Sciences, University of South Africa
[3]Nursing Department, School of Nursing, University of Kwa-Zulu Natal, South Africa

Background: Antiretroviral adherence for offenders living with HIV/AIDS in the correctional service facilities remains a challenge. The text highlights challenge in ensuring consistent antiretroviral medication adherence among offenders with HIV/AIDS in correctional facilities. This study aims to explore and describe the Professional nurses' Experiences Regarding Antiretroviral Adherence by Incarcerated Individuals Living with HIV and AIDS in Correctional Services, Limpopo Province South Africa. Method: A qualitative, exploratory, descriptive, and contextual approach was used. The setting was the Department of Correctional Services Management Areas A and B facilities in Vhembe District. The population was professional nurses working in correctional healthcare facilities who were selected using a purposive sampling method. Data was collected through semi-structured telephone interviews. Interviews were audio-recorded and transcribed verbatim. The thematic analysis method was used to analyse data. Results: Three themes and subthemes emerged. (1) professional nurses' experiences regarding offenders from foreign countries; (2) manipulative behaviors, and (3) misuse of antiretroviral therapy (ART) medication by offenders. Conclusion: Understanding professional nurses' adherence experiences for offenders in the correctional setting is essential to achieve adequate patient outcomes and to save lives. The study highlights the need for specific intervention regarding antiretroviral adherence, enhancing health-related quality of life for offenders in prisons. The researcher is committed to peruse her academic journey in any tertiary institution when opportunity arises.

Table1, Results: Themes and sub-themes

Themes	Subthemes
1. Professional nurses' experience regarding incarcerated individuals from foreign countries	1.1 Lack of policies addressing the needs of foreign nationals.
	1.2. Staff unpreparedness
2. Professional nurses' experiences of incarcerated individuals' manipulative behaviors	2.1 System manipulation for personal gain.
	2.2 Exploiting legal procedures.
	2.3 Misuse of grievance system
3. Professional nurses' experiences of misuse of medication by incarcerated individuals.	3.1. Faking a medical condition
	3.2. Misuse of Prescribed Medication
	3.3. Demanding Unnecessary transfers

Presenter:

Mapholisa Ntavhanyeni

Sefako Makgatho Health Sciences University, South Africa

Anti-Tuberculosis Drug Resistance in a Pulmonary Tuberculosis Referral Health Facility in Etinan, Akwa Ibom State, Nigeria

Anne E. Asuquo[1], **Ibokette David Micheal**[1], **Anietie Moses**[2], **Benjamin Pokam Thumamo**[3] and **Aniekan A. Eyo**[1]

[1]University of Calabar, Nigeria
[2]University of Uyo, Nigeria
[3]University of Buea, Cameroon

This study investigated the prevalence of Tuberculosis, drug-resistant TB and associated resistance genes among pulmonary tuberculosis (PTB) patients at a referral facility in Etinan, Nigeria. The 12-month cross-sectional study enrolled 220 presumptive PTB patients. Sputum samples were evaluated using GeneXpert assays (MTB/RIF and MTB/XDR) for simultaneous TB detection and resistance profiling. Molecular characterization of resistance genes (*katG, inhA*, *embB*, and *gyrA*) was performed using Polymerase Chain Reaction (PCR) and phylogenetic sequencing. Data were analyzed using SPSS version 29. This study found a 18.6% prevalence of PTB, significantly higher infection rates in males (30.5%; $p < 0.001$) especially those within the 31–40 age group (27.8%; $p = 0.02$). Socioeconomic factors of the patients were significantly associated with both education level ($p < 0.001$) and income ($p = 0.005$) while HIV seropositivity was significantly associated with PTB ($p < 0.001$). The drug resistance profiles varied with the assays: Rifampicin Resistance (RR-TB): 3.2% ($n = 7$) using MTB/RIF assay. The MTBB/XDR assay identified 5 Isoniazid Resistance while PCR analysis of the seven resistant isolates identified four specific resistance genes: *embB*: 85.7% ($n = 6$), *katG*: 71.4% ($n = 5$), *gyrA*: 42.9% ($n = 3$) and *inhA* : 28.6% ($n = 2$). The prevalence of Multi-Drug Resistant TB (MDR-TB) was 12.2%, polyresistant-TB (71.4%), MDR-TB (28.6%), and Pre-XDR-TB (28.6%). The isolates are closely related to known M. *tuberculosis* strains, including H37Rv, NO157, 5521, and 02-R1179. The 18.6% prevalence of PTB and various categories of drug resistance and their genes in the study population represent a significant TB burden. Routine integration of both GeneXpert MTB/RIF and MTB/XDR assays into clinical practice is vital for rapid diagnosis and robust drug stewardship to curb the transmission of resistant TB in Akwa Ibom State.

Presenter:

Anne Ebri Asuquo
University of Calabar, Nigeria

Effects of Dietary L-glutamate, L-aspartate, and their Combination on Growth Performance, Diarrhea Severity, Intestinal Integrity, and Nutrient Digestibility of Weaned Piglets Challenged with *Enterotoxigenic echerichia coli*

Supatirada Wongchanla, Youngmin Park, Sangwoo Park, Shuhan Sun and **Yanhong Liu**
University of California, USA

L-glutamate (Glu) and L-aspartate (Asp) are functional amino acids that support intestinal health and resilience. This study evaluated the effects of dietary Glu, Asp, or their combination on growth performance, diarrhea incidence, intestinal integrity, and nutrient digestibility in weaned pigs challenged with F18 enterotoxigenic *Escherichia coli* (ETEC). Pigs were assigned to five dietary treatments: control, 1% Glu (GLU), 1% Asp (ASP), a Glu + Asp combination (GAC), and an antibiotic control. ASP and GAC increased ($P < 0.05$) body weight gain on d 21 post-infection (PI), with ASP-fed pigs exhibiting the greatest ($P < 0.05$) body weight on d 14 and 21 PI. GLU, ASP, and GAC improved ($P < 0.05$) average daily gain and gain-to-feed ratio from d −7 to 21 PI. Among treatments, ASP showed the strongest performance responses and increased ($P < 0.05$) average daily feed intake from d 0 to 14 PI. GLU and ASP reduced ($P < 0.05$) diarrhea scores on d 4 PI and decreased ($P < 0.05$) overall diarrhea frequency. ASP and GAC reduced ($P < 0.05$) fecal β-hemolytic coliform shedding on d 7 PI, with further reductions ($P < 0.05$) observed in GAC-fed pigs on d 14 PI. On d 5 PI, GLU or ASP tended to reduce ($P < 0.10$) ileal CLDN1 expression, while ASP tended to increase ($P < 0.10$) jejunal OCLN. On d 21 PI, GAC tended to increase ($P < 0.10$) jejunal *MUC2* expression. Additionally, GAC increased ($P < 0.05$) apparent and standardized ileal digestibility of lysine, Glu, and Asp, whereas ASP increased ($P < 0.05$) digestibility of dry matter and Asp. In conclusion, dietary Glu and/or Asp improved growth, nutrient utilization, and diarrhea outcomes during ETEC challenge. These findings support Glu and Asp as potential nutritional strategies to reduce antibiotic reliance in weaned pigs.

Presenter:
Supatirada Wongchanla
University of California, USA

Investigating Pandemic Polarization with Agent-Based Models

David Knoke
University of Minnesota, USA

This PowerPoint presentation examines how political partisanship in the United States influenced the Covid-19 pandemic. It is based on a chapter in my recent book *Network Collective Action: Agent-Based Models of Pandemics, Riots, Social Movements, Insurrections and Insurgencies* (Springer Nature 2025). It describes “To Mask Or Not To Mask”, a computer simulation written in NetLogo software. The model was intended to assess whether a few simple assumptions about differential partisan masking behaviors and viral transmissibility, informed by national mask-wearing data collected near the beginning of the pandemic, could explain its tragic collective outcome. Across repeated experiments with varied parameters, the recurrent results were that higher proportions of Republicans than Democrats succumbed to infections. Pandemic political polarization was just one symptom of the ongoing decline over the past half century in American democratic norms and values, growing disbelief in science and medicine, and rising distrust in institutional authorities. Fanners of the flames of ideological hostility are political party elites, social movement activists, and media platforms that caricature opponents as enemies. In this toxic brew, refusing to wear a face mask symbolizes resistance to governmental restrictions on personal liberties, on a par with resistance to gun control and affirmative action. Political polarization widens when society is fragmented into densely interconnected subgroups and weak or absent intergroup connections, creating echo chambers and filter bubbles. People falling into online echo chambers receive only filtered information which they already believe, thereby reinforcing their confirmation biases. These polarizing forces have only strengthened since Covid-19 and threaten even greater societal destruction whenever the next inevitable pandemic erupts.

Presenter:
David Knoke
University of Minnesota, USA

Stochastic Modelling of Co-infection Dynamics: An Analysis of Dual Disease Transmission in Individuals

Sunil Maity[1,2], and **Debjani Mondal**[1]
[1]Department of Mathematics, National Institute of Technology Patna, India
[2]Host-Pathogen Interactions program, Texas Biomedical Research Institute, USA

This work stochastically models and analyzes the emergence of two diseases in a single individual, a realistic scenario, using the continuous-time Markov chain (CTMC) modelling approach. The branching process approximation is used to calculate the extinction threshold of the stochastic model and the probability that the disease will disappear. The probabilities of disease extinction assessed by numerical simulations and the probability derived from the branching process are found to be in good agreement. In order to evaluate the influence of demographic stochasticity on the disease transmission dynamics, we analyse and compare the disease dynamics of both deterministic and stochastic models. Analytical and numerical results show that stochastic and deterministic models make different predictions and have different asymptotic dynamics. It has been discovered that if the disease emerges from people who have a major disease rather than people who have a minor disease or people who have both a major and minor disease, the disease is more likely to become extinct. A sensitivity analysis is undertaken to show how the model parameters affect the basic reproduction numbers and the probability that a disease will become extinct, both locally and globally. Using stochastic realizations, we can predict how long an epidemic is likely to last, and we see that the transmission of the disease by people who are already carrying a major disease results in the lowest epidemic duration. Finally, in the frame of the stochastic model, we estimate the probability distribution of the final size of the epidemic.

Presenter:

Sunil Maity
National Institute of Technology Patna, India & Texas Biomedical Research Institute, USA

Hidden Pathways of Resistance: How Environmental Fungicides Undermine Clinical Antifungals

Daniel Assis Santos

Federal University of Minas Gerais (UFMG), Brazil

Cryptococcosis is a life-threatening disease caused by environmental fungi of the *Cryptococcus* genus. It disproportionately affects immunocompromised individuals, particularly people living with HIV/AIDS. Globally, it accounts for approximately 19% of AIDS-related deaths, making it a significant public health concern. This elevated mortality is often linked to delayed diagnosis and treatment, as well as the increasing problem of antifungal resistance. One of the primary drugs used in both the induction and maintenance phases of cryptococcosis treatment is fluconazole, a triazole antifungal. However, fluconazole resistance is becoming increasingly prevalent and is considered a major factor contributing to poor treatment outcomes. This resistance can emerge during prolonged treatment or alternatively, patients can be infected with *Cryptococcus* strains that are already resistant, having acquired resistance mechanisms in the environment before infecting a human host. A growing body of evidence points to the role of agricultural fungicides in this environmental emergence of antifungal resistance. In our study, we evaluated the impact of several fungicidal agrochemicals from different chemical classes—including azoles, strobilurins, and fungal replication inhibitors—on the development of resistance in *Cryptococcus* strains. Our results revealed that exposure to these agrochemicals induced the overexpression of efflux pumps, which play a crucial role in reducing intracellular drug concentrations and thereby contributing to resistance. Additionally, in some strains exposed to azole fungicides, we observed upregulation of the ERG11 gene, which encodes the target enzyme of fluconazole, 14-alpha-demethylase. Interestingly, despite the increased expression, no mutations were detected in the ERG11 gene itself, suggesting that resistance was due to regulatory, rather than structural changes. To assess whether this *in vitro* resistance translated into *in vivo* consequences, we infected mice with the resistant strains. The results demonstrated that the resistance phenotype was maintained *in vivo*, underscoring the clinical relevance of environmentally induced resistance. In a subsequent phase of our research, we observed that fungicide exposure also triggered the expression of enzymes commonly associated with bacterial resistance to antibiotics. This led us to investigate further and ultimately discover a novel mechanism by which environmental fungi such as *Cryptococcus*, *Candida albicans,* and *Candida auris* modify fluconazole. After contact with agrochemicals, these fungi were found to chemically alter fluconazole. This structural modification increased the molecular size of the drug, causing steric hindrance that prevented effective binding to 14-alpha-demethylase, rendering the antifungal inactive. In conclusion, our findings demonstrate that the use of agricultural fungicides can induce cross-resistance to clinical antifungals in pathogenic yeasts. This resistance arises through complex mechanisms that involve metabolic and enzymatic pathways, some of which were previously thought to be limited to gene expression regulation. These insights highlight the urgent need to reassess the environmental use of antifungal agents and their broader implications for human health, particularly in regions with high burdens of opportunistic fungal infections.

Presenter:
Daniel Assis Santos
Federal University of Minas Gerais (UFMG), Brazil

Lactiplantibacillus sp. LH01 as an Adjuvant to Reduce Antibiotic use in Recurrent Urinary Tract Infections

Jesús Alonso Amezcua López[1], **Blanca Rosa Aguilar Uscanga**[2], **Daniel Pérez-Rulfo Ibarra**[3], **Ixtlilxochitl Flores Fong**[4] and **Josué Raymundo Solis Pacheco**[5]

[1]Human Milk Research Laboratory, Department of Pharmacology, University Center of Exact Sciences and Engineering, Universidad de Guadalajara, Mexico
[2]Child Growth and Development, Paediatrics Speciality, Department of Human Reproduction Clinics, University Health Sciences Centre, Universidad de Guadalajara, México
[3]Department of Food and Nutrition, University Health Sciences Centre, Universidad de Guadalajara, México
[4]Nutrition, Academy of Biochemistry, Genetics and Food Technology, Centro Universitario UTEG, Health Sciences Campus, Mexico

Antimicrobial resistance is an escalating global health concern that severely compromises the management of recurrent infections. Recurrent urinary tract infections (UTIs) represent a particularly challenging condition in paediatric patients with structural urinary tract abnormalities and extensive prior antibiotic exposure, where infections are frequently caused by multiantibiotics-resistant and extended-spectrum β-lactamase (ESBL)-producing pathogens.

To address this clinical need, a novel probiotic strain, *Lactiplantibacillus* sp. LH01, was isolated and characterized from human milk and officially registered. Its clinical potential was evaluated in a pediatric patient with bilateral hydronephrosis, a history of repeated hospitalizations, and recurrent UTIs caused by ESBL-producing *Escherichia coli* and *Klebsiella pneumoniae*.

Administration of *Lactiplantibacillus* sp. LH01 was associated with a marked reduction in UTI recurrence and a sustained clinical improvement. *In vitro* assays demonstrated an 89% inhibitory activity against ESBL-producing *E. coli*. Notably, subsequent urinary cultures revealed loss of the ESBL phenotype and restoration of susceptibility to multiple antibiotics that had previously failed, suggesting a potential role in modulating antimicrobial resistance rather than solely suppressing bacterial growth. No adverse events or safety concerns were observed during treatment.

These findings support *Lactiplantibacillus* sp. LH01 as an innovative and clinically relevant candidate for development as a Live Biotherapeutic Product. This probiotic-based approach may represent a novel adjunctive strategy to reduce antimicrobial resistance and improve outcomes in paediatric patients with recurrent UTIs, particularly in settings where therapeutic options are increasingly limited.

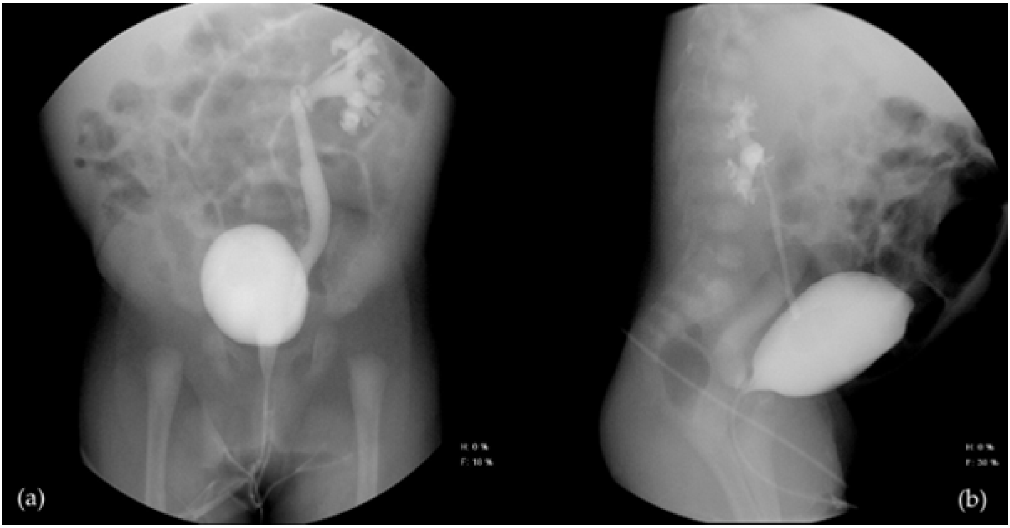


Figure 1. Voiding cystourethrogram: (a) (left kidney, anteroposterior view): Grade IV vesicoureteral reflux is observed, with dilation of the ureter, renal pelvis, and calyces. Partial preservation of the papillary impressions is noted; (b) (right kidney, lateral view): Grade V vesicoureteral reflux is evident, with severe dilatation of the pelvicalyceal system and a tortuous ureter. Loss of normal calyceal morphology and obliteration of the papillary impressions are observed.

Presenter:

Jesús Alonso Amezcua López

Universidad de Guadalajara, Mexico

Microbial Signatures Associated with HPV Infection: Differential Genus-Level Abundance in Cervicovaginal Microbiota Revealed by 16S rRNA Sequencing Analysis

Soudabeh Sabetian

Infertility Research Center, Shiraz University of Medical Sciences, Iran

Objective: To investigate cervicovaginal microbiome alterations associated with HPV infection and cervical lesion severity through reanalysis of publicly available 16S rRNA sequencing data.

Methods: Raw 16S rRNA sequencing data were retrieved from the NCBI Sequence Read Archive (SRA) under BioProject PRJNA1270007, including cervicovaginal samples from women with different HPV statuses and cervical cytology classifications. Sequencing reads were processed using a standardized amplicon analysis workflow, including quality filtering, denoising, and amplicon sequence variant (ASV) inference using the DADA2 pipeline. Taxonomic classification was performed using the SILVA reference database. Microbial community structure was evaluated using alpha and beta diversity metrics, and differential abundance analysis was conducted to identify taxa associated with HPV status and lesion severity.

Results: Distinct microbial community shifts were observed between HPV-positive and HPV-negative samples. HPV-positive and high-grade lesion samples showed reduced dominance of Lactobacillus species and increased relative abundance of anaerobic and opportunistic bacterial taxa. In contrast, HPV-negative and lower-grade samples exhibited more stable, Lactobacillus-dominated microbial profiles. Diversity analyses demonstrated increased microbial heterogeneity with increasing lesion severity, indicating progressive disruption of cervicovaginal microbial homeostasis.

Conclusion: HPV infection and cervical lesion progression are associated with stepwise dysbiosis of the cervicovaginal microbiome, characterized by depletion of protective Lactobacillus species and enrichment of anaerobic taxa. These findings support the role of microbial community instability in HPV-related cervical pathogenesis and highlight potential microbial signatures associated with disease progression.

Presenter:
Soudabeh Sabetian
Shiraz University of Medical Sciences, Iran

Liquid Chromatography–Mass Spectrometry Profiling, Antioxidant and Allelopathic Activities of Leaf Extracts from *Eucalyptus torquata and Eucalyptus campaspe*

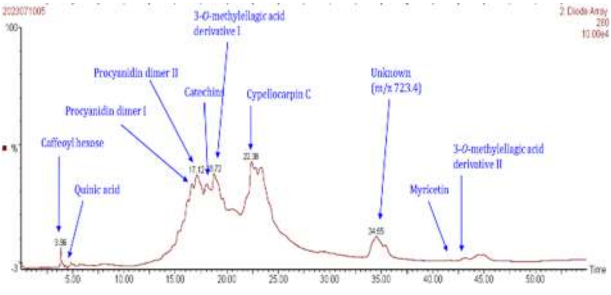
Ferjani Dhaouadi, Hela Sakka, Samia Ayari, Yassine Mrabet, Ismail Amri, Oumayma Kochti, Mouldi Saidi, Abdennacer Boulila and **Naceur Mejri**

Centre National des Sciences et Technologies Nucléaires (CNSTN), Tunisia

Eucalyptus species are recognized as rich sources of bioactive compounds with potential applications in agriculture and environmental protection. The present study investigated the chemical composition, antioxidant capacity, and allelopathic effects of leaf extracts from *Eucalyptus torquata* and *Eucalyptus campaspe*. Different solvents, including methanol (80%), water, and ethyl acetate, were used to prepare extracts, and their phytochemical contents were quantified.

Results showed that methanolic extracts exhibited the highest concentrations of total phenolic compounds, flavonoids, and condensed tannins compared with aqueous and ethyl acetate extracts. Liquid chromatography coupled with mass spectrometry (LC–MS) analysis identified several bioactive compounds, including caffeoyl hexose, gallic acid, rutin, catechin, and myricetin, known for their antioxidant and phytotoxic activities. The antioxidant potential was evaluated using DPPH and ABTS radical scavenging assays. Methanolic extracts demonstrated strong

Fig. 1 Chromatograms of phenolic and flavonoid compounds identified by LC-MS in methanolic leaf extracts of (A) E. torquata and (B)E. campaspe



antioxidant activity with low IC50 values,

indicating high free radical scavenging capacity.

Furthermore, phytotoxic assays revealed significant inhibitory effects of methanolic extracts on seed germination and seedling growth of selected weeds and wheat. The inhibitory effect increased with extract concentration, suggesting a dose-dependent response. These findings highlight the potential use of eucalyptus leaf extracts as natural bioherbicides and eco-friendly alternatives to synthetic chemicals in sustainable agriculture.

In conclusion, *Eucalyptus torquata* and *Eucalyptus campaspe* leaf extracts represent promising natural sources of antioxidant and allelopathic compounds, supporting their potential application in weed management and environmental protection strategies.

Presenter:

Ferjani Dhaouadi
Centre National des Sciences et Technologies Nucléaires (CNSTN), Tunisia

Antimicrobial Potential of Zno-Zns and Activated Carbon Composite

Marta Mediavilla[1,2], **Aida Villa**[2] and **Luis Valencia**[2]

[1]Engineering Faculty, Central University of Venezuela, Venezuela

[2]Environmental Catalysis Group, Antioquia University, Colombia

The rapid increase in bacterial resistance to conventional antibiotics has created a pressing demand for new antimicrobial strategies. This study reports the synthesis and evaluation of a ZnO–ZnS composite supported on activated carbon derived from banana peel, tested against *Escherichia coli* and *Staphylococcus aureus* as representative resistant strains. The composite was prepared by impregnation of banana peel with zinc sulphate, followed by pyrolysis, and characterized by X-ray diffraction (XRD) and scanning electron microscopy coupled with energy-dispersive X-ray spectroscopy (SEM–EDX). XRD confirmed the presence of crystalline ZnO and ZnS phases within the carbon matrix, while SEM–EDX revealed a porous surface with homogeneous distribution of zinc and sulfur. Antimicrobial performance was assessed using agar diffusion method. Table 1 presents the results of quantifying the inhibition zones and their comparison with the positive control (tetracycline).

Table 1. Inhibition diameter values in mm for the composite

Bacterial strains	**Tetracycline (30 μg)**	**Composite (10.0 mg)**	**Composite (25.0 mg)**
S. Coli	30.0 ± 0.0	14.5 ± 0.7	18.5 ± 0.7
S aureus	30.0 ± 0.6	14.5 ± 0.7	20.5 ± 0.7

The inhibition diameters are indicating no appreciable differences in the inhibitory behavior of the composite against gram-negative or gram-positive bacteria. It is supposed that the generation of reactive oxygen species such as H_2O_2, OH^-, and O_2^- causes DNA and protein damage, lipid peroxidation, and unregulated cell signaling. The release of Zn^{2+} ions through direct interaction with bacterial membranes enhances permeability; additionally, Zn^{2+} ions can interact with nucleic acids and deactivate enzymes involved in the bacterial respiration system.These findings suggest that ZnO–ZnS/carbon composites from agro-industrial residues may serve as sustainable antimicrobial materials to address the global challenge of antibiotic resistance.

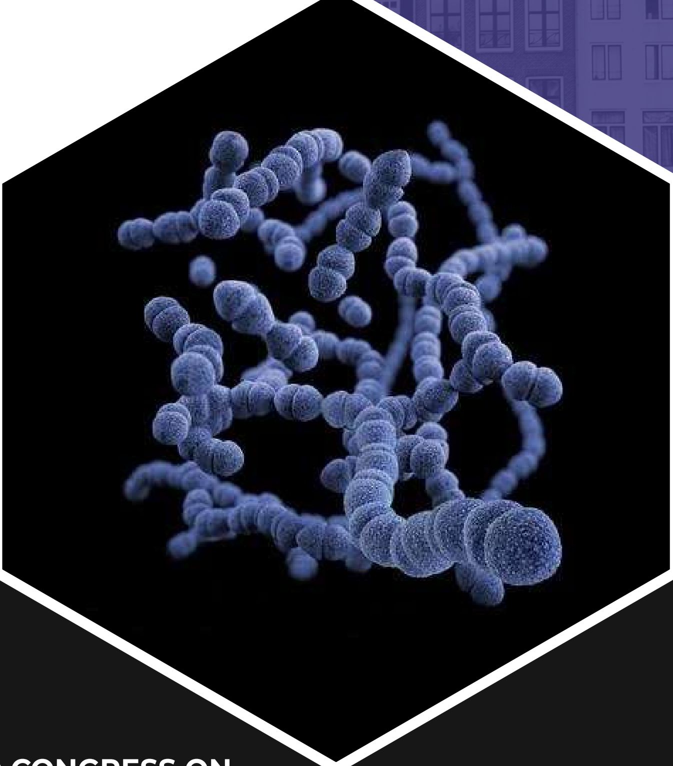
Presenter:

Marta Beatriz Mediavilla Quintero

Central University of Venezuela, Venezuela & Antioquia University, Colombia

PEERS ALLEY MEDIA

DAY 02



4th WORLD CONGRESS ON

INFECTIOUS DISEASES AND ANTIMICROBIAL RESISTANCE

JUNE 26-27, 2026

SPEAKER TALKS

From Debt to Development: Evaluating the Effects of External Debt, Political Instability, and Inflation on Economic Growth in The Democratic Republic of Congo

Amini J. Byamungu and **Diping Zhang**
Zhejiang University of Science and Technology, China

This paper examines the interplay between external debt, political instability, inflation, and economic growth in the Democratic Republic of Congo (DRC), one of the wealthiest nations on the planet, yet a fragile state grappling with protracted socio-political crises. Using World Bank data from 1994 to 2022, the study employs a dual modeling approach, combining linear techniques (Ordinary Least Squares, OLS, and Johansen co-integration) with the Logistic Smooth Transition Autoregressive (LSTAR) model to investigate both linear and non-linear dynamics. The results reveal a significant negative linear effect of external debt on growth, with no long-run relationship. The regime-switching (LSTAR) model uncovers a non-linear, U-shaped relationship, indicating an optimal external debt threshold of 17.16% of the Gross Domestic Product (GDP). Below this threshold, debt hampers growth; conversely, above it, debt stimulates growth, aligning with the Debt Laffer Curve. Trade openness emerges as the most influential positive driver of growth, while inflation exerts a significant negative impact. However, political instability failed to affect economic growth. The study emphasizes the importance of balancing debt sustainability, trade liberalization, and macroeconomic stability to achieve resilient and inclusive economic development. Policy implications include maintaining debt levels above the 17.16% threshold to avoid growth impediments, directing borrowing toward high-productivity sectors, and implementing structural reforms to enhance trade competitiveness and macroeconomic stability. These findings offer vital perspectives for policymakers in the DRC and similar resource-dependent, politically fragile economies.

Results: The economic growth of the DRC can be divided into two distinct phases, as illustrated in Figure 1. The first phase, characterized by negative growth, spanned from 1993 to 2001. In contrast, the second phase, marked by positive growth, occurred from 2002 to 2022. Since 2018, the economy has been experiencing an upswing, largely driven by a surge in commodity prices. In 2022, GDP growth reached nearly 9%, approaching the peak of 9.4% that was achieved in 2014.

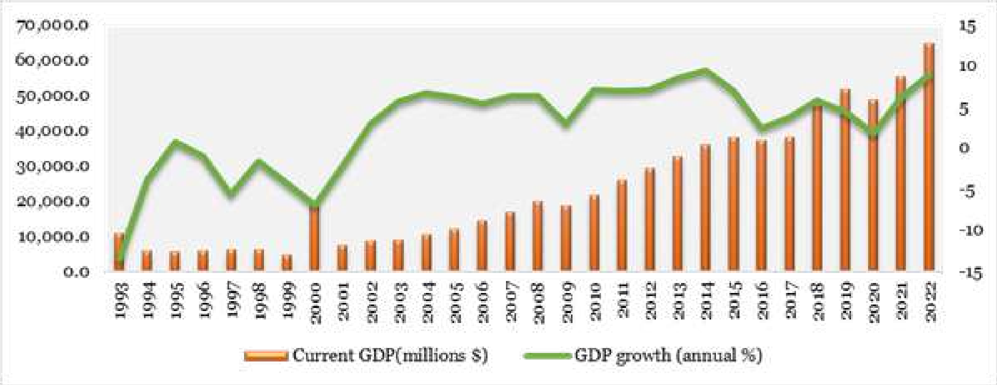


Fig. 1 GDP growth rate in DRC. Source: WDI, WB databank, and author calculations.

Table 1 LSTAR regression with GDP Growth

Variable	Coefficient	Std. Error	t-Statistic	Prob.
EDST - Linear Part	-0.312725	0.123611	-2.529917	0.0251
EDST - Non-Linear Part	0.325786	0.09948	3.2749	0.006
Regressors independent of the regime				
GDPG(-1)	0.290705	0.134187	2.166422	0.0494
GRCF	0.0008201	0.071303	0.115021	0.9102
POPG	1.879727	4.20101	0.447447	0.6619
TRADE	14.15282	2.862129	4.944857	0.0003
PISX	-1.247556	1.697652	-0.734872	0.4755
INFX	-0.002575	0.00112	-2.298591	0.0388
Intercept	-11.60481	14.29919	-0.811571	0.4316
Threshold Approach				
Threshold	**17.16496*** **	R-squared		0.929289

CI of Threshold	[16.40; 17.92]	Adjusted R-squared		0.874897
Smoothing parameter	2.087035	F-statistic		17.08482
Linearity test	3.680972**	Prob(F-statistic)		0.000007

Notes: Superscripts *, **, *** indicate statistical significance at 10%, 5%, and 1% levels, respectively.

The results presented in Table 1 reveal that the stock of external debt exerts a negative and significant impact on economic growth in the first regime. However, in the second regime, this negative effect diminishes substantially and transitions into a positive relationship. Contrary to our expectation, this evidence strongly supports the existence of a U-shaped (non-linear) relationship between the stock of foreign debt and economic growth in the Democratic Republic of Congo (DRC) in contrast with empirical studies on other African economies that often reveal inverted U-shaped relationships (Alsamara et al. 2024; Kitutila W. 2024; Stungwa 2024). The findings imply that at low levels (below 17.16% of GDP), external debt negatively impacts growth, but once external debt crosses the threshold (17.16% of GDP), its effect becomes positive, meaning additional borrowing stimulates economic growth. The findings align with the Debt Laffer Curve theory, which posits that at low levels, debt may hinder growth due to inefficiencies, poor allocation of resources, or lack of productive investment, whereas moderate debt levels can foster growth by financing productive investments and stimulating economic development.

The LSTAR model evaluates the optimal threshold at 17.16% of GDP. These results are quite similar to those obtained by Kazadi (2023) using the ESTAR model. The empirical evidence suggests that the government should exercise caution in accumulating external debt, as low levels may prove counterproductive, while moderate-to-high levels can be beneficial if effectively managed. This underscores the critical role of prudent debt utilization and sustainable fiscal policies to ensure that borrowing contributes consistently to economic growth.

The estimated slope of 2.087035 indicates a smooth, increasing transition between regimes, supported by a non-significant p-value (0.3494), which suggests the absence of a sharp threshold effect. This implies that the relationship between external debt stock (EDST) and GDP growth (GDPG) evolves gradually, with economic growth responding progressively rather than instantaneously to changes in debt levels. Consequently, policymakers continuously monitor debt dynamics over time.

The coefficients of the regressors are in line with endogenous growth theory. The lagged GDP growth (GDPG(-1)) significantly influences the current, highlighting the importance of sustaining growth momentum through macroeconomic stability and productivity-enhancing investments. Gross capital formation (GRCF) and population growth (POPG) show insignificant impacts (p-values = 0.9102 and 0.4477, respectively), suggesting the need for higher-quality investments in high-return sectors and human capital development to unlock their growth potential. Trade openness (TRADE) is highly significant (coefficient = 14.15282, p-value < 0.0001), emphasizing the critical role of trade liberalization and export diversification in driving growth. While political instability (PISX) and inflation (INFX) exhibit negative coefficients, only inflation is statistically significant (p-value = 0.0485), underscoring the necessity of tight monetary policies to mitigate inflationary pressures and support economic stability.

Presenter:
Amini Jephté Byamungu
Zhejiang University of Science and Technology, China

Unmasking Melioidosis - A Journey through Diverse Presentations

Vaishnavi R, Swarnalingam Thangavelu, Kumar J S and **Ravi Kishor Allu**
SRM Medical College Hospital and Research Centre, India

Background: Melioidosis, caused by *Burkholderia pseudomallei*, is an emerging infectious disease in India with varied clinical manifestations and high mortality, particularly among patients with underlying comorbidities. Delayed diagnosis is common because the disease mimics several infectious conditions.

Methods: This retrospective case series included five adult patients with culture-confirmed Melioidosis admitted to a tertiary care teaching hospital in South India between June 2024 and June 2025. Clinical features, laboratory findings, treatment, and outcomes were analysed.

Results: Four patients had type 2 diabetes mellitus, while three had chronic kidney disease. Clinical presentations included liver abscess with septicaemia, pneumonia with bacteremia, neuromelioidosis, necrotising soft tissue infection with septic shock, and relapsing Melioidosis. Blood cultures were positive for *Burkholderia pseudomallei* in all cases. All isolates were susceptible to ceftazidime, meropenem, and trimethoprim–sulfamethoxazole. Intensive therapy with intravenous ceftazidime or meropenem followed by oral eradication therapy was administered. Two patients recovered, whereas three succumbed to severe sepsis and multiorgan dysfunction.

Conclusion: Melioidosis demonstrates diverse and aggressive clinical manifestations with significant mortality. Early clinical suspicion, prompt microbiological diagnosis, and timely initiation of targeted therapy are crucial for improving patient outcomes.

Presenter:
Vaishnavi R
SRM Medical College Hospital and Research Centre, India

Towards Real-Time Precision Agriculture: Evaluating ViT-Base/16 and ViT-Base/32 Variants for High-Accuracy Plant Pathology Detection

Sajja Ratan Kumar[1], **M. Appala Srinuvasu**[1], **A. Vamsidhar**[2] and **B. Dinesh Reddy**[3]

[1]Anil Neerukonda Institute of Technology & Sciences(ANITS), India,
[2]Raghu Engineering College, India,
[3]Vignan'S Institute of Information Technology, India.

Objectives: The primary objective of this research is to evaluate the trade-off between diagnostic precision and computational efficiency in the automated classification of rice leaf diseases, specifically Bacterial Blight, Blast, Brownspot, and Tungro. The study aims to determine the optimal configuration for Vision Transformer (ViT) architectures in agricultural contexts.

Scope: The scope of this study encompasses a comparative analysis of two architectural variants—**ViT-Base/16** and **ViT-Base/32**—across incremental dataset scales. Model generalization is analyzed using training sizes of 100, 300, and 500 samples to simulate varying data availability in real-world farming environments.

Methods Used: The methodology employs a transfer learning framework utilizing the **google/vit-base-patch16-224-in21k** and **vit-base-patch32-224-in 21k** models. The training and testing samples are sourced from the **benchmark Plant Village dataset**, a standard repository for plant pathology. Performance is quantified through test accuracy and total training latency, comparing the impact of patch resolution on self-attention mechanisms.

Results: Experimental results demonstrate a significant correlation between patch size and resource consumption as shown in **Figure 1.** While both models showed susceptibility to overfitting at the 100-sample scale, they achieved high reliability as data volume increased. The **ViT-Base/16** variant attained a peak test accuracy of **100.00%** at 500 samples, capturing fine-grained textural signatures. Conversely, the **ViT-Base/32** variant provided a high-efficiency alternative, reaching **98.68%** accuracy while reducing total training time by approximately **58.7%** (from 2355.3s to 972.3s).

Conclusion: The study concludes that while the 16-patch configuration is optimal for high-precision laboratory diagnostics, the 32-patch architecture is a more viable framework for real-time agricultural deployment on

resource-constrained edge devices. By quantifying the accuracy-latency trade-off, this work establishes a benchmark for deploying Transformer-based models on resource-constrained hardware within smart farming infrastructures.

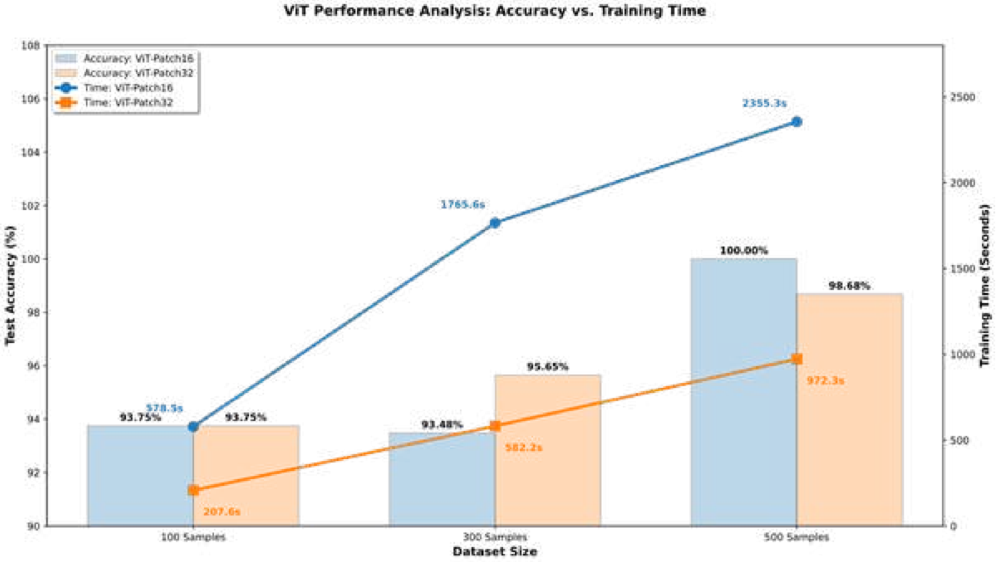


Figure 1: Comparative performance analysis of ViT-Base variants across varying dataset scales.

Presenter:

Sajja Ratan Kumar

Anil Neerukonda Institute of Technology & Sciences(ANITS), India

Biosynthesis of Silver Nanoparticles and their Applications as Next-Generation Antibiotics

Narasimha Golla
Professor & Dean (R&D) Head, Department of Virology
Sri Venkateswara University, India

Nanotechnology is a novel interdisciplinary science that serves as a nexus between the basic sciences, and it is no exception in the life sciences. As multi-drug resistance in pathogens has made antibiotics less effective, nanoparticles are the next line of defense. Silver nanoparticles have been found to have applications in various fields, such as inter-chelating agents. Due to their enhanced responsiveness to environmentally friendly technology for quantifiable synthesis, several developed nations have seen significant growth in the biosynthesis of Ag NPs. The biological method, however, is in the highest demand because it is quicker, safer, less expensive, and more environmentally friendly than other techniques. In addition, the importance of Ag NPs is extensively examined in light of their numerous applications, including antifungal, anti-inflammatory, antibacterial, antiviral, and bio-catalytic activities, as well as in anticancer medicine. materials for electrical batteries, optical receptors, catalysis in chemical reactions, biolabeling agents, sensors, bioactive materials, and antimicrobial agents in the biomedical fields. The significant texture of silver is its broad-spectrum antimicrobial property, which is associated with microbial colonization and biomaterial-related infections. Recent reports indicate that fungi, Viruses, and bacteria are susceptible to silver nanoparticles. In our lab, metallic silver nanoparticles (BioAgNPs) were synthesized using an eco-friendly approach by reacting silver nitrate ($AgNO_3$) with the cell-free filtrate of various microbial sources. *viz* fungi (*Aspergillus niger*, *Aspergillus flavas*, and *Agaricus bisphoris*), Actinobacteria (*Actinomycetes*), and the plant parts (leaves, flowers, stems, etc). Using plant sources as reducing agents for AgNP formation is most attractive due to the cost-effectiveness and time-consuming nature of the process. In our studies, various plants, such as Piper betle, Ocimum leaves, Azadirachta indica, Ficus religiosa, and Ziziphus, are used to synthesize AgNPs. The synthesized AgNPs were characterized using UV-visible spectroscopy, FTIR, SEM, and DLS to further assess their efficient biosynthesis and morphological properties, including size, shape, and stability. The probable mechanism for the extracellular biosynthesis of silver nanoparticles was explained. The synthesized silver nanoparticles exhibited good antimicrobial agents, such as antibacterial (Gram-positive and Gram-negative) and antifungal (*Asper-*

gillus niger), and could be used as next-generation antibiotics in modern medicine

Presenter:

Narasimha Golla
Sri Venkateswara University, India

Impact of Network Sparsity on Graph Based Classification in Biological Systems: Insights from Resting State Functional Connectivity in Autism

Kiran Raj V and **Anoop Jacob Thomas**
Indian Institute of Information Technology Tiruchirappalli, India

Biological systems are increasingly represented as complex networks to capture interactions across multiple scales. These interactions play an important role in understanding system behaviour along with analytical tasks including prediction and diagnosis. However, such data pose a significant challenge in terms of feature extraction and modeling due to higher dimensionality and noise factors. These issues in biological networks manifest into weak or spurious connections which are addressed through thresholding, resulting in network sparsity which can significantly alter the network topology. These alterations consequently affect graph-theoritic measures used in feature extraction. To examine the impact of network sparsity and predictive performance, a resting state functional connectivity was analyzed from the ABIDE dataset across a range of threshold values. Graph-theoretic measures involving centrality measures were computed across multiple threshold levels to generate network representations with varying sparsity. These measures involving degree centrality, betweenness centrality, clustering coefficient and eigenvector centrality were then used to train a linear Support Vector Machine classifier to distinguish patients with Autism Spectrum Disorder (ASD) from Typical Development (TD) participants to evaluate sparsity-dependent behaviour. Experimental results indicated strong dependence of classifier performance on network sparsity levels. Among the centrality measures, clustering coefficient achieved the highest accuracy of 79.17% with Sensitivity and Specificity of 83.3% and 75.0% respectively at a threshold of 0.75 for a site-specific dataset. Furthermore, the sensitivity and specificity varied across sparsity levels for certain graph measures revealing distinct trends across these measures, particularly improved sensitivity when the network is more sparsely distributed. This methodological approach is relevant to many conditions that affect network-level organization of the brain, including those related to Central Nervous Systems. The choice of network construction can significantly influence downstream analytical outcomes, where preprocessing choices such as thresholding can have a direct influence on feature stability and model performance.

Presenter:

Kiran Raj V
Indian Institute of Information Technology, Tiruchirappalli, India

From Mathematical Modeling to Public Health Action: Data-Driven Analysis and Control of HIV–COVID-19 Syndemic Dynamics

Anupam Priyadarshi

Department of Mathematics, Institute of Science, Banaras Hindu University, India

The emergence of interacting infectious diseases (syndemics) has revealed critical limitations in classical single-disease modeling frameworks. In particular, the coupled dynamics of HIV/AIDS and COVID-19 pose a significant challenge for public health systems, especially in high-burden regions such as India. In this talk, I will present a data-driven mathematical modeling framework for HIV–COVID-19 syndemic dynamics, integrating epidemiological data, nonlinear dynamical systems, and optimal control theory. The key novelty of this work lies in the incorporation of an exposed HIV compartment within a co-infection model, enabling the explicit modeling of early-stage infection and post-exposure prophylaxis (PEP) interventions—features that are largely absent in existing syndemic models. In addition, the framework combines real-data calibration (*via* nonlinear least-squares fitting), rigorous global stability analysis, and optimal control strategies, thereby bridging the gap between theoretical epidemiology and data-driven decision-making.

I will first introduce the compartmental structure and demonstrate the mathematical well-posedness, positivity, and boundedness of the system. The talk will then focus on threshold dynamics and global stability results, derived using Lyapunov-based techniques, which characterize the transition between disease-free and endemic states. Using epidemiological data from India, I will show how data-driven parameter estimation enhances predictive accuracy and reveals the role of HIV-induced immunosuppression in amplifying COVID-19 transmission and severity. Furthermore, I will present optimal control strategies for minimizing co-infection burden, highlighting that integrated interventions outperform single-disease control policies. The results provide actionable insights for designing coordinated public health strategies in resource-constrained settings. Finally, I will discuss how this framework can be extended toward AI-assisted epidemiological modeling, including parameter inference, real-time forecasting, and adaptive intervention design, positioning mathematical modeling as a key tool in next-generation infectious disease analytics.

This talk aims to provide a unified perspective combining nonlinear dynamics, data-driven modeling, and control theory for understanding and mitigating complex infectious disease interactions.

Presenter:
Anupam Priyadarshi
Banaras Hindu University, India

AI-Driven Early Warning Systems for Childhood Diarrhea Outbreaks in India: A Prescriptive Modeling Approach

Monalisha Pattnaik, Deepti Rani Pattanaik and **Chandra Sekhar Jena**

Sambalpur University, India

Diarrhea in childhood continues to be a major cause of illness and death among children under five years old in India. Even with numerous health initiatives, the systems for early detection and preventive measures are still restricted. This study seeks to create an AI-based early warning system to forecast and categorize diarrhea incidence in children under five by utilizing a prescriptive modeling technique. The main goal is to improve predictive precision, address class imbalance, and pinpoint crucial factors affecting childhood diarrhea. The research employs data derived from the National Family Health Survey (NFHS-5, 2019–21) Children's Recode (KR) file, concentrating on five states vulnerable to diarrhea-Bihar, Chhattisgarh, Odisha, Jharkhand, and Uttar Pradesh. The dataset underwent preprocessing and was split into training 80% and testing 20% portions. A range of AI and Machine Learning (ML) algorithms were utilized, incorporating both traditional models and sophisticated deep learning frameworks. Due to the unbalanced characteristics of the dataset, the evaluation of model performance was mainly conducted using the Area Under the Precision-Recall Curve (AUPRC), in addition to accuracy measurements.The results show that AI-based models, especially deep learning systems, greatly surpass conventional machine learning techniques in terms of predictive accuracy and classification effectiveness. The creation of feature importance scores enhances interpretability and bolsters evidence-based decision-making.The suggested AI-driven framework shows significant promise as a preliminary alert and decision-assistance tool for identifying diarrhea in children under five. It provides important clinical and policy perspectives, encouraging prompt public health actions and aiding in the alleviation of diarrheal disease burden in India.

Presenter:

Monalisha Pattnaik

Sambalpur University, India

Nano Biosensors for Microbial Contaminants and their Impacts on Food Industry

Manas Kumar Dhal
Department of Zoology, Shivaji College, University of Delhi, India

Health and food safety experts continue to have serious concerns about foodborne infections. Worldwide, reports of foodborne-related mortality average 0.42 million respectively. High-concern pathogens include bacteria like *Salmonella, Escherichia coli, Campylobacter,* and *Listeria monocytogenes*, which are known to produce Shiga toxins. Among the aquatic pathogens of great concern are *Schistosoma japonicum, leptospirosis, Vibrio cholerae*, and others. The global incidence of foodborne illnesses remains high, even with significant efforts being made in the areas of food quality control to monitor the presence of these pathogens of concern in various sources. These factors make it necessary to create new, quicker pathogen-detection techniques that may be used with real-time surveillance plans. In place of more time-consuming and unsuitable techniques for large-scale surveillance, biosensor-based methods have become unique tools for the quicker identification of food pathogens. In a nutshell, biosensors are devices that detect infections by biochemical reactions involving biorecognition components such as tissues, isolated enzymes, antibodies, genetic materials, or aptamers. The majority of biosensors rely on the correlation between electrical, thermal, or optical signals when pathogen biomarkers are present. The use of molecular and nanotechnology makes it possible to identify pathogens at incredibly low pathogen concentrations quickly and with high sensitivity. As a matter of fact, the incorporation of magnetic, silver, iron, and gold nanoparticles (NP) into biosensors has proven to enhance their detection capabilities. The main use of nanomaterials and biosensor-based instruments for the identification of pathogens in food is the subject of this chapter. Furthermore, it emphasises how nanoparticles have improved biosensor devices. Particular benefits are provided by nanomaterials for pathogen detection. The sensitivity and selectivity of the biosensors are improved by the more efficient interaction with pathogenic agents made possible by the nanoscale and high specific surface area. Lastly, the capacity of biosensors to bind to certain molecules, like antibodies or nucleic acids, makes it easier to identify the pathogens of interest.

Presenter:

Manas Kumar Dhal
University of Delhi, India

Intelligent AI-Driven Predictive Analytics for Real-Time Infectious Disease Surveillance and Early Outbreak Detection

Vimala Roselin J
Assistant Professor, Kristu Jayanti University, India

This paper examines how Artificial Intelligence (AI) and Machine Learning (ML) techniques for the early prediction and monitoring of infectious disease outbreaks at an early stage. The topic is highly important because catching diseases quickly can help safeguard public health, slow down epidemics, and get us ready for pandemics. In this research, researchers pulled together healthcare records, social media data and environmental data were collected and analyzed using advanced AI models. Machine learning algorithms such as Decision Tree, Random Forest, and Deep Learning were applied to identify disease patterns and predicts outbreak risks. The study revealed that AI-based surveillance systems can identify infectious diseases faster and more accurately than traditional methods. Real-world value comes from healthcare authorities being able to make quicker decisions and improve their emergency response strategies. This research shows how important computer science is becoming in the battle against diseases and in addressing global health challenges.

Presenter:
Vimala Roselin J
Kristu Jayanti University, India

Deep Learning Techniques for Cervical Cancer Image Segmentation: Architectures, Challenges and Future Directions

S. Ravi, Saranya A and T. Kalaichelvi

Department of Computer Science, Pondicherry University, India

Cervical cancer is a tremendous concern worldwide, with limited or without early detection and efficient screening in low-resource settings. Detecting abnormity regions using Pap smear and colposcopy in the medical images is crucial for cervical cancer diagnosis. This survey investigates novel deep learning algorithms used to identify cervical cancer, emphasizing segmentation methods such as CNN-based architectures, U-Net, and its derivatives. The research work analyzes current datasets in-depth, evaluates essential performance indicators, and explores the issues of generalization, class imbalance, and segmentation accuracy. Furthermore, the survey identifies future research objectives to better deep learning incorporation into clinical practice, segmentation approaches, and cervical cancer therapy. Its vital insights for academics and healthcare professionals trying to improve cervical cancer diagnosis and treatment by bridging the gap between research and real-world applications.

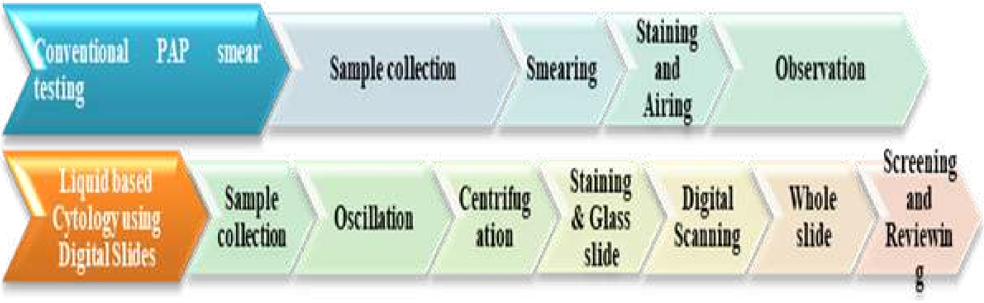


Fig. 1 Two prevalent procedures screening of cervical cytology [2].

Table 1. A Systematic Review of Collaborative Models for Cervical cancer detection in segmentation

Author	Method	Dataset	Merits	Demerits
XiaoQing Zhang [1]	U-Net network model	6692 cervical images	Efficiency and accuracy	Overfitting observed despite early stop and data increase methods
Youyi Song [2]	Intensity-based methods	Hematoxylin and Eosin (HE) dataset	Adaptive shape priors accuracy.	------
Kurnianingsih [3]	Mask R-CNN ResNet10	Herlev Pap smear dataset	Accuracy	Higher processing power
Elima Hussain [4]	U-Net and Mask R-CNN	Herlev dataset	Improved accuracy	Issues with overlapping cells
Hanna Sartor [5]	CNN	CT scans from 75 cervical cancer patients	Faster and more accurate delineation	Manual segmentation inaccuracies
Peng Guo [6]	Mask R-CNN and Mask X R-CNN	Kaggle Intel MobileODT dataset	Segmentation accuracy	Poor lighting and motion blur
Yu-Chun Lin .[7]	U-Net for tumor segmentation	MR images from 169 patients	High accuracy in tumor segmentation	Limited to DW MR imaging
Ch. Rajarao [8]	Normalized Graph Cut	ERUDIT dataset	Reduces noise	No specific limitations mentioned
Zhikai Liu [9]	U-Net-based multi-class segmentation	Peking Union Medical College dataset	Faster processing	Unclear organ boundaries
Tao Wang [10]	Iterative Level Set refinement segmentation	ISBI2015 public dataset	Low contrast	Overlapping cells, staining issues
Zijie Yue [11]	LACNN, AFCN, and FPA	Cervigram dataset with 609 images	High Hausdorff Distance values for acetowhite	Poor segmentation quality

Yosuke Kano [12]	2D and 3D U-Net models	DWI images	High accuracy	Challenges in reducing inter-contour errors
Reza Mohammadi [13]	ResU-Net Deep CNN	113 cervical cancer patient images	Improved reproducibility in brachytherapy	Poor contrast
Jinjie Huang [14]	GAN (Generative Adversarial Networks)	Harbin Maria Obstetrics and Gynecology dataset	High accuracy and robustness	Complexity of cell images
Yizhan Fan [15]	U-Net structure	Anhui Provincial Cancer Hospital dataset	Emphasis on recall value enhances tumor	Small targets and unclear boundaries
Guangqi Liu [16]	Mask R-CNN	Cx22 dataset	Validates the impact of false-negative objects	Lack of high-quality datasets hampers performance
Krishna Prasad Battul [17]	Contrast Local Adaptive Histogram Equalization (CLAHE)	Herlev dataset	Scales network width, depth, and image size.	Difficulty in feature design and selection
Die Luo [18]	Dual-Supervised Sampling Network (DSSNet)	Tongji Hospital, ISBI2014, DIC-HeLa	Wide-bottleneck residual blocks	Datasets may not generalize well
Jinhee Park [19]	Encoder-weighted learning	Intel and MobileODT dataset	Improves model convergence	ROI segmentation challenges
Jiahao Wang [20]	CNN	Independent cohort of 75 cervical cancer images	Improved efficiency	Needs better accuracy
Erlend Hodneland [21]	Dice-Sorensen similarity coefficient	MRI dataset	Human experts in segmentation	Accuracy still needs improvement

Juebin Jin [22]	Adam algorithm	------	High accuracy and reliability	Low reliability in some instances
Nahida Nazir [23]	Otsu method	Dataset of 2100 cervical cell images	Cell boundaries better than the Otsu method	Noise, over-staining issues
Zhen Li [24]	DeepLabv3+ model	High-resolution post-acetic acid images	Training for 50 epochs enhances	Data not publicly available
M.A. Devi [25]	Boykov's Graph Cut-Based segmentation	Herlev dataset	High classification accuracy	Noise and intensity variations

Presenter:

Prof. S. Ravi
Pondicherry University, India

Therapeutic Activities of Transition Metal Complexes with a 3ES4PThiosemicarbazone Based Ligands

K. Gour[1], **Sampada Payal**[2] and **P Ashtraputre**[2]
[1]Priyadarshini Bhagwati College of Engineering, India
[2]Institute of Science, India

Schiff base complexes are known for their remarkable versatility, finding applications across medicine, catalysis, materials science, environmental protection, and agriculture. To synthesize a novel Schiff base ligand derived from 3ES4PTthiosemicarbazone& evaluate the therapeutic activities of the synthesized metal complexes, including antibacterial, antifungal & enzyme inhibition potential of these complexes to assess their possible pharmacological applications. In this study, a novel Schiff base ligand was synthesized from thiosemicarbazone&3ETS and further complexed with cobalt (II) and copper (II) Metal. These newly formed complexes were characterized using FT-IR, UV-Vis spectroscopy, XRD, SEM, and CHNS elemental analysis, confirming their four-coordinate square-planar structures. Biological evaluations revealed promising outcomes: the copper complex exhibited notable antifungal activity, while both the ligand and its metal complexes showed moderate antibacterial and antifungal properties. Enzyme inhibition studies demonstrated that the compounds effectively inhibited digestive enzymes such as lipase, trypsin, and pepsin, with a stimulatory effect observed on amylase activity. Overall, the findings highlight the therapeutic potential of these Schiff base metal complexes as multifunctional bioactive agents, opening avenues for future research in drug development and biochemical modulation.

Presenter:

Kavita Sandip Gour
Priyadarshini Bhagwati College of Engineering, India

Breeding Habitat Distribution and Adult Insecticide Susceptibility of *Aedes* Mosquitoes in Selected NCR Districts of Delhi, India

Lalthazuali[1], **Purnima Srivastava**[1] and **Sukhvir Singh**[2]
[1]Bhagwant University, India
[2]National Centre for Disease Control, India

Dengue is an important vector-borne disease transmitted mainly by *Aedes aegypti* and *Aedes albopictus*, and its increasing incidence in the National Capital Region (NCR) of Delhi necessitates continuous monitoring of vector susceptibility to insecticides. The present study aimed to evaluate the adult insecticide susceptibility status of *Aedes* mosquitoes and identify major breeding habitats in selected districts of NCR, including Ghaziabad and Gautam Buddha Nagar (Noida) in Uttar Pradesh and Gurugram in Haryana. Entomological surveillance was conducted monthly from July 2021 to September 2022 in two localities from each district. Immature stages of mosquitoes were collected from different breeding habitats and reared under laboratory conditions. Adult susceptibility tests were performed using WHO standard tube assay protocols against Deltamethrin (0.05%), Permethrin (0.75%), and Fenitrothion (1%).

The study identified coolers, plastic containers, flower pots, tyres, refrigerator trays, and overhead tanks as the major breeding habitats of *Aedes* mosquitoes. Breeding prevalence was highest during monsoon and post-monsoon seasons, with increased House Index (HI), Container Index (CI), and Breteau Index (BI), indicating elevated dengue transmission risk. Adult susceptibility assays showed that *Aedes* populations were fully susceptible to Deltamethrin, with mortality ranging from 98.9–100% across all study sites. However, reduced susceptibility was observed against Permethrin, with mortality ranging from 94.7–95.9%, while Fenitrothion showed lower mortality (74.2–90.9%), indicating resistance in several populations. Knockdown rates after one hour of exposure were highest with Deltamethrin and lowest with Fenitrothion.

The findings indicate emerging insecticide resistance among *Aedes* mosquitoes in NCR regions and highlight the importance of regular resistance monitoring and integrated vector management strategies for effective dengue control. One representative table showing adult susceptibility status and one figure illustrating major breeding habitats may be included in the results and discussion section for better interpretation of findings.

Presenter:
Lalthazuali
Bhagwant University, India

Pandemics, Power and Prediction: What Colonial Bengal's 1918 Influenza Pandemic Reveals about the Preparedness for Future Global Pandemics

Saumitra Basu
Indian National Science Academy(INSA), India

Can a research on historical pandemic can truly provide an early indications or true insights or preparedness for any pandemic diaster for present and future world? This question instills the present researcher to think over this issue in a new perspective and "1918-1920 Spanish Influenza" is an illuminating lens in this regard which reflects as a witness to a procession of death march in the backdrop of war, famine and colonial brutality. The aim of this presentation is to analyze pandemic as a model to understand long-term consequences of pandemic diseases and the way of its preparedness. In this light, the paper hopes to investigate how inequalities and brutality of governance influenced disease spread and mortality, and tries to connect this historical insights with contemporary global health crises such as COVID-19 and antimicrobial resistance (AMR). Methodologically, the research uses a multidisciplinary approach including archival sources, news papers, micro films and socio-epidemiological analysis to understand every intersections of the disease prevalence, and it comparatively situates these findings within recent global health experiences to establish historical continuities. In the future, pandemics will come and come in new forms, driven by overpopulation, environmental degradation, the use of advanced technology, and the unequal distribution of health, and with it the future world will face AMR, which will be considered a slow pandemic. Combining facts with predictions, author tries to portray public health models which will not only integrate socio-political and historical variables to understand colonial pandemic experiences as a retrospective but also essential for combating the next generation of global pandemic disease threats.

Presenter:
Saumitra Basu
Indian National Science Academy(INSA), India

Multisource AI Diagnostics: Harmonizing Imaging and Omics for Improved Patient-Level Predictions

Rosy Sarmah
Tezpur University, India

Recent advancements in multi-omics and imaging technologies have paved the way for integrating different data types to improve robust, data-driven prediction and modality-wise comparison. As an initial step toward this broader objective, the radiogenomics component has already been implemented to validate key pipeline elements on real datasets. Specifically, radiomic feature extraction and prioritization have been operationalized (including 107 features per region across intensity, shape and texture features, along with ANOVA F-test–based feature ranking), alongside transcriptomic differential analysis using DESeq2 with standard filtering criteria (adjusted $p < 0.05$ and $|\log2 \text{ fold-change}| > 1$). Cross-dataset comparison of DEG lists has been used to derive consistently dysregulated genes, which are then aligned with top-ranked radiomic features to prioritize candidates for downstream association analysis.

Building on these foundational components, a tri-modal artificial intelligence (AI) framework is envisioned to integrate imaging, clinical and genomic modalities through standardized preprocessing within each modality. For the imaging branch, regions of interest will be delineated, and quantitative radiomic descriptors (first-order, shape, and texture families such as GLCM/GLRLM) will be extracted under reproducible settings, followed by feature screening and selection (e.g., ANOVA F-test with SelectKBest) to retain informative signatures. For the genomic branch, expression profiles will be analyzed to identify statistically significant molecular signatures using established differential analysis strategies with multiple-testing control and effect-size thresholds. For the clinical branch, structured variables (demographics, laboratory indices, clinical scores, comorbidity indicators, and treatment history) will be curated, normalized, and encoded to enable learning from heterogeneous clinical records.

Modeling in the planned tri-modal framework will be performed in two stages. First, modality-specific deep learning models will be trained to learn compact embeddings and to generate unimodal prediction scores. Second, a multimodal fusion module will combine unimodal representations to produce a final prediction with calibrated confidence estimates. To quantify the contribution of each modality, systematic comparisons and evaluation is conducted using AUROC, F1-score, precision–recall metrics, and calibration measures. Interpretability is incorporated using XAI-based feature attribution methods to identify salient predictors within each modality and to support transparency in multimodal decision-making.

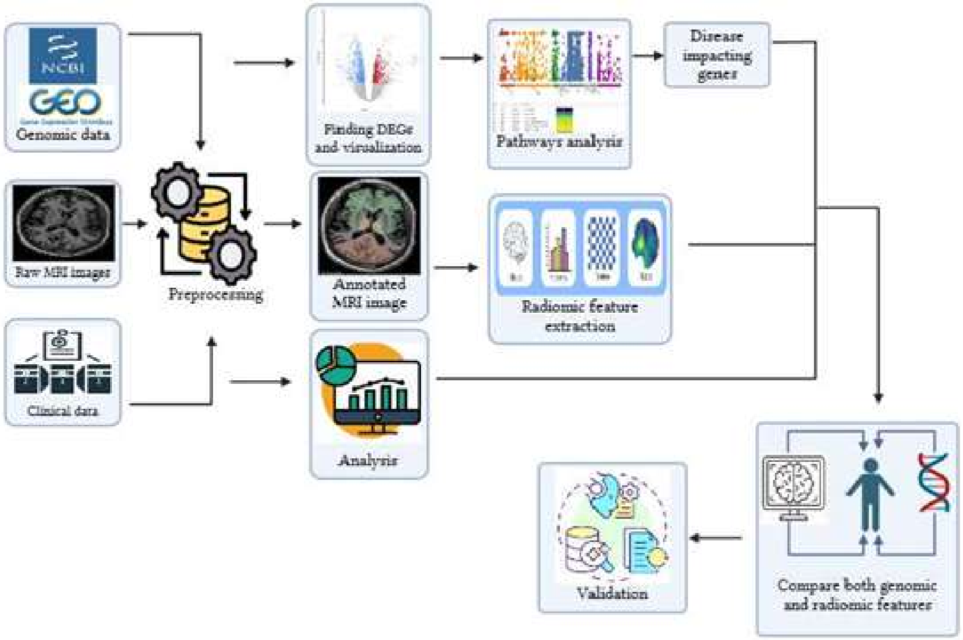


Fig: Workflow of the tri-modal framework

Presenter:

Rosy Sarmah
Tezpur University, India

Targeting Drug-Resistant Pathogens using *Daphne papyracea* Wall. ex G. Don: An *in vitro* Study of it's Antimicrobial Potential

Priyanka Sharma, Dimple Guleria, Shikha Dhiman and **Amit Kumar Sehgal**
Department of Biosciences, Himachal Pradesh University, India

The rise in drug resistance among bacteria and fungi has become a serious challenge in managing infectious diseases. In the present study, the antimicrobial efficacy of different solvent extracts (acetone, methanol and petroleum ether) of *Daphne papyracea* Wall. ex G. Don roots was evaluated against selected pathogenic microorganisms, including ESKAPE-related bacteria (*Streptococcus mutans, Staphylococcus aureus, Streptococcus pneumoniae, Escherichia coli, Klebsiella pneumoniae, Pseudomonas aeruginosa)* and *Candida albicans.* The antimicrobial activity was assessed using the agar well diffusion method and minimum inhibitory concentration (MIC) assays. Among the tested extracts, the acetone extract exhibited the highest antibacterial activity, with maximum zones of inhibition observed against *S. mutans* (22.10 ± 0.02 mm), *S. aureus* (22.05 ± 0.03 mm) and K. pneumoniae (22.15 ± 0.01 mm). Notable activity was also recorded against *E. coli* (22.33 ± 0.52 mm) and *P. aeruginosa* (18.21 ± 0.05 mm). In contrast, methanol and petroleum ether extracts showed comparatively lower but concentration-dependent antibacterial effects. Antifungal activity against *C. albicans* was relatively lower across all extracts, with petroleum ether showing slightly higher inhibition (9.76 ± 0.07 mm) compared to acetone and methanol extracts. Minimum inhibitory concentration (MIC) assays further supported these findings. The lowest MIC value was recorded for *S. mutans* (0.078 mg/mL) across all extracts, indicating strong susceptibility. The acetone extract demonstrated notable activity against *S. aureus* and *C. albicans* (0.625 mg/mL), while moderate MIC values were observed for *P. aeruginosa* and *S. pneumoniae* (1.25 mg/mL). Higher MIC values were recorded for *E. coli* and *K. pneumoniae* (2.5 mg/mL), suggesting comparatively lower sensitivity. These findings support the traditional medicinal use of *D. papyracea* and highlight its potential as a source of bioactive compounds for developing new antimicrobial agents to combat drug-resistant infections.

Presenter:
Priyanka Sharma
Himachal Pradesh University, India

Clock and Clot: Impact of Processing Time on the Quality of Fresh Frozen Plasma – A Comparative Analysis of Coagulation Parameters

Shubhi Yadav[1], **Tulika Chandra**[2] and **Rajeev Misra**[3]

[1]Department of Transfusion Medicine, Balrampur Hospital, India
[2]Department of Transfusion Medicine, King George's Medical University (KGMU), India
[3]Department of Community Medicine, King George's Medical University (KGMU), India

Fresh frozen plasma (FFP) is a vital blood component used for replacement of coagulation factors in bleeding disorders, liver disease, and massive transfusion protocols. Its quality depends on proper preparation and storage, with national and international guidelines recommending freezing within 6–8 h to preserve factor stability. However, delays in process-ing may compromise coagulation efficacy. This study aimed to evaluate the impact of processing time on coagulation parameters of FFP at different preparation and testing intervals. A comparative observational study was conducted over one year (September 2020–August 2021) in the Department of Transfusion Medicine, a tertiary care centre in Northern India. A total of 110 eligible whole blood donors (18–65 years) were enrolled. FFP units were divided into two categories: Category A (n=60; prepared within 4, 6, and 8 h) and Category B (n=50; prepared within 4 h but tested at 4, 6, 8,and 10 h). Coagulation parameters were assessed using Stago STA R Max3 analyzer. The mean donor age was 31.8±8.7years, with mean hemoglobin 13.5±0.9 g/dL. In Category A, PT and aPTT were significantly prolonged with delayed preparation ($p=0.017$ and $p=0.001$, respectively), while fibrinogen and Factor VIII remained stable. Paired comparisons confirmed significant increases in PT and aPTT between 8 h versus 4 h. In Category B, PT and aPTT remained relatively stable, but Factor VIII declined significantly over 10 h ($p=0.001$). Timely preparation of FFP within 4–6 h is crucial for preserving coagulation integrity. PT and aPTT are sensitive to processing delays, and Factor VIII is particularly vulnerable to extended storage before freezing. These findings emphasize strict adherence to preparation timelines and quality control protocols to optimise transfusion efficacy

Presenter:
Shubhi yadav
Balrampur Hospital, India

Design, *In silico* Targeting, and Characterization of Curcumin Prodrug Microspheres for Brain-Specific Delivery in Alzheimer's Therapy

Shakuntala Chopade[1], Priya Kumari[1], Arulmozhi Sathyanarayanan[2], Kunal Pimpalkar[2], Ajay Kumar[3], Dileep Kumar[4]

[1]Department of Pharmaceutical Chemistry, Bharati Vidyapeeth University, Poona College of Pharmacy, India
[2]Department of Pharmacology, Bharati Vidyapeeth University, Poona College of Pharmacy, India
[3]Department of Pharmacology, Sardar Patel College of Pharmacy, India
[4]Department of Pharmaceutical Chemistry, Manipal College of Pharmaceutical Sciences, Manipal Academy of Higher Education (MAHE), India

Background: Alzheimer's disease (AD) is a complex neurodegenerative condition characterized by limited treatment effectiveness, attributed to inadequate blood-brain barrier (BBB) permeability and low medication absorption. Curcumin and ibuprofen possess anti-inflammatory and neuroprotective properties but are limited by pharmacokinetic constraints.

Objective: To synthesize a curcumin–ibuprofen mutual prodrug (CIP), formulate it into chitosan-based microspheres (CIPM), and evaluate its neuroprotective potential for brain-targeted delivery in AD.

Methods: CIP was synthesized *via* ethylenediamine carbodiimide (EDCI) mediated esterification and confirmed through IR, NMR, LC-MS, and DSC. CIPM microspheres were prepared using emulsion cross-linking, characterized by scanning electron microscopy, drug entrapment efficiency (85.5%), zeta potential, particle size analysis and DSC. In silico tools (SwissADME, Pro-Tox-II) and molecular docking assessed ADMET profiles and target binding (AChE, BACE1, β-secretase). Network pharmacology identified overlapping targets between curcumin and AD. *In vivo* evaluation was conducted in a TMT (Trimethyltin)- induced neurodegeneration rat model through behavioral Morris Water Maze (MWM), Novel Object Recognition(NOR), Social Recognition Test (SRT), biochemical and histological assessments.

Results: CIP demonstrated strong binding affinity with AD-related targets (−10.0 to −8.5 kcal/mol) and favorable ADMET properties. Network analysis identified 226 overlapping targets and key hub genes. CIPM significantly

improved cognitive performance, antioxidant enzyme levels, and neuronal integrity compared to individual drugs and showed comparable efficacy to donepezil.

Discussion:

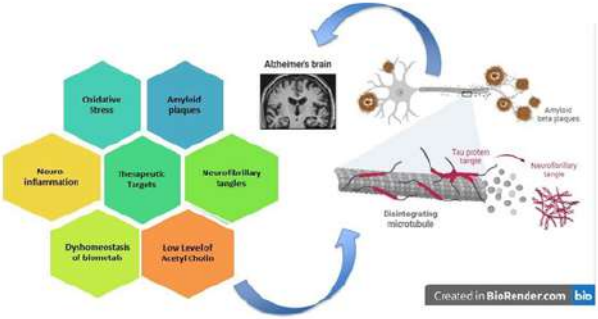


Figure 1: Alzheimers Disease

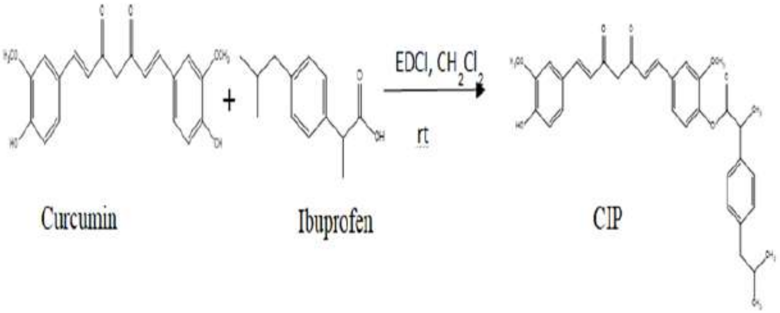


Figure 2: CIP Synthesis Scheme

The present study demonstrates that the curcumin–ibuprofen conjugate, when delivered through chitosan-based microspheres, effectively enhances brain targeting and overcomes pharmacokinetic barriers. The formulation not only improved drug bioavailability but also showed superior neuroprotective and cognitive benefits compared to individual drugs. Molecular docking and network pharmacology further confirmed its multi-target potential, suggesting a synergistic mechanism in modulating key AD pathways. These outcomes highlight CIPM as a promising candidate that warrants further pharmacokinetic and clinical validations for Alzheimer’s therapy.

Conclusion: The curcumin–ibuprofen prodrug-loaded microspheres present a promising brain-targeted treatment approach for Alzheimer's disease by improving bioavailability, engaging multiple targets, and providing neuro-protection.

Presenter:
Shakuntala Santosh Chopade
Poona College of Pharmacy, India

Artificial Intelligence for Infectious Diseases Learning and Research: Microbiology Students' Perceptions, Ethical Considerations and Challenges at the University of Port Harcourt

Sandra Eberechukwu Augustine and Comfort N owate
University of Port Harcourt, Nigeria

The COVID-19 pandemic that ravaged the world showed that infectious diseases and their causative microorganisms are everywhere, with little or no geographical or regional limitations. This highlights the need for adequate knowledge of microorganisms that cause various infectious diseases, diagnosis, transmission and resistance patterns, treatment, prevention, and control, through focused learning and evidence-based research. Artificial Intelligence has simplified knowledge acquisition and research processes by offering tools that adapt learning and research to individual learners' needs and interests. However, the manner in which Microbiology students at the University of Port Harcourt perceive the use of AI tools for infectious disease learning and research remains unknown in the literature. This study, therefore, investigates Microbiology students' perceptions, ethical considerations, and challenges regarding the use of AI tools for infectious disease learning and research at the University of Port Harcourt. It employs descriptive survey and correlational designs to answer six research questions and test six hypotheses from a population of 350 400-level Microbiology students. The study used a sample of 185 respondents selected through simple random sampling. An interview and a questionnaire titled, Students' Perceptions, Ethical Considerations, and Challenges of Using Artificial Intelligence for Infectious Diseases Learning and Research (SPECAIIDLR) will be expert-validated, pilot-tested, subjected to Cronbach's alpha reliability testing, and used for data collection. Data analysis will be performed using qualitative analysis, frequencies, percentages, means, standard deviations, t-tests, and Chi-squared test. The findings tools in the curriculum towards on the use and integration of responsible AI tools in the curriculum towards the prevention, treatment, and control of infectious diseases.

Presenter:
Sandra Eberechukwu Augustine & Comfort N owate
University of Port Harcourt, Nigeria

SIOOT Oxygen-Ozone Therapy against Multidrug Resistant Bacteria Perspectives and Future Remarks

Marianno Franzini

Scientific Society of Oxygen Ozone Therapy (SIOOT), Italy

Introduction: Antibiotic resistance is one of the most pressing global health threats, reducing the effectiveness of standard antimicrobial therapies and contributing to increased morbidity, mortality, and healthcare costs. In response to this challenge, ozone therapy has emerged as an adjunctive treatment to existing antibiotics for multidrug-resistant (MDR) bacterial infections. In particular, the protocols approved by the Italian Scientific Society of Oxygen-Ozone Therapy (SIOOT) and the clinical analyses of Professor Marianno Franzini have contributed to a better understanding of ozone's dual mechanism of action in infection control. All of this convinced me to initiate a trial in 2018 after reading the paper by Wentworth P Jr. et al., "Evidence for antibody-catalyzed ozone formation in bacterial killing and inflammation." Science. 2002;298:2195–2199., which suggested that the immune system generates highly potent (ozone-like) oxidants with possible bactericidal, anti-inflammatory, and redox signaling roles.

Methods: This review summarizes data from experimental studies, model analyses, and clinical reports on the use of medical ozone in MDR infections. Mechanistic analyses focus on two main pathways: (1) direct bactericidal activity of ozone and its reactive species through oxidative damage to microbial membranes and thiol groups, and (2) systemic immunomodulation through low-dose ozone exposure. The latter is mediated by secondary messengers such as 4-hydroxynonenal, which activate Nrf2 signaling, regulate inflammasomes, promote macrophage activity, and improve mitochondrial function.

Results: Evidence indicates that ozone exerts rapid, broad-spectrum bactericidal effects, largely independent of classical resistance mechanisms. When administered systemically within a hormetic dose range, ozone enhances host innate immunity through redox-sensitive signaling pathways and promotes tissue resilience. Modeling studies suggest synergistic effects when ozone is combined with antibiotics, accelerating pathogen clearance compared to antibiotic monotherapy. Clinically, ozone has demonstrated efficacy as an adjunct in the treatment of chronic wounds and necrotizing infections caused by MDR pathogens.

Conclusions: Ozone therapy, when precisely dosed and integrated into standardized medical protocols, offers a compelling adjunct approach in the management of antibiotic-resistant infections. Rather than replacing antibiotics, ozone enhances their efficacy and may reduce the selective pressure that leads to resistance. The future integration of ozone into antimicrobial stewardship programs could support more sustainable and systemic infection control strategies, in line with global health imperatives.

Presenter:
Marianno Franzini
Scientific Society of Oxygen Ozone Therapy (SIOOT), Italy

Health and Safety Hazards and Associated Organisational and Social Support Factors for Deathcare Workers: A Global Scoping Review

Mary Aku Ogum[1], **Nkosi Nkosi Botha**[1], **Cynthia Esinam Segbedzi**[2], **Anita Asiwome Adzo Baku**[3], **Victor Kwasi Dumahasi**[4], **Ruby Victoria Kodom**[5], **Samuel Maneen**[1], **Ivy Selorm Tsedze**[6] and **Edward Wilson Ansah**[1]

[1]Department of Health, Physical Education and Recreation, University of Cape Coast, Ghana,
[2]Jasikan College of Education, Department of Arts and Social Sciences Studies, Ghana,
[3]Department of Health Services Management, University of Ghana Business School, Ghana,
[4]Institute of Environmental and Sanitation Studies, Environmental Science, College of Basic and Applied Sciences, University of Ghana, Ghana,
[5]Department of Health Services Management/Distance Education, University of Ghana, Ghana,
[6]Ho Teaching Hospital, Ghana

Background: Deathcare workers, including mortuary workers, embalmers, funeral directors, and undertakers, are routinely exposed to occupational health and safety risks. Despite recommendations from the International Labour Organisation (ILO) and the World Health Organisation (WHO), many deathcare facilities lack adequate engineering controls, administrative measures, and personal protective equipment (PPE) required for safe work practices.

Objective: To synthesise global evidence on the work practices, occupational hazards, and organisational and social support systems of deathcare workers to inform policy, practice, and future research.

Scope: The review covered global evidence on occupational hazards, workplace safety practices, and support systems among deathcare workers.

Methods: The scoping review was conducted with the PRISMA-ScR and JBI methodological guidelines. A comprehensive search was conducted across multiple international databases. After screening and data extraction, 64 peer-reviewed full-text studies were included and analysed using qualitative thematic synthesis.

Results: The review identified a range of occupational hazards, including physical and ergonomic injuries, biological and chemical exposures, psychosocial stressors, and indoor air pollution. Exposure levels varied across settings and were influenced by workers' characteristics, workplace safety culture, and the availability of safety controls. Inadequate engineering and administrative controls, insufficient PPE supply and utilisation, and poor adherence to donning and doffing procedures contributed to elevated occupational risks. Many facilities also lacked structured social support systems, counselling services, and compensation schemes. Workers adopted both positive and negative coping strategies to manage occupational challenges.

Conclusion: The use of inappropriate equipment, inadequate training, limited supervision, insufficient medical screening and vaccination, and the absence of post-exposure prophylaxis undermine workplace safety. Strengthened policy interventions are needed to improve occupational health and safety in deathcare settings through enhanced training, supportive supervision, counselling services, compensation mechanisms, and the consistent provision and proper use of PPE.

Presenter:
Mary Aku Ogum
University of Cape Coast, Ghana

INDEX

BOOKMARK DATES

5TH WORLD CONGRESS ON

INFECTIOUS DISEASES AND ANTIMICROBIAL RESISTANCE

June 2027 | Vienna, Austria

PARTNER WITH US
CONFERENCE CO-ORGANIZATION AND JOURNAL PARTNERSHIPS!!

Greetings!!

We are reaching out to explore meaningful collaboration opportunities with professionals and organizations who share our vision of advancing scientific knowledge and global outreach. Please find below two key areas where we are currently seeking partnerships:

Collaboration 1: Conference Co-Organization

We would be delighted to collaborate with you in organizing conferences—either in your own country or in any other location of your preference.

If you, or a group of your colleagues or scientific contacts, are interested in hosting a conference, we welcome the opportunity to partner with you under a flexible and supportive collaboration model.

At Peers Alley, we have a strong and experienced team that manages both the scientific and operational aspects of conference planning. Our dedicated marketing team will actively promote the event, attract a diverse lineup of expert speakers, and ensure strong participation. We also leverage our extensive, curated database of researchers and professionals across various scientific disciplines to maximize outreach and engagement.

While our team oversees the scientific agenda, logistics, and event management, your local or regional insights will help shape the program for greater impact. Our approach is simple and collaborative—your event terms are our terms.

Collaboration 2: Partnerships with Journals and Publishing Houses

Peers Alley is interested in collaborating with publishing houses, academic publishers, and independent journal owners to support the growth and sustainability of scholarly journals.

We can help increase quality manuscript submissions through our extensive conference network and researcher database. For journals requiring additional support, we are open to collaboration, joint management, acquisitions, or taking responsibility for journal operations.

Our partnership model is flexible, and we are open to mutually agreeable terms and conditions.

With our robust researcher database and outreach capabilities, we are confident in our ability to significantly increase the volume and quality of manuscript submissions for your journals.

If you are open to exploring potential synergies, we would be glad to connect at your convenience.

For further communication, please contact us at: contact@peersalley.com

Warm regards,
Peers Alley Media
701 West Georgia Street,
Suite 1500, Vancouver, V7Y 1C6, Canada

BOOKMARK YOUR DATES

5th World Congress on

Infectious Diseases and Antimicrobial Resistance

JUNE 2027 | VIENNA, AUSTRIA