Infectious Disease World Conference

IDWC 2025

World Vaccines R&D Conference

WVRDC 2025

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Joint Event On

2nd Edition of the Infectious Diseases World Conference & World Vaccines R&D Conference

17-19 October 2025

Venue

Millennium Hotel Paris CDG, France

IDWC & WVRDC 2025

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ABOUT US

Precision Global Conferences

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17-19 October 2025

KEYNOTE SESSIONS | DAY 1

Sergey Suchkov[1-6]*, Roger D. Kamm[9], Daniel Scherman[10], Shawn Murphy[7], David Smith[11], Hiroyuki Abe[8], Holland Cheng[12], Noel Rose[8,13]

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The transformation of Personalized and Precision Medicine (PPM) as a Unique Healthcare Model to Be Set Up for Infectious Diseases Monitoring & Management

A new and upgraded approach to the diseased states and wellness, and to re-shape tomorrow's healthcare whilst doing it today, resulted in a new global trend in the healthcare services, namely, ***Personalized and Precision Medicine (PPM).*** PPM as a Unique Entity demonstrating an integration of Fundamental, Healthcare & Life Sciences, ***Biodesign-driven BioTech, Translational ART*** and ***IT Armamentarium***, is based on the new developmental strategy driven by ***Biomarkers-*** and ***Biotargeting***-related biomachines. So, it would be extremely useful to integrate data harvesting from different databanks for applications such as pre-early predictive diagnostics, precise prognostication and personalization of further treatment to thus provide more tailored measures for the diseases bodies and persons-at-risk resulting in improved outcomes and more cost effective use of the latest health care resources.
PPM as being the Grand Challenge to forecast, to predict and to prevent is rooted in a big and a new SCIENCE generated by the achievements of (i) ***Systems & Synthetic Biology***; (ii) ***Biodesign-driven Translational***

applications and ***Biotech-driven Biomanufacturing***; (iii) ***Bioindustry*** and ***Biomarketing*** of the next step generation. The latter, being a Grand Brick laid into the frame of National Bioeconomy, says and confirms that the efficiency and efficacy of the Bioeconomy are determined and dictated by the innovative trends,generated by fresh knowledge and their transfer into the scientific, bioindustrial and social areas to maintain the national stability and extensive development of the country.

The core strategic tool to operate the transdisciplinary approach is rooted in a unique tandem consisting of (i) ***integrated platforms of Fundamental Sciences (Basics) and innovative OMICs biotechnologies*** on one hand, and (ii) the algorithms of ***Bioinformatics***, on the other one.

The importance of PPM in the healthcare management of several diseases is well-documented. And advances in genomics and computing are transforming the capacity for the characterization of biological systems, and researchers are now poised for a precision-focused transformation in the way they prepare for, and respond to, infectious diseases. But still, very little is known about the role of ***precision genomics*** and ***immunogenetics*** in susceptibility or resistance to infectious diseases. And despite being a forerunner, PPM is not yet routinely applied in infectious patient care.

Meanwhile, new technologies are supporting the rapid identification of infective agents and targeted approaches based on the genetic resistance of pathogens to antibiotics. For instance, recent technological advances have enabled the development of antimicrobials that can selectively target a gene, a cellular process, or a microbe of choice. These strategies bring us a step closer to developing personalized therapies that exclusively remove disease-causing infectious agents. This information can lead to revising the data banks that can be used for personalized predicting diseases, improving PPM-driven treatment, and also personalized prevention strategies specific to infectious pathogens.

PPM-driven management of infectious diseases plays a critical role in trust for government, health-care organizations, science, and pharma. The improvement in biomedical technologies, availability of large clinical and OMICS data and appropriate application of applied bioinformatics-related algorithms may allow precision in vaccines and public health and restore trust. For this scope, the next step education is a crucial step for the successful implementation of PPM in the clinic, and with this part, we would like to encourage learning about PPM and the impact in the communicable (including infectious) disease field.

Infectious disease management essentially consists in identifying the microbial cause(s) of an infection, initiating if necessary antimicrobial therapy against microbes, and controlling host reactions to infection. In canonical (PPM-ignored) clinical microbiology, the turnaround time of the diagnostic cycle (>24 hours) often leads to unnecessary suffering and deaths; approaches to relieve this burden include rapid diagnostic procedures and more efficient transmission or interpretation of molecular microbiology results. While genomics-supported PPM generally aims at interrogating the genomic information of a patient, drug metabolism polymorphisms, for example, to guide drug choice and dosage, PPM concepts are applicable in infectious diseases for the rapid identification of a disease-causing microbe and determination of its antimicrobial resistance profile, to guide an appropriate antimicrobial treatment for the proper management of the patient and, in particular, for persons-at-risk. The implementation of point-of-care testing for infectious diseases will require acceptance by medical authorities, new technological and communication platforms, as well as reimbursement practices such that time- and life-saving procedures become available to the largest number of patients.

PPM has indeed arrived for the diagnosis of infectious diseases. More than that, it has arrived once and for all in the areas of clinical microbiology, molecular epidemiology and many other areas. With the current capabilities, cost, and speed of sequencing technologies, the field has finally reached a point where rapid genomic surveillance and analysis can start to become a standard part of the response

to infectious disease outbreaks. Just as broadscale human genome sequencing revolutionized the treatment of many noncommunicable diseases, pathogen genome data are poised to drive a similar revolution in the response to infectious diseases.

Healthcare is undergoing a transformation, and it is imperative to leverage new technologies to support the advent of PPM. This is the reason for developing global scientific, clinical, social, and educational projects in the area of PPM and TraMed to elicit the content of the new trend. The latter would provide a unique platform for dialogue and collaboration among thought leaders and stakeholders in government, academia, industry, foundations, and disease and patient advocacy with an interest in improving the system of healthcare delivery on one hand and drug discovery, development, and translation, on the other one, whilst educating the policy community about issues where biomedical science and policy intersect

Biography

Sergey Suchkov was born in the City of Astrakhan, Russia, in a family of dynasty medical doctors. In 1980, graduated from Astrakhan State Medical University and was awarded with MD. In 1985, Suchkov maintained his PhD as a PhD student of the I.M. Sechenov Moscow Medical Academy and Institute of Medical Enzymology. In 2001, Suchkov maintained his Doctor Degree at the National Institute of Immunology, Russia.

From 1989 through 1995, Dr Suchkov was being a Head of the Lab of Clinical Immunology, Helmholtz Eye Research Institute in Moscow. From 1995 through 2004 - a Chair of the Dept for Clinical Immunology, Moscow Clinical Research Institute (MONIKI). In 1993-1996, Dr Suchkov was a Secretary-in-Chief of the Editorial Board, Biomedical Science, an international journal published jointly by the USSR Academy of Sciences and the Royal Society of Chemistry, UK.

Maria Jose Tintel Astigarraga
Veterinary Pathology, PATHVET, Asunción, Paraguay,
Molecular Biology, FIOCRUZ, Rio de Janeiro, Brazil.

Artemisinin as an antiretroviral alternative for Feline Immunodeficiency Virus (FIV)

VFIV is the only non-primate lentivirus that causes an AIDS-like syndrome, but not always the death of cats. They can live as carriers and transmitters of the disease for many years. The virus's actions depend on the species, coinfections, viral genome, and the age of the host. FIV has the ability to infect CD4 lymphocytes, as well as regulatory T cells, CD8 T lymphocytes and B lymphocytes, monocytes, macrophages, and dendritic cells. This virus

can also be involved in the infection of some CNS cells such as microglia, astrocytes, and cerebral macrophages, causing chronic encephalopathies, resulting in various clinical signs that disrupt the normal development of their functions. The pathophysiology of FIV, like human HIV, focuses on the progressive destruction of the cat's immune system, making it vulnerable to a variety of diseases and secondary complications. FIV primarily affects CD4 T

cells, which are crucial for immune function. Replication of the virus in these cells leads to a decrease in their number and function, as well as alterations in cytokine production and an overactive immune response that can cause inflammation and tissue damage. Several studies in human medicine have revealed a broad spectrum of applications for artemisinin in antitumor, immune regulation, antibacterial, and antiviral functions over the years. The antiviral effects against human HIV consist primarily of inhibiting the activation of cellular transcription factors, interfering with the viral replication cycle, inducing cell apoptosis, and preventing the virus from binding to host cells. Studies on the antiviral effect of artemisinin in humans may provide new insights into combating the emerging feline viral disease for which no effective antiviral drugs are available.

Biography

Veterinary Medicine. Graduated from the National University of Asunción (UNA). Complementary training in the Department of Pathophysiology at the University of the Center of the Province of Buenos Aires (UNICEN). Training in the Veterinary Pathology service at the Paulista State University (UNESP). Postgraduate in Oncohematology in small animals at the Centre for Veterinary Medical Specialties (CEMV). Member of the Argentine Society of Veterinary Oncology (SAOV). Postgraduate Professor in Veterinary Cytology for Veterinarians on the web. Specialist in Veterinary Anatomohistopathological Diagnosis at the National University of the Northeast (UNNE). PhD candidate in Health Sciences, Oswaldo Cruz Foundation (Fiocruz). Founder of the Centre for Veterinary Pathology of Paraguay (PATHVET), responsible for the Department of Pathology. PRONII-CONACYT researcher. Research Line; Vector-Transmitted Diseases (VTE) with several relevant publications and presentations. Author of the books Ehrlichiosis: an Emerging Zoonosis (2017) and Feline Leishmaniasis: often forgotten, other times unknown (2022).

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ORAL SESSION | DAY 1

Lisa Indar * and SasteeKissoondan

Caribbean Public Health Agency, Port of Spain, Trinidad & Tobago

Strengthening Regional Health Security: The Caribbean Public Health Agency's Coordinated Approach to the COVID-19 Pandemic

Background: The Caribbean small-island development states are characterised by its tourism dependence, interconnected, porous borders, under-resourced populations, and varying health and surveillance capacities. Travel/Tourism are key economic drivers yet facilitate the introduction and spread of infectious diseases, providing a conduit for local outbreaks to become pandemics, as the first cases of COVID-19 and its variants were imported.

Method: The Caribbean Public Health Agency (CARPHA) led the regional public health response to COVID-19, as mandated,whichincorporated robust, multi-sectoral collaboration and coordination with Heads of Government, Ministers, health, security, and tourism leads, regional and international entities; provision of surveillance and response, technical guidance, laboratory services, risk communications, resource mobilization, vaccination support, capacity building and instruments to promote tourism recovery and healthier, safer tourism (HST) to its 26 Member States.

Result: CARPHA produced 265 situation reports, 64 technical guidelines, 104 vaccine updates, 11 regional documents, 44 videos, 73 infographics, 78 travel briefs, 136 country reopening plans,175 infographics, trained>14,000 persons; and tested 165,164 samples from 17 CMS (27.38% positive; identification of 3,658 samples with variants of concern). For tourism recovery, CARPHA trained ~9,000 peoplein preventing COVID-19 in the hospitality sector; provided real-time surveillanceandalerts for visitor illnesses in cruise ships (1641 COVID-19 alerts) and accommodation settings (34 alerts; 1001 businesses) that triggered rapid responses; issued 140 HST awards and joint tourism safety communication with tourism entities.

Conclusion: CARPHA implements an integrated, multi-faceted and multi-sectoral response to public health threats, like COVID-19. CARPHA continues to work with countries and partners to strengthen regional health security.

Biography

Dr. Indar is an innovative public health scientist/specialist with 20 years regional and international experience in managing and executing regional public health surveillance and response, with demonstrated, robust leadership, management, coordination, multidisciplinary technical expertise (public health, emergency and response, food safety, environmental health, travellers' health), health diplomacy, communications and resource mobilization skills. She has a Ph.D (with high commendation), MSc (Distinction) and a BSc (Honors).

Dr. Indar currently holds the position of Ad Interim Executive Director of the Caribbean Public Health Agency (CARPHA), as of July 2024, having served in her substantive post of Director, Surveillance, Disease Prevention and Control Division (D-SDPC) for the past four years, and the Assistant D-SDPC prior. Most recently, Dr. Indar, through her stewardship, has successfully led CARPHA through its health responsepost-Hurricane Beryl, regional response to Mpox and COVID-19, and the development and implementation of novel, regional mass gatherings surveillance for the ICC Men's T20 Cricket World Cup (June 2024).

Jessie Caridad Martín Sujo
Research group of Smart Society, La Salle - Ramon Llull University, Barcelona, Spain

Using Hybrid AI Models to Predict COVID-19 Outbreaks and Optimize Regionalized Vaccination Strategies

The COVID-19 pandemic has highlighted the need for effective predictive tools to anticipate outbreaks and optimize vaccine distribution.In this study, a hybrid Long Short-Term Memory (LSTM) and logistic regression model is used to predict COVID-19 outbreaks in Spain.Although a preliminary analysis using ARIMA did not show clear seasonal patterns, the hybrid model achieved an accuracy of 93%.While the initial data showed an unbalanced distribution, when balancing techniques were applied, the overall accuracy decreased to 87%. This reduction is offset by a significant improvement in the ability to correctly identify the absence of outbreaks, which is crucial for planning preventive interventions.It is worth noting that the implemented model allows for the visualization of a risk map by autonomous community, highlighting the areas with the highest probability of outbreaks, which highlights the importance of personalizing vaccination strategies according to regional dynamics. This study demonstrates the value of artificial intelligence in improving vaccination and prevention strategies, highlighting that with more robust data, including information on vaccination coverage for other infectious diseases and demographic and epidemiological variables, the model can be improved and provide key insights for addressing future pandemics.

Biography:

I am a Ph.D. specialized in Natural Language Processing (NLP), with solid research experience and a focus on the cutting edge of Artificial Intelligence. With four years of experience in Data Science, I work as a data analyst, machine learning engineer, and business intelligence analyst. As a programming lecturer in the Healthcare Engineering program, I am passionate about exploring challenges in the healthcare field, applying my knowledge of NLP, machine learning, and programming to develop innovative solutions that optimize processes and analytics in the healthcare sector.

Benson Jacob*, Anumol Kurian, Eoghan de Barra
International Health and Tropical Medicine, Royal College of Surgeons in Ireland, Dublin, Ireland.

Understanding what matters to patients in antimicrobial stewardship in hospitals. PERSPECT study update.

Background: There is a growing consensus that the involvement of patients in healthcare-based research and as equal partners in healthcare decision-making enhances their opportunity to improve service and outcomes. Our research is focused on the patient perspective in the successful implementation of antimicrobial stewardship in a hospital set-up with the following objectives.
To explore patient knowledge, understanding and perceptions of antimicrobial resistance and the role of patients in AMS (Antimicrobial Stewardship)
To identify barriers and facilitators of patient engagement in AMS programmes.

Methods: A questionnaire survey using previously validated questions on antimicrobial resistance and stewardship was conducted among 360 hospitalised patients from six patient groups (Cystic fibrosis, Haematology/Oncology, Bone and joint infection, Renal, Outpatient parenteral antibiotic therapy (OPAT), general Infectious Disease). Sixty patients from each group were recruited using purposive sampling. Quantitative data were analysed using descriptive analysis. 36 semi-structured interviews were conducted followed by the questionnaire survey and the qualitative data were analysed using NVIVO.

Results: Male participants made up 56% (n=202), female participants made up 43% (n=156), and 1% (n=3) chose not to respond. Most respondents were from the 20-55 age group (84%).
93% had never heard the term “antimicrobial stewardship” but showed an understanding and awareness of antimicrobial resistance. 56% reported receiving advice from the doctor when prescribed antibiotics. Preference for approaching healthcare professionals with antibiotic treatment questions was doctors 67%, nurses 21% and pharmacists 12%. Overall, 87% responded that they would complete the entire prescribed course of antibiotics even if they felt better after taking 2-3 doses; this figure rose to 94% among the cystic fibrosis group.
68% of respondents were happy to ask the doctor questions about the type of infection they were being treated for and the risk involved in receiving antibiotics, with the cystic fibrosis and OPAT groups leading this list with 83% and 82%, respectively.

Conclusion: Patients appear to have a good understanding of AMR and are open to discussing infection treatment plans with healthcare professionals, though they may not be familiar with the terminology used. The next phase of our study will use qualitative methods to explore how patients might have a role to play in AMS.

Biography

I work as an infectious disease clinical Research Nurse Manager at Beaumont Hospital, Dublin. I am a second-year PhD student at the Royal College of Surgeons in Ireland. I received the Irish Research Council fellowship in 2023 for this PhD project.
I have a master's degree in public health and clinical and translational research and a professional diploma in health economics apart from a bachelor's degree in nursing.
I have enormous experience in working and coordinating observational studies, clinical trials and biobank studies related to infectious diseases.

Andjelka Stojkovic
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[2]Department of Paediatrics, Faculty of Medical Sciences, University of Kragujevac, Kragujevac, Serbia

Level of Prevention of RSV Infection in Infants

Respiratory syncytial virus (RSV) is a significant health problem worldwide, especially in children younger than 6 months. RSV is not recognized by cytotoxic T-lymphocytes, or there is a polymorphism for interleukin-10, or there is a deficient production of interferon (INF)-beta or there is a cross-reaction between elevated immunoglobulin-E and downregulation of INF-alpha due to high expression of the receptor (FcεRIα) on dendritic cells, due to which prolonged ciliary damage and corticosteroid-resistant airway inflammation are manifested. The previous prevention with a humanized IgG1k monoclonal antibody (Palivizumab) was expensive and provided short-term immunoprophylaxis with a half-life of 2–3 weeks, which is why five doses were administered over five consecutive months and were administered to children from risk groups, primarily premature infants under 35 weeks of gestational age with accompanying disease. Modern technology has enabled the production of a humanized IgG1k monoclonal antibody (Nirsevimab), which achieves a half-life of 71 days with one intramuscular injection at the beginning of the season and can be used in all children up to five years of age, which achieves more comprehensive protection against RSV infection, prolonged for a longer period in the first and second years of life. Expansion of the Nirsevimab immunization calendar is currently being considered in many countries around the world. Immunoprophylaxis of pregnant women with “vaccine for mothers” provides a lower level of protection of infants against RSV infection compared to Nirsevimab. In addition to immunoprophylaxis against RSV, hygienic measures to protect against respiratory virus infection, isolation of patients with RSV infection, control of cross-transmission of viral and atypical infections in hospital and non-hospital environments, and testing with a rapid test at the beginning of the RSV season are carried out. Treatment of children suffering from RSV infection is symptomatic and in accordance with the severity of the clinical picture (mild to severe respiratory insufficiency).

Biography

Andjelka Stojkovic is a full professor of the Faculty of Medical Sciences at the University of Kragujevac and a member of the Department of Pediatrics. She is the Head of Department for pulmonology, allergology, and clinical immunology, and in a previous mandate, she was the Director of the Clinic for Pediatrics in the University Clinical Centre. She is a member of several domestic (SMS) and international (ERS, EAACI, ECFS) professional associations in the field of paediatrics, pulmonology, and allergology. She holds a diploma from the Serbian Medical Society (SMS). She serves as a member of the presidency of the Paediatric Assembly of Serbia and the Association for Preventive Paediatrics of Serbia. Currently, her research interests are in the domains of paediatric asthma, allergic diseases in children, respiratory infections, use of probiotics, hypovitaminosis D, inhalation therapy in children, benefits of the vaccination program for children in Serbia, rare respiratory diseases, particularly cystic fibrosis in children, and nitric oxide therapy in newborns. He is the author of the monograph “Phenotypes of Asthma in Children” and is preparing a second monograph on the prevention of diseases associated with the “atopic march”.

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KEYNOTE SESSIONS 02 | DAY 1

Joao Paulo Tardivo[1]* and Mauricio S Baptista[2]

[1]Department of Vascular Surgery, Centro Universitário, Faculdade de Medicina do ABC – Brazil.

[2]Institute of Chemistry, Universidade de São Paulo -SP – Brazil.

Diabetic Foot Ulcer & Photodynamic Therapy: Tardivo Protocol with High Salvage Rate

Background data: Saving an infected diabetic foot has been a significant challenge throughout medical history. The high amputation rates among diabetes patients in various countries confirm this reality. Additionally, microbial resistance to antibiotics makes this syndrome increasingly difficult to treat, severely impacting the quality of life for diabetics.Poorly controlled diabetes over the years causes significant damage to the entire circulatory system. When poor peripheral blood perfusion is associated with an infected diabetic foot ulcer, the chances of saving the foot decrease even further.

Objective: Drastically reduce the number of amputations in diabetic patients.

Materials and methods: To address this challenge, we created the **Tardivo Algorithm**, an easy-to-apply tool that identifies and classifies the diabetic foot, assigning a risk score and guiding the best clinical or surgical management.

Most cases that arrive at healthcare facilities already present some degree of infection. In these situations, **Photodynamic Therapy** plays a fundamental role in treatment, combating localized infection in ulcers, both superficial and deep and eliminates development of resistance. Additionally, this therapy treats osteomyelitis and often restores the bone tissue itself, avoiding major surgical debridement. Generally, treatment is performed on an outpatient basis.

Results: Published studies show that the Tardivo Algorithm is very effective to cure the diabetic feet. 85.5% of the diabetes patient with score equal or smaller than 12 presented avoided amputation. This method was evaluated and validated by the IWGDF, Venezuela and Indonesia. Other publications demonstrate excellent results with the use of Photodynamic Therapy, not only in Brazil but also in Italy and China, where the method is considered promising.

Conclusion: Tardivo Protocol prevented rescue in 85% of diabetic feet.The most important aspect is the improvement in the quality of life for these patients and their families.

Biography

He graduated with a degree in medicine from the ABC Medical School in 1976. He completed a Specialization in Medical Residency in the areas of general surgery and clinical angiology from 1977 to 1982. He obtained the title of Specialist in Angiology and Vascular Surgery granted by the Brazilian Medical Association. He holds a PhD and Master's degree in Health Sciences from the ABC Medical School and has been researching lasers since 1988, when he was the Founding Medical Director of the Medical Center for Laser Studies and Treatment, emphasizing clinical applications. Since 1999, he has been conducting experimental and clinical studies in photodynamic therapy, where he was responsible for developing a low-cost light source, the RL50, enabling its application in public health. He has developed methods for treating wounds, herpes, onychomycosis, and infected wounds in diabetic feet with photodynamic therapy. He was an associate professor of vascular surgery at FMABC until 2023. He currently works as a vascular surgeon and coordinator of the diabetic foot outpatient clinic at Hospital de Clínicas de São Bernardo do Campo and clinical director at Centro de Medicina Tardivo&Tardivo.

Migena Qato*,Najada Como, Esta Kokla, Suada Sulaj
Mother Teresa Hospital, Tirana, Albania.

West Nile Virus Infection, An Update on Epidemiological, Clinical and Diagnostic Data in Albanian Adults

Introduction: West Nile Virus (WNV) is a re-emerging pathogen, whose natural cycle can lead to an accidental infection of humans. The vast majority of WNV infections are asymptomatic. However, a significant number of patients present with a flu-like clinical presentation, while a small percentage, especially the elderly or immunosuppressed subjects, present the most severe form of this infection: Neuroinvasive Disease.

Objective: Highlighting our experience during the outbreak of West Nile Virus (WNV) Infection in Albanina adults and evidence epidemiologicsl clinical, laboratory and neuroimaging characteristics of WNV Neuroinvasive Disease.

Material and methods: We collected epidemiological, clinical and diagnostic data from a total of 84 patients hospitalized in the Infectious Diseases Service in the period July-September 2024. The diagnosis was determined by the detection of antibodies in CSF, serum and/or urine.

Results: Epidemiological The study included 84 cases, males 66.7%, females 33.3%. The average age was 68 years and the most affected age group was 71 years-80 years (42.8%) and 61-71 years (29.76%). The majority of patients were residents of the areas of Lushnja 18, Fier 14, Tirana 11 & Berat 8. Clinical The most frequent symptom was fever 96.7% (Continuous/intense fever in 52 in 16 cases , continuous/high in 36 and Intermittent high in 32 cases), altered consciousness 55.9%, headache 25%, asthenia 47.61% and nausea/vomiting 16.66%. Co-existing pathologies which were also identified as risk factors resulted in: HTA 50, IKK 2, SRK 3, POST AVC 4, D.Mellitus 30, HIV 1Laboratory Inhemocytograms and biochemical analysis, significant alterations stood out: leukopenia 2.3%, lymphocytosis 77.3%, thrombocytopenia 26.19% and thrombocytosis 3.5%. Elevated LDH in 53.5%, CK 46.4%, Hepatic enzymes ALT 63.1%, AST 72.6%. Inflammatory tests showed an increase in all patients: PCR in 78.57% of cases, Fibrinogen 48.80%, Ferritinemia 36.90%. Antibodies to WNV were detected in CSF in 53.57% of patients, in serum 91.66% and urine 44%. Imaging showed cerebral edema in 53 cases, chronic hypodensity in 5, cerebral atrophy in 29

Conclusion: Although severe clinical forms of WNV infection are rare, theydhould be considered statistically significant, considering the morbidity and mortality associated with it.

Biography

Dr. Migena Qato is a board-certified Infectious Disease Specialist and holds a PhD in Medical Sciences. She completed her residency in Infectious Diseases at the University Hospital for Infectious Diseases, QSUT, from 2008 to 2012. Alongside her clinical work, she serves as a lecturer in the Department of Infectious Diseases at the University of Medicine in Tirana.
Dr. Qato has authored and co-authored numerous scientific articles published in both national and international journals, including Medico Research Chronicles, ENCEP, the Albanian Medical Journal etc.Her scientific contributions span a wide range of topics in infectious diseases, with active participation in international and national conferences.

Infectious Disease Specialist, University Hospital "Mother Teresa" (QSUT), Tirana, Albania
Lecturer, Department of Infectious Diseases, Faculty of Medicine, University of Medicine, Tirana

Dr. Qato is fluent in English and Italian and is known for her clear communication and engaging speaking style. She brings both academic depth and practical clinical insight to her presentations, making her a valued contributor in the field of infectious diseases.

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ORAL SESSIONS 2 | DAY 1

Kefeng Qin

Department of Infectious diseases, Huzhou Central Hospital, Affiliated Huzhou Hospital of Zhejiang University Medical School. Huzhou, Zhejiang, China

Multiple immune responses to acute respiratory virus infections following the Covid-19 pandemic

Following COVID-19 pandemic caused by SARS-COV-2, the phenomenon of immune debt has emerged worldwide, significantly changing the epidemiological of respiratory infections. Acute respiratory viral infections (ARVIs) are the leading cause of morbidity and mortality in children worldwide and have a significant impact on the health of adult patients. The post-COVID-19 model of ARVI remains largely unstudied internationally. In order to study the epidemiology of ARVI in the second year after the COVID-19 pandemic, we examined the ethology of patients with fever in our hospital from June to August 2024.Among the total 12,108 febrile patients, 5,734 (47.4%) were males, 6,373 (52.6%) females, 4,803 (39.7%) children (aged ≤ 12 years), and 7,303 (60.3%) adults (aged ≥ 13 years). The total number of patients who were positive for 7 pathogens was 7,167 (59.2%),including 2,094 cases (17.3%) of adenovirus (ADV), 1,295 (10.7%) of human rhinovirus (HRV), 984 (8.1%) of Mycoplasma pneumoniae (MP), 2,433 (20.1%) of SARS-COV-2, and 349 (2.9%) of influenza A virus (IAV). There were 3 cases of influenza B virus (IBV) and 9 cases of respiratory syncytial virus (RSV). There is also co-infection with some pathogens.ADV and SARS-COV-2 infections account for a large proportion. There is also co-infection with some pathogens.We have further analysed the distribution of cases in ARVI patients in the 13 weeks from June 1 to August 31, 2024, and found that during the week of July 21-27, there was a spike in febrile patients, which was mainly due to the outbreak of SARS-COV-2 infection. Other pathogens, including ADV, HRV,MP, and IAV, were circulating at low levels and did not record a new peak of infection. Multiplex immunoassays were performed on the plasma of patients with positive nucleic acid or co-infection of 7 pathogens, nucleic acid negative patient with fever and health volunteers.The concentration level data of 48 factors ofimmunity and inflammation were obtained. The data were analysed using ANOVA and post-hoc Tuley HSD test, and it was found that pathogen infection led to changes in the levels of some factors. The immune or inflammation reactions were divided into three groups. Levels of CTACK, G-CSF,IFN-a2, IL-1ra, IL-4, IL-6, IL-12p40, MIF,MIP-1b, SCGF-b, TRAIL orVEGF presented with very significant differences in different pathogen infections ($P<0.01$). Levels of GRO-a, HGF, IL-1a, IL-2Ra, IL-9, IP-10, MIG or TNF-b were increased when patients with fever but nosignificantdifferences between different pathogen infections($P<0.01$). Levels of Eotaxin, FGF, GM-CSF, IFN-g, IL-1b, IL-2, IL-3, IL-5, IL-7, IL-8, IL-10, IL-12(p70), IL-13, IL-15, IL-16, IL-17,

IL-18, LIF, MCP-1, MCP-3, b-NGF, PDGF-bb, RANTES orSCFdid not change with significant differences with different pathogen infections (P>0.05).Based on these results, we have found that the epidemiological and immune response profile of ARVI is unique and complicated. Our finding would helpthe clinical manifestations and management strategies.

Biography

Kefeng Qin, MD, PhD, is professor and Chief Scientist in Huzhou Central Hospital, the affiliated Huzhou hospital Zhejiang University School of Medicine. He has been working in NIH, University of Toronto, Northwestern University, University of Maryland and University of Chicago as a scientist in the field of virology, including HSV, HIV and SARS-COV-2 research, and neurodegenerative diseases, including prion, doppel and Alzheimer's disease. Researchpapers have been published in Nature, JBC, JNS, etc.

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Precision Genome-driven Epidemiology and Biostatistics for Infectious Disease Control

Policy formation in the field of individual health promotion and protection is one of the priority tasks of national healthcare systems. Canonical health care is becoming increasingly unaffordable in most of the countries, yet it remains ineffective in preventing or effectively treating chronic diseases (including infectious ones). The medicine of the XXI century is ***Personalized & Precision Medicine (PPM)***, by protecting and preserving human health throughout the life. In this regard, an upgraded model of healthcare service, which includes the philosophy, principles and armamentarium of PPM and aimed at identifying the disorder at its early (subclinical) stage, is being created and set up.

PPM focuses on predictive and preventive measures that contribute to the development of individualized strategies for managing a healthy lifestyle that stabilize morbidity rates and can help to improve the working capacity of the population.PPM provides procedures for disease prediction and for the prediction of consequences and complications. In this regard, the biomarker-based analysis is intended as a first step towards a more personalized and precision treatment and clinical utility.

Advances in genomics and computing are transforming the capacity for the characterization of biosystems, and practitioners are now poised for a precision-focused transformation in the way they prepare for, and respond to, infectious diseases. In addition, advances in the speed and granularity of pathogen genome generation have improved the capability to track and understand pathogen transmission, leading to potential improvements in the design and implementation of population-level

public health interventions.

Meanwhile, despite being a forerunner PPM is not yet routinely applied in infectious patient care. Since, for instance, with the increase in antimicrobial agent resistance and a decreasing antimicrobial pipeline, there is a need for coordinated efforts to promote appropriate use of antimicrobial agents. Such “antimicrobial agent stewardship” measures encourage the appropriate use of antimicrobials by promoting the selection of the optimal drug regimen. PPM can help solve the crisis of antimicrobial resistance (AMR) by changing the way antimicrobial agents are developed and prescribed.

One thing is clear, as we embark into an era of increasing antimicrobial resistance coupled with the routine use of advanced immune modulating agents delivering deep, potent immune suppression, the role of PPM to better understand the clinical outcomes of infectious complications becomes more critical. Efforts to fund and support this nature of clinical and translational research is imperative. Finally, research into personalized medicine will serve as the foundation to develop cellular and immunotherapies specific for infectious pathogens.

For this scope, the next step PPM-oriented and driven education is a crucial step for the successful implementation of PPM in the clinical applications in infectious diseases, and with this part, we would like to encourage learning about PPM in the communicable disease field.

Additionally, new biodesign-driven technologies are supporting the rapid identification of infective agents and targeted approaches based on the genetic resistance of pathogens to antibiotics. This information can lead to revising the data that can be used for personalized predicting diseases, improving the usage of precision biomarkers and personalized treatment, and also personalized prevention strategies specific to infectious pathogens.

Improved patient (or persons-at-risk) outcomes with the application of the above-mentioned biomarker tests must consider not only increased survival or quality of life, but also improved ***clinical decision support (CDS) & making*** leading to the avoidance of unnecessary therapy or toxicity captured within the rapid learning system.

Opportunities exist at every stage of disease initiation and progression to develop a ***Personalized Health Plan(PHP)*** addressing lifestyle, risk modification and disease management, and later, ***Personalized Health Management & Wellness Program (PHM&WP).***So, a combination of genomic and phenome-related biomarkers is becoming of great significance to be applied in PPM and need to be translated into the daily practice to predict risks of the disease chronification and thus of disabling.

Meanwhile, advances in biomedical informatics and IT technologies brought on and suiting the goal by applying mathematical modeling to secure constructing and maintaining unified biobanks and databanks necessary for personal health monitoring, for instance, by the increasing availability of electronic medical records (EMRs), electronic patient registry (EPR, telemedicine and mHealth tools and cloudy technologies have allowed for the proliferation of data-centric tools and inter-hospital network communications armamentarium, especially in the context of ***personalized & precision healthcare (PPH).***

Advances in genomics and computing are transforming the capacity for the characterization of biological systems. The set would include the use of genome-based approaches to inform molecular diagnosis and individual-level treatment regimens. In addition, advances in the speed and granularity of pathogen genome generation have improved the capability to track and understand pathogen transmission, leading to potential improvements in the design and implementation of population-level public health interventions. So, we outline several trends that are driving the development of PPM-based epidemiology of infectious disease and their implications for the ability to respond to outbreaks.

Going beyond the detection of the pathogen is crucial to transforming the diagnosis of microbial infections. Consideration of the evolutionary and ecological principles between the host and their microbiome might provide "new strategies for restoring and maintaining human health." Innovative diagnostics that can identify host, microbiome, environmental and pathogen biomarkers are crucial to PPM-based approach. That Big Data can then be used to design optimal therapeutic strategies for patients that can restore them to health by coordinating agents that can target the pathogen, the host and the microbiome thereby intervening appropriately in the ecological balance in the patient. These strategies bring us a step closer to developing personalized therapies that exclusively remove disease-causing infectious agents. And we would advocate the preservation of our beneficial microbes and provide an overview of promising alternatives to broad-spectrum antimicrobials. Specifically, we emphasize that the newest approaches can not only improve patient care, but preserve antimicrobial agents for the future. We can advance directly to the phase of preclinical validation of disease biomarkers and their underlying mechanisms, and the results can be translated into precision diagnosis enabling patient stratification for individualized therapy. Taken together, the activities proposed will demonstrate the clinical feasibility and advantages of PPM in managing chronic and acute infectious diseases.

As you might see from the above-mentioned, PPM has drastically changed and is keeping on changing the landscape of healthcare. In reality, PPM is the new revolution in medicine which is dramatically modifying the traditional paradigm in medicine with huge consequences for health care systems. And putting PPM-tools in a public health perspective requires an apprehension of the current and future public health challenges.

A symbiotic relationship between infectious diseases, their risks, epidemiological studies, public health and PPM may exist. In this sense, accurate diagnosis of malaria and the resilient capacity that the malaria parasite has in acquiring resistance to anti-malarial drugs (based on the phenotypic variations) form immediate barriers to the control and elimination of this disease. Those variations mentioned could be dependent on geo location or differential transmission setting or even the different ring developmental stage. So, PPM-based and driven OMICS- and IT-armamentarium would secure the advances in spectroscopic-based technologies which is able to reveal unique 'molecular fingerprint', and thus providing the much needed rapid phenotyping (rather than genotyping) platform in the field.

Moreover, PPM could help to improve precision diagnosis and individualized treatment of asthma, whilst determining some specific strategies for probing the situation in the tropics with special conditions to be considered for applying this strategy. The clinical impact of the advances in PPM for asthma in the tropics is mainly related to component resolved diagnosis, and would need to be improved

via identification of the biomarkers of the next step generation (including interactome- and network-related ones) that allow and accurate definition of phenotypes and endotypes of this heterogeneous disease to secure the proper choice pf personalized treatments.

These examples show how PPM-driven approach to wildlife health has in turn the potential to provide deeper insights into human health and the possibility of stemming and alleviating the impacts of parasite-induced diseases. The integration of the currently emerging PPM-related Initiative with the concepts of EcoHealth and One Health has great potential to deliver a deeper and broader interdisciplinary-based understanding of both wildlife and human parazyte-provoked and infectious diseases.

So, PPM has indeed arrived for the diagnosis of infectious diseases. More than that, it has arrived once and for all in the areas of clinical microbiology, molecular epidemiology and many other areas. Epidemics of the most diverse viruses will continue to occur due to factors that we are not completely able to control. The difference now is that we have powerful PPM-based technologies and tools to win this fight. In this connection, the healthcare providers, public policy sector, and consumer industries will be required to develop new and creative models and products. And, no doubt, next generations will speak about the XXI century as a time, when medicine became preventive and personalized, and its outcomes – predictive and guarantied.

Biography

Sergey Suchkov was born in the City of Astrakhan, Russia, in a family of dynasty medical doctors. In 1980, graduated from Astrakhan State Medical University and was awarded with MD. In 1985, Suchkov maintained his PhD as a PhD student of the I.M. Sechenov Moscow Medical Academy and Institute of Medical Enzymology. In 2001, Suchkov maintained his Doctor Degree at the National Institute of Immunology, Russia.

From 1989 through 1995, Dr Suchkov was being a Head of the Lab of Clinical Immunology, Helmholtz Eye Research Institute in Moscow. From 1995 through 2004 - a Chair of the Dept for Clinical Immunology, Moscow Clinical Research Institute (MONIKI). In 1993-1996, Dr Suchkov was a Secretary-in-Chief of the Editorial Board, Biomedical Science, an international journal published jointly by the USSR Academy of Sciences and the Royal Society of Chemistry, UK.

Semra Soydam*, Gamze Varan, Buse Türegün Atasoy, Serhat Ünal

Vaccine Institute, Hacettepe University, Ankara, Turkey

Limitations of BCG and Booster Vaccine Research

STuberculosis (TB) is an infectious disease that primarily affects the lungs. TB is transmitted from person to person through the air. Individuals with pulmonary TB release *Mycobacterium tuberculosis* bacilli into the air when they cough, sneeze, or spit. Inhaling just a few of these bacilli is enough for a person to become infected. Approximately one-quarter of the world's population is estimated to harbor a latent TB infection. People infected with the tuberculosis bacterium have a lifetime risk of developing active TB disease of about 5–10%. Immune-weakening factors such as HIV, malnutrition, diabetes, or tobacco use significantly escalate the risk of disease.

Bacillus Calmette–Guérin (BCG) is the only currently licensed vaccine against tuberculosis and is included in routine vaccination programs in around 180 countries. BCG, a live-attenuated strain of Mycobacterium bovis isolated from cattle, has been the sole licensed vaccine to significantly contribute to TB control for over 80 years. It is administered in many countries as part of standard childhood immunization schedules. While BCG is estimated to provide approximately 80% protection against TB meningitis and miliary TB in infants and young children, it is not effective as a therapeutic vaccine for latent infection. Moreover, its efficacy against pulmonary TB is limited, and a second booster dose administered during school age has not been shown to confer additional protection.TB remains particularly dangerous for individuals infected with Human Immunodeficiency Virus (HIV) or those with suppressed immune systems, where morbidity and mortality rates are exceedingly high.

According to WHO, despite global vaccination efforts, approximately 1.7 million people die from tuberculosis every year. TB remains among the top 10 causes of death worldwide and is the second leading infectious killer, only behind COVID-19 and ahead of HIV/AIDS. The emergence of multidrug-resistant TB (MDR-TB) and extensively drug-resistant TB (XDR-TB)—caused by strains resistant to first-line treatments like isoniazid and rifampicin—has made treatment of advanced disease increasingly difficult.

In this presentation, we will present an overview of ongoing booster vaccine development efforts for the treatment of tuberculosis, followed by a summary of the research conducted at the Hacettepe Vaccine Institute.

Biography

After graduating from the Department of Biology, Faculty of Science, Anadolu University in 2004, she worked as a Research Assistant at the Department of Biology, Ankara University until 2011, and as an Assistant Professor at Niğde University between 2011 and 2013. Between 2013 and 2019, she worked on the potency analyses of vaccines, blood products, and monoclonal antibodies at the Biotechnological Products Laboratory Unit of the Turkish Medicines and Medical Devices Agency, Ministry of Health. Since 2019, she has been a faculty member in the Department of Vaccine Technology, Vaccine Institute, Hacettepe University. She continues to work on Vaccine Technology, Recombinant Production, Molecular Diagnostic Methods, Biotechnology, and Cell-Based Identity and Potency Analyses.

Zhiqiang Cao*, Dan Zhao, Xiaojing Wen, Ying Ma, Xiaomei Li, Luodan Suo
Beijing Center for Disease Prevention and Control, Beijing Research Center for Respiratory Infectious Diseases, School of Public Health, Capital Medical University, China.

Incremental Effectiveness of Emergency Vaccination against Varicella Outbreak at an Elementary School in Beijing, China, 2019: An Observational Cohort Study

Background: The effect of varicella emergency vaccination (EV) has not been fully evaluated. Meta-analysis on the vaccine effectiveness of varicella EV for controlling outbreaks shows significant heterogeneity, with effectiveness ranging from 0% to 92% for the first dose as EV and from 0% to 89% for the second dose as EV. This poses a challenge for the use and evaluation of EV in the event of a varicella outbreak.

Methods: We conducted an observational cohort study on the impact of EV on the varicella incidence rate in a primary school in Beijing where a disease outbreak occurred. Participants were categorized into five groups based on their immune status: Unvaccinated group, First Dose as EV group, One Dose no-EV group, Second Dose as EV group and Two Doses group. Incidence rate of varicella was calculated by person-time according to different immunization statuses. Multivariate Cox proportional hazards models were applied to assess the effectiveness of the varicella vaccination on disease incidence rate among those students. EV status was treated as time-dependent covariate. For students who received a first-dose as EV or second-dose as EV, disease exposure was quantitatively assessed separately for the time period before and after their transition to vaccinated status. To account for confounding factors, baseline characteristics such as sex, grade, and interval between immunization history and risk exposure were included as control variables in the multivariate analysis. The incremental effectiveness of EV was further examined, limited on the students with classroom exposure for the sensitive analysis.

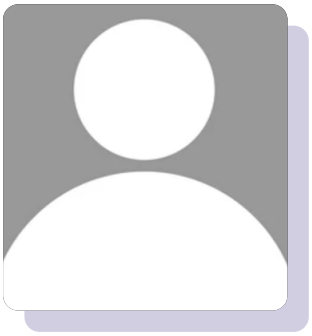
Results: Demographic characteristics, vaccination details, and disease onset information were 100% (918/918) collected. The crude attack rate was 44% (11/25), 8% (3/36), 11% (24/215), 3% (6/176) and 2% (8/466) among Unvaccinated group, First Dose as EV group, One Dose no-EV group, Second Dose as EV group and Two Doses group, respectively. Compared to the Unvaccinated group and One Dose no-EV group, the first dose varicella vaccine as EV and the second dose as EV offered incremental effectiveness of 90% (95% CI 65%–97%) and 79% (95% CI 47%–92%), respectively.

Conclusions: Both the first dose and the second dose as EV contributed to lower rates of varicella incidence and offered incremental vaccine effectiveness in an outbreak setting. Our study underscores the importance and benefits of initiating emergency varicella vaccination early to reduce the disease

incidence rate in an elementary school setting where there was no complete coverage of the two doses of varicella vaccine and an outbreak occurred.

Biography:

Dr. Cao is a Research Scientist at the Immunization Prevention Institute, Beijing CDC, holding an M.D. and Ph.D. in Epidemiology and Medical Statistics from China CDC. His research focuses on vaccine-preventable diseases and population vaccination coverage. Dr. Cao's expertise spans population cohort studies, clinical trial statistical analysis, viral variation and evolution, and real world epidemiology studies. He applies advanced statistical methodologies to immunization program data, generating evidence to strengthen public health strategies. Driven by a commitment to disease prevention, his work translates complex epidemiological findings into actionable insights for optimizing vaccine policy and improving population health outcomes.



Stephen Jeffrey Dollery
Biological Mimetics, Inc, USA

UVC-MDP: A Radiation-Shielded Inactivation Platform for Potent, Safe, and Scalable Whole-Microbe Vaccines

Despite the success of OPV and IPV in suppressing poliomyelitis, both approaches carry intrinsic limitations that complicate the endgame of eradication: OPV's risk of reversion to vaccine-derived disease and IPV's reliance on neuropathogenic strains with associated biosecurity, cost, and supply constraints. We present a unifying inactivation platform—Ultraviolet-C with manganese–decapeptide–phosphate (UVC-MDP)—that preserves conformational epitopes during irradiation and enables safe, high-yield production of whole-virion and whole-cell vaccines. Using this chemistry, we generate ultraIPV™ from attenuated polioviruses and demonstrate three key attributes relevant to eradication: (i) complete inactivation, eliminating risk of vaccine-associated disease; (ii) compatibility with non-pathogenic/attenuated strains, reducing biocontainment burden; and (iii) markedly increased doses per milligram of input virus, with antigenicity retained after freeze–thaw, supporting resilient, lower-cost manufacturing.

To test breadth beyond polio, we apply UVC-MDP (and, for comparison, γ-irradiation) to Acinetobacter baumannii, a WHO priority pathogen. In a neutropenic murine pulmonary challenge with virulent AB5075, both inactivated whole-cell candidates protect against lethal infection; passive transfer of immune sera recapitulates protection, indicating sufficiency of humoral immunity. Extending platform generality, we produce MRSA whole-cell immunogens and evaluate them in a stringent tibia-implant model. Vaccination drives high levels of bacterial clearance, and protection correlates with the retained protein-antigen profile of the inactivated preparations, consistent with the platform's epitope-preserving mechanism.

Collectively, these data position UVC-MDP as a versatile, manufacturable technology for vaccines where traditional attenuation or chemical inactivation degrade protective epitopes. The platform directly addresses eradication needs for polio (safety, supply, cost), while enabling rapid prototyping against drug-resistant bacteria. We will discuss mechanism, quality-control assays for confirming complete inactivation and epitope integrity, and a translational path that emphasizes scalable production, reduced biosecurity risk, and equitable access. Take-home: irradiation guided by biochemical radioprotectants can unlock whole-microbe vaccines that are safer to make, cheaper to scale, and more protective in vivo.

Biography:

Stephen J. Dollery, Ph.D. is a Staff Scientist at BMI where he leads research in multiple fields. To advance his goal of improving global health, Dr. Dollery applies his expertise in molecular structure, molecular biology and immunology to lead several vaccine and diagnostic projects and to direct funding and development efforts. Dr. Dollery has been the Principal Investigator on the Company's NIH-NIAID SBIR grant entitled, "Whole-cell Vaccine Development lt blue sq2for MRSA." Dr. Dollery is a renowned expert in the mechanisms of viral entry has been the first author on six peer-reviewed scientific publications in the past four years alone. Dr Dollery is deeply involved with developing the companies "ultra" and immune-refocused vaccine platforms (A. baumannii, polio, influenza) and diagnostics (HPV, malaria, Leishmania).

Dr. Dollery received his doctorate in Microbiology and Immunology while studying the virus entry pathways of human herpesviruses. He continued training, and was then employed by, the NIH as a postdoctoral researcher and then a fellow in the Molecular Structure Section of the Laboratory of Viral Diseases

Joint Event on

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17-19 October 2025

POSTER | DAY 1

Vassiliki C. Pitiriga[1]*, Myrto Papamentzelopoulou[2], Dimitrios Nikoloudis[3], Kanella E. Konstantinakou[3], Irene V. Vasileiou,[3] Konstantina S. Sakellariou,[3] Natalia I. Spyrou[3] and Athanasios Tsakris[1]

[1] Department of Microbiology, Medical School, National and Kapodistrian University of Athens, Athens, Greece.
[2] Molecular Biology Unit, 1st Department of Obstetrics and Gynecology, National and Kapodistrian University of Athens, Athens, Greece.
[3] Bioiatriki Healthcare Group, Kifisias and Papada Street, Athens, Greece.

Comparison of Levels and Duration of T Cell Immunity Between Vaccinated COVID 19 Naïve Individuals with and Without Detectable IgG Antibody Levels

Background: The essential management of vaccination schedules requires a thorough knowledge and measurement of the individual's immunoprotection level, interaction and persistency at both humoral and cellular levels following SARS-CoV-2 vaccination.

The goal of this study was to investigate the possible relationship between the levels and duration of SARS-CoV-2 T cell response and IgG measurements in a particular cohort consisting of individuals who were COVID-19 naive and had received SARS-CoV-2 vaccination.

Methods: We performed a retrospective descriptive analysis utilizing data retrieved from the electronic medical records of consecutive COVID 19 naïve and vaccinated adult individuals who underwent COVID-19 immunity screening at BIOIATRIKI private healthcare center from September 2021 to September 2022. T-cell response was evaluated using the IGRA methodology T-SPOT®.COVID (Oxford Immunotec, Oxfordshire, UK). SARS-CoV-2 IgG antibody levels were evaluated with SARS-CoV-2 IgG II Quant assay (Abbott Laboratories).

Results: A cohort of 262 individuals, comprising 148 females (56.5%) and 114 males (43.5%), with ages ranging from 17 to 92 years (mean age: 59.47±15.5 years) were included in the study.

The mean time elapsed post-exposure/vaccination for all participants was 137.12 ± 78.7 days (range: 14-364 days). Individuals with a positive antibody response demonstrated statistically significant higher T-SPOT results compared to those with undetectable antibody levels. Specifically, the mean rank was 125.7 in set A and 158.73 in group B (Mann-Whitney Test, p=0.006). No significant difference

was observed between the two groups in the time period post-vaccination, with mean times after vaccination being 136.38±78.68 days in group A and 140.6±79.5 days in group B (T test, p=0.74).

Conclusions: Our findings indicate that the activation of humoral immunity following SARS-CoV-2 vaccination is associated with higher levels of produced cellular immunity compared to low or undetectable antibody levels.

Biography:

Experienced academic and healthcare leader with 20+ years in Medical Microbiology, specializing in clinical diagnostics, antimicrobial resistance, and healthcare-associated infections. Associate Professor at NKUA's Medical School, teaching and mentoring students since 2009. Published 52 papers with 1,587 citations and an h-index of 24 (Scopus, 2024). Held key leadership roles in hospitals and biomedicine organizations. Passionate about advancing clinical microbiology, infection control, and medical education through research, innovation, and collaborative teamwork in academia and healthcare.

Maria Lucia Brito Ferreira*, Livia Brito Bezerra de Albuquerque, Maria Iris Moraes Machado. Vanessa Cristina Fragoso Cassiano Alencar, Bruno Paulo Teles Chaves, Mauricea Novaes Costa Pereira, Marcilio José de Oliveira Filho, Nathalia Saraiva Ramos Cruz, Norma Lucena Cavalcanti Licínio da Silva

University of Liverpool - Royal University, Brazil

Challenge for diagnosing emerging and remerging viral infections of Central Nervous System - a Brazilian Northeast Reference Center experience

Objectives: To present diagnosticsand discuss probable mechanisms ofemerging and remerging viral infectionsat the Reference Center in a public Brazilian Northeast hospital.

Methods: We diagnosed patients, using neurological examination, magnetic resonance image, serological and spinal fluid viral biomarkers identification, from 2014 to 2024.This research has been approved by Oswaldo Cruz Foundation, Institute Aggeu Magalhaes Ethics Committee registered as CAAE nº 511.06.115.8.000.5190.

Results: Eleven patients of both genders, aging from 2 to 73 years old, were diagnosed withemerging and reemerging viruses as Coxsackie B2,B3,B4, Eritrovirus B19, ZikaV, ChikV, Herpes zosterV, West NileV, Sars Cov19, and a possible case of OropoucheV. Different neurological manifestations posed constant challenges.

Conclusions: The diagnostic of emerging and remerging viruses requires great neurologic skills. It is important to consider cellular and humoral responses, genetic susceptibility and vaccine reactions that can contribute to the diagnosis and sequelae of viral infections in the Nervous System.

Biography

I am a Neurologist and Coordinator of the neuroinfection and neuroimmunology center in the public health service - Hospital da Restauração- Recife, Pernambuco, Brazil.

Juan Li[1]*, Luzhao Feng[2], Yuan Ma[2], Luodan Suo[1]

[1]Department of Immunization and Prevention, BeijingCenter for Disease Prevention and Control, China

[2]School of Population Medicine and Public Health, Chinese Academy of Medical Sciences & Peking Union Medical College, China.

Effectiveness of Influenza Vaccines inPreventing Acute Cardiovascular Events Within 1 year in Beijing, China

Background: Cardiovascular disease is the leading cause of death globally and in China, with accumulating evidence linking acute respiratory infections to increased risk of acute cardiovascular events. Influenza vaccination, effective in preventing acute respiratory infections, may also reduce cardiovascular complications, but controversies persist regarding its protective effects across different populations and study designs. Previous research has highlighted inconsistencies due to confounding biases, varying study populations, and limited data from Chinese populations using self-controlled case series (SCCS) designs, which better control for non-time-varying confounders.

Objective: This study aimed to investigate the protective effect of influenza vaccination against acute cardiovascular events within one year using an SCCS design, based on hospitalization data from Beijing, China. It sought to clarify the duration of protection, variations across subgroups (e.g., age, cardiovascular history), and potential confounding by acute respiratory infections, providing evidence to optimize cardiovascular disease prevention strategies.

Methods: Participants included 1,647 permanent Beijing residents (median age 65 years, 38.43% female) who received influenza vaccination between 2016–2018, had no subsequent vaccinations within two years, and experienced at least one acute cardiovascular event within two years post-vaccination. The SCCS design defined a 2-year observation period: exposure period (29–365 days post-vaccination) and control periods (0–28 days and 366–730 days post-vaccination). Relative incidence (RI) and 95% confidence intervals (CI) were calculated, adjusting for acute respiratory infections and seasonal effects. Stratified analyses by age, cardiovascular history, and other factors were performed.

Results: The risk of acute cardiovascular events during 29–365 days post-vaccination was 0.76 times the baseline (RI=0.76; 95% CI: 0.68–0.84). Protective effects were more pronounced in younger participants (P=0.043) and those without cardiovascular history (P<0.001), with no significant impact from acute respiratory infections (P=0.986) or vaccination frequency (P=0.272). Influenza vaccination reduced risks of ischemic stroke (RI=0.58; 95% CI: 0.49–0.69) and myocardial infarction (RI=0.74; 95% CI: 0.55–0.99)

within one year. Sensitivity analyses confirmed stability, and protection persisted for at least two years.

Conclusion: Influenza vaccination reduces the risk of acute cardiovascular events for at least one year, with stronger protection in younger individuals and those without prior cardiovascular disease. These findings support influenza vaccination as a potential primary and secondary prevention strategy for cardiovascular disease, highlighting its public health significance in China.

Biography :

Juan Li, Ph.D. in Epidemiology and Health Statistics from Peking University, is a researcher at Beijing CDC, focusing on vaccine-preventable disease surveillance and evaluation. She has over 40 papers, 4 compiled/translated works, led/participated in 10 projects, and won the 2017 Chinese Preventive Medicine Association's Science and Technology Third Prize and the 2020 Beijing March 8th Red Banner Medal. Academic roles include Beijing health popularization expert and association committee member.

Ying Ma*, Dan Zhao, Juan Li, Xiaomei Li, Zhiqiang Cao, Wei Yao, Jiang Wu, Luodan Suo

Beijing Center for Disease Prevention and Control, Beijing Research Center for Respiratory Infectious Diseases, China

Effectiveness of Vaccination Against Covid 19 Related Hospitalization in Elderly Adults Aged 80 Years and Over During the Period of Omicron Circulation in Beijing, China: A Retrospective Cohort Study Using Linked Regional Healthcare Data

Background: A large wave of COVID-19 caused by SARS-CoV-2 Omicron subvariants began in Beijing in early December 2022. We evaluated the COVID-19 vaccine effectiveness (VE) in mitigating the risk of COVID-19-related hospitalization during the epidemic.

Methods: We conducted a retrospective cohort study linking regional healthcare data and vaccination registry routinely collected in Beijing. All electronical medical records on COVID-19 related hospital discharges of the elderly inpatients aged 80 years and over during November 2022 and February 2023 were included in the study. Poisson regressions were used to estimate incidence risk ratio (IRR) of COVID-19 related-hospitalization or death. VE was calculated as 1 minus IRR ×100%.

Results: A total of 53,789 individuals aged 80 and above were included, 30531 individuals were in the vaccine group (56.76%) and 23258 individuals in the unvaccinated group (43.24%). 17916 (33.31%) were diagnosed with COVID-19. The analysis revealed that the VE of booster vaccination in preventing COVID-19-related hospital, severe/critical COVID-19 and in-hospital death were 63.5% (95%CI: 59.8%–66.9%), 66.9% (95%CI: 60.1%–72.6%) and 79.4% (95%CI: 77.0%–81.5%), the VE of primary series were 56.0% (95%CI:51.4%–60.2%), 66.8% (95%CI:59.0%–73.0%) and 66.4% (95%CI: 63.0%–69.5%).

Conclusion: Booster vaccination significantly reduced the risk of COVID-19-related hospitalization, critical illness or in-hospital deaths in the elderly inpatients during an Omicron dominant period. Offering booster dose and regularly monitoring the coverage and VE of COVID-19 vaccines remains the main stay for mitigating impacts of upcoming epidemics.

Biography :

Ma Ying is a public health professional at the Beijing Center for Disease Control and Prevention, focusing on the research field of vaccine - preventable diseases. She participates in the research on the protective effect of COVID - 19 vaccines on the elderly. By analyzing the real - world data of vaccinated elderly people, she clarifies the protective effects of the vaccines against severe illness and hospitalization. Dedicated to safeguarding vulnerable groups, she now shares the research results to optimize the immunization strategies for the elderly population and help enhance this group's resilience in responding to the epidemic.

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17-19 October 2025

KEYNOTE SESSION | DAY 2

Bene Ekine Il-Afolabi

ZEAB Therapeutic Ltd, Universal Scientific Education & Research Network (USERN), London, England, United Kingdom

Cancer Pathogens and the Future of Vaccines in Cancer Treatment

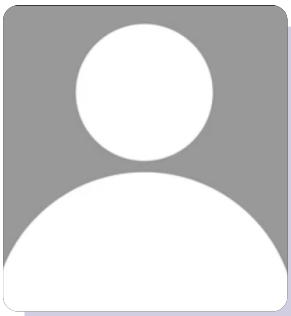
The accumulating evidence and establishment of the consensus that living organisms constitute not only blood, organs and tissues, but includes microbiota (bacteria, fungus, virus, parasites) is gaining attention in the pathogenesis of cancers. Globally, millions are affected by pathogen-related cancers. Humans are made up of resident microbiota that are implicated in the health and sickness paradigm. The role of these resident microbiotas is demonstrated in homeostasis maintenance, such as hydrolysis of glucoraphanin to sulforaphane by myrosinase or gut microbiome. Sulforaphane inhibits the Kelch-like ECH-associated protein mediated degradation of NrF2, allowing NrF2 to migrate from cell cytoplasm into the nucleus where it binds to antioxidant responsive element in the promoter regions of NrF2 target genes, including GSTM1 (family of Glutathione-S-Transferase, which is phase II antioxidant enzymes), thus increasing their transcription, activities and resulting in decrease in reactive oxygen species (ROS), reactive aldehydes (RAs) and factors involved in inflammation. Interindividual variations in microbiota occur, which gives rise to inter-individual heterogeneity in drug response. Pathogens are agents of mutations and play a pivotal role in tumour growth and cancer evolution, acting as hidden drivers. Infectious agents such as Human Papillomavirus (HPV), Epstein-Barr Virus, and Helicobacter pylori disrupt host cellular homeostasis and facilitate tumour development. Recent therapeutic strategies are exploring pathogen-specific immunotherapies, such as immune checkpoint inhibitors, vaccine' therapy, and cutting-edge gene-editing technologies like CRISPR. Advancing technologies that aim at the oncogenic pathway as antifungal, antibacterial, and antiviral are highlighted in addition to integration with conventional cancer treatments. This review highlights the urgency of enhancing cancer prognosis through multidisciplinary methods with the view of cancer pathogens.

Biography

Bene is a graduate of River State University of Science & Technology in Applied Biology (Medical Microbiology option); with an MRes degree at University of East London, United Kingdom.

She had her PhD study & worked at the Department of Natural Sciences, Middlesex University, UK. Trained in practical approach to toxicology in drug development (American College of Toxicology/British Toxicology Society). Bene had Harvard University part-sponsored training in Cancer Biology &Therapeutic, and received a 2nd Harvard award for a complementary training in COVID-19 and Mental Health for Medical Professionals. Bene has her expertise in evaluation and passion in improving the health and wellbeing. Her open and contextual evaluation model based on responsive constructivists creates new pathways for improving healthcare. Researching in Microbiology, Molecular Biology and Cancer: Her current focus of research (which has yielded

eight designed drug models), is on the Investigation of molecular mechanism of colorectal cancer and due to the year 2020 pandemic, has been involved in drug development for COVID-19; she set up a diagnostic laboratory for COVID-19 testing service, and now expanding diagnostic scope. Bene has been speaking in several conferences and published over seven peer reviewed articles, as well as written a chapter in Springer Nature book series on Cancer & Immunology. And a manuscript on COVID-19 was submitted to the Chief Medical Officer of United Kingdom to assist in response to the pandemic. Bene sits on journals' editorial boards, and review panels. Bene sits on congress' committee Board (European Congress on Human Genetics 2024, Oncology & Cancer Conference 2024). She is expanding through her years of research evaluation and teaching to establish Hospital projects in Africa, starting with Nigeria's state-of-the-art Hospital project. Bene is the Founder & CEO of ZEAB Therapeutic LTD, UK, ZEAB Medical Centre, Lagos Nigeria; as well as the founder of two non-profit organizations: Citizen's Wellbeing Intervention UK, and Earthwise & Citizens' Empowerment Nigeria. She was recently endorsed by and in collaboration with the Ministry of Environment Nigeria for promotion of transition to Green Renewable system. She is a member of the Medical Research group council at University of East London, a research consultant with Norxin Medical research Cooperation. She is honoured with an affiliation to Universal Scientific Education & Research Network (USERN), London, England United Kingdom.



Mordoh José*[1],Schwab Erika[1], Carri Ibel[2], Aris Mariana[1] Bravo Alicia Inés[1] Barrio María Marcela[1]

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[2] La Jolla Institute for Immunology, La Jolla, CA, USA

Vaccimel Immunization Is Associated with Enhanced Response to Treatment with Anti-PD1 Monoclonal Antibodies in Cutaneous Melanoma Patients – A Case Report Study.

VACCIMEL plus BCG and GM-CSF is an immunotherapeutic treatment (IT) that has been assayed in stages IIB, IIC, and III cutaneous melanoma patients. In the adjuvant randomized Phase II study CASVAC-0401, VACCIMEL-treated patients had longer distant-metastases-free survival (DMFS) than those treated with IFNα2b. Five years after locking the data, an actualization was performed. The benefit in DMFS was maintained in the VACCIMEL group versus the IFNα2b treated group (p=0.035), with a median DMFS of 96 months for VACCIMEL and 13 months for IFNα2b. DMFS was also analyzed as a single cohort in patients (n=30) who had been treated with VACCIMEL. The median DMFS was 169 months, and at 48 months follow-up it was 71.4 %, which was not statistically different from DMFS of previously published results obtained in adjuvancy with ipilimumab, pembrolizumab, nivolumab or dabrafenib/trametinib. VACCIMEL induced a polyclonal cellular immune response against melanocytic differentiation antigens (MDA), cancer-testis antigens (CTA), and neoantigens derived from both the patient's tumor and VACCIMEL, as demonstrated in PRE- and POST-VAC PBMC cultured *ex vivo* with HLA-restricted peptides and quantified by IFNγ ELISPOT.

The feasibility of combining VACCIMEL with anti-immune checkpoints inhibitors (ICKi) was analyzed. Remarkably, 5 pts relapsing after VACCIMEL achieved complete responses (CR) with anti-PD-1 IT without added toxicity. Assuming that anti-PD-1 synergized VACCIMEL responses, we performed analogous *ex vivo* assays, stimulating available PBMC from 8 pts treated with VACCIMEL, with HLA-restricted peptides ± nivolumab (10 µg/ml) and evaluated their responses by IFNγ ELISPOT. Overall, IFNγ+ responses increased for 13/30 peptides tested. Two pts (#2, #5) were studied in depth. Pt#2 who relapsed 29 months after VACCIMEL, received pembrolizumab (200 mg Q3W), and achieved CR lasting >24 months. PBMC collected after 10 months of therapy (anti-PD1IT-PBMC) retained reactivity to Tyrosinase and gp100, which was induced only after vaccination, since they had been detected in POST but not in PRE-VAC PBMC. Compared to PRE and POST-VAC PBMC, anti-PD1 IT-PBMC had higher Ki67+ CD4 and CD8 T cells, higher HLA-DR+, CD69+, CD137+ activation markers, the highest effector memory and lowest TEMRA fractions. Upon peptide stimulation, POST-VAC and anti-PD1 IT-PBMC similarly increased effector memory and reduced central memory/naïve T cells, which prevailed in PRE-VAC PBMC. Anti-PD1 IT PBMC after *ex vivo* TAA stimulation enhanced their activation phenotype and showed the lowest proportion of PD1+ T cells.

In Pt#5 (HLA-A*0201+), PRE- and POST-VAC PBMC were cultured ± nivolumab and tested in a calcein-*

*lysis assay targeting an HLA-A*0201+ CM line expressing relevant TAA. Nivolumab increased POST-VAC PBMC lysis from 11.5% to 24.2% (E:T 30:1), whereas PRE-VAC PBMC remained weakly cytotoxic.

These results demonstrate that VACCIMEL-induced T cell responses persisting long after treatment and remain functional under anti-PD-1 IT, suggesting that VACCIMEL expands clones whose enhanced lytic activity may contribute to favorable outcomes with checkpoint blockade.

Biography

José mordoh, m.d., ph.d., was born in buenos aires, argentina. He graduated cum laude as medical doctor at the faculty of medicine, university of buenos aires. He obtained his phd under the supervision of prof. Luis f. Leloir, nobel prize in chemistry, 1970. After obtaining a guggenheim fellowship, he made his post-doctoral studies at the pasteur institute, france, under the direction of prof. Francois jacob, nobel prize in medicine 1965. After returning to buenos aires as a scholar of the leukemia society of america, he founded the laboratory of cancerology at the fundación instituto leloir. In 1994 he co-founded the alexander fleming institute, the biggest private oncology hospital in latin america. Presently he is director of the center of oncological research of the cancer foundation (cio-fuca). He is professor of molecular medicine and molecular oncology at the university of buenos aires. For the last 30 years his research has focused on cancer immunotherapy, and more specifically on the development of immunotherapy in cutaneous melanoma. He is an emeritus member of the american association for cancer research.

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17-19 October 2025

ORAL SESSION | DAY 2

Debra Hawkins*, Kacy Aderhold, Susan Dresser,
University of Oklahoma Health Sciences Center, USA.

From Awareness to Action: Improving Sepsis Screening in Rural Hospitals

Sepsis is a life-threatening condition requiring early recognition and timely intervention to improve patient outcomes. Despite advances in sepsis protocols, rural hospitals continue to face significant barriers in sepsis management due to resource limitations, workforce shortages, and inconsistencies in protocol adherence. Studies indicate that rural healthcare settings often struggle with delayed identification of sepsis, contributing to increased morbidity and mortality. Addressing these challenges through structured education and quality improvement initiatives is essential to enhancing compliance with evidence-based sepsis protocols.

This quality improvement project aimed to assess the impact of a structured sepsis education program combined with compliance audits on nursing documentation accuracy and adherence to sepsis screening guidelines in two rural critical access hospitals. The project followed a three-phase approach: a pre-intervention audit, a targeted educational intervention, and a post-intervention audit. In the pre-education phase, a three-month retrospective chart review evaluated baseline adherence to sepsis documentation and protocol compliance among nursing staff. Results revealed low baseline accuracy rates, averaging 52.57% at Hospital A and 49.70% at Hospital B, indicating a critical gap in early sepsis recognition and adherence to standardized protocols.

The educational intervention phase involved a one-month structured training program for nursing staff, focusing on sepsis pathophysiology, early recognition, and evidence-based treatment guidelines, including the Surviving Sepsis Campaign recommendations. The training emphasized timely sepsis screening, appropriate documentation, and escalation of care protocols, integrating case-based learning and interactive workshops to reinforce key concepts. The post-education audit, conducted over three months, demonstrated a substantial improvement in documentation accuracy and protocol adherence, with rates increasing to 88.33% at Hospital A and 81.56% at Hospital B. Additionally, the frequency and accuracy of sepsis screening during routine nursing assessments improved significantly, highlighting the effectiveness of education in reinforcing best practices.

This project underscores the critical role of structured education and continuous auditing in bridging gaps in sepsis recognition and management in resource-limited settings. Findings support the integration of ongoing sepsis education and quality improvement initiatives to enhance early detection, reduce treatment delays, and improve patient outcomes. Future efforts should focus on sustaining these improvements through periodic refresher training, automated screening tools, and interprofessional collaboration to standardize sepsis care across rural healthcare settings. By demonstrating the effectiveness of targeted interventions in improving adherence to sepsis protocols, this project provides a replicable framework for other rural hospitals aiming to optimize sepsis care and reduce preventable mortality.

Biography

Debra Hawkins, BSN, RN, CCRN, is an advanced practice nurse leader and Clinical Nurse Specialist doctoral candidate at the University of Oklahoma Health Sciences Center. With over 12 years of diverse experience in emergency, critical care, and rural healthcare, she specializes in improving clinical outcomes through education, quality improvement, and evidence-based practice. In addition, Debra is a decorated Girl Scout leader and a past recipient of the Girl Scout Leader of the Year award for Western Oklahoma, demonstrating her commitment to mentorship and community engagement.

Natalle Do Socorro Da Costa*[1], Wilson Rogério Soares E Silva[2]

[1]Federal Institute Pará, Brazil
[2]Estácio de Belém College, Brazil

Epidemiological Profile of Dengue in Belém Over the Last 10 Years

Dengue fever remains one of the most significant public health challenges in Brazil, particularly in tropical regions such as the Amazon caused to proliferation of the *Aedes aegypti* mosquito. This study aims to outline the epidemiological profile of dengue in the municipality of Belém, Pará, over a 10-year period (2014–2024), focusing on identifying the most affected demographic groups and analyzing temporal trends. The research is based on secondary data obtained from DATASUS, Brazil's national public health database.

Methodology:

Data were collected regarding dengue incidence by age group, educational level, income, race/ethnicity, and predominant viral serotype. The dataset was analyzed using descriptive statistics and temporal comparisons, with visual tools applied to highlight patterns and seasonal variations.

Preliminary Results:

The highest incidence of dengue was observed among individuals aged 20 to 59, followed by adolescents between 15 and 19 years old. Most cases were reported among people with incomplete secondary education and monthly income up to two minimum wages. Regarding race/ethnicity, a higher occurrence was found among people identified as "branco" (mixed race), reflecting the city's demographic composition. Serotype analysis revealed DENV-1 . A marked increase in case numbers was recorded during the Amazonian winter (rainy season), particularly between January and April.

Conclusion:

The findings indicate a rising trend in dengue cases in Belém, especially during the rainy season, when stagnant water facilitates the proliferation of the *Aedes aegypti* mosquito. The persistence of transmission and the circulation of multiple serotypes underscore the need for continuous surveillance and tailored prevention strategies, especially targeting the most socioeconomically vulnerable groups.

Biography:

Bachelor's degree in Biomedicine from the Federal University of Pará (2007), Master's degree in Genetics and Molecular Biology from the Federal University of Pará (2010) and PhD in Genetics and Molecular Biology from the Federal University of Pará (2015). Professor at Estácio-Castanhal from 2014 to 2019. She is currently coordinator and professor of the Biomedicine course at Estácio de Belém College. She has experience in the area of Genetics, Microbiology with an emphasis on Molecular Biology.

Lu Shengye*, Yan Wende
Department of Hematology, Peking University People's Hospital, China.

Prevalence of HEV and Occult Infection Among Chinese Hematopoietic Stem Cell Transplant Donors

Objective: This study aims to investigate the prevalence of hepatitis E virus (HEV) infection among hematopoietic stem cell transplant donors in China and its associated factors, while evaluating the impact of donor HEV infection status on recipient HEV infection risk.
Methods: A single-center retrospective cohort study design was employed, enrolling 7,168 hematopoietic stem cell donors who underwent pre-transplant examinations at the Hematopoietic Stem Cell Transplantation Center of Peking University People's Hospital between January 1, 2018, and December 31, 2023. The study covered 31 provinces (autonomous regions and municipalities) in China. Serological testing assessed HEV infection prevalence, and logistic regression analyzed risk factors for occult HEV infection.
Results: Among 7,168 donors, 1,201 (16.76%) tested seropositive for HEV. This included 1,184 (16.52%) with anti-HEV IgG positivity, 39 cases (0.54%) were HEV IgM positive, 22 cases (0.31%) were HEV IgG/IgM double positive, and no HEV RNA positive cases were detected. The HEV seropositivity rate showed a significant decline in 2021, decreasing from approximately 18% to 14%. Geographic analysis revealed that Guizhou, Sichuan, Yunnan, Chongqing, and Hubei ranked among the top five provinces/municipalities nationwide in HEV positivity rates. HEV infection rates showed a negative correlation with regional Human Development Index (HDI) scores. Among the 4,099 donors studied, 880 (21.47%) were HEV seropositive; no HEV-derived infections were detected in their corresponding recipients. Further analysis confirmed that all recipients with clinically confirmed HEV infection had HEV-negative donors and negative HEV infection markers themselves, ruling out the possibility of donor-to-recipient transmission via occult infection. Multivariate analysis revealed that age 45–65 years (OR = 3.67, 95% CI: 3.19–4.22) and age ≥65 years (OR = 4.51, 95% CI: 2.70–7.37) were risk factors for HEV occult infection. Conversely, female gender (OR = 0.58, 95% CI: 0.46–0.68), being of Hui ethnicity (OR = 0.37, 95% CI: 0.13–0.84), and self-pay medical care (OR = 0.80, 95% CI: 0.67–0.96) were protective factors. Comparative biochemical analysis revealed significantly higher levels of AST, GGT, PTA, creatinine, and fibrinogen in the past infection group compared to the healthy group ($P < 0.05$). GGT levels were also significantly higher in the current infection group than in the healthy group ($P < 0.01$), but no significant differences existed between the past and current infection groups ($P > 0.05$).

Conclusion: This study first reveals the epidemiological characteristics and associated risk factors of HEV occult infection from the perspective of hematopoietic stem cell donors. It confirms that occult HEV infection in donors does not lead to HEV-derived infection in recipients, providing scientific basis for developing more efficient donor screening strategies.

Biography

Lu Shengye, Associate Chief Physician, Department of Hematology, Peking University People's Hospital; Deputy Director, Medical Information Center, Peking University People's Hospital; Principal Investigator of the parallel project "Intelligent Clinical Decision Support System for Novel Acute Leukemia" under the Beijing Research Ward Excellence Program.

KilYong Choi[2]* and Inchun Kim[1]

[1]Department of Health and Safety Convergence Science, Korea University of Seoul, Republic of Korea.

[2]Department of Environmental Energy Engineering, Anyang University of Anyang-si, Gyeonggi-do.

Determinants of Respiratory Health Impairment from Chronic Chemical Exposure in Small-Scale Manufacturing Enterprises

This study evaluated environmental awareness and respiratory disease incidence among residents in Banwol-dong (exposure area) and a control area, and examined links with environmental factors. A 2021 survey of 20 residents used a 5-point Likert scale to assess awareness, and indoor PM10, PM2.5, temperature, and humidity were measured with a DT-9881M device. Cohort analysis using NHIS data (2002–2022) assessed chronic disease onset. Women showed higher awareness of water ($p=0.0039$) and soil pollution ($p=0.007$). Respiratory diseases and asthma were significantly higher in the exposure area ($p<0.0001$), especially with ≥5 years residence, underscoring the need for region-specific environmental health policies.

Key Words: Health effect, Industiral complex, Environmental pollutants, Environmental awareness.
Funding: The Mental Health Technology Project of the Korea Environmental Industry & Technology Institute(KEITI) was funded by the Ministry of Environment (Grant No. 2021003320007).

Biography

Dr. KilYong Choi has over 20 years of experience in environmental health research and policy development, with a focus on carbon neutrality, climate change, and environmental disease prevention. In recent years, he has led major projects on pediatric respiratory diseases, air pollution and health monitoring, and environmental health assessments around industrial complexes and coal-fired power plants. He actively contributes to national committees, including those on noise, chemical safety, and architecture, while serving as a technical advisor to multiple agencies. Currently, he is Academic Director of the Korean Society for Environmental Health and Toxicology and Executive Director of the Korean Society for Indoor Environment.

Mohamed Z. Sayed-Ahmed*[1,2,3], Heba Mohammed Rahmo4, Samir Mohammed Abd-Elghany4, Amira Ibrahim Zakaria4, Khalid Ibrahim Sallam4

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[3]Department of Internal Medicine and Infectious Diseases, Faculty of Veterinary Medicine, Mansoura University ,Mansoura, Egypt

[4]Food Hygiene and Control Department, Faculty of Veterinary Medicine, Mansoura University, Mansoura, Egypt

Health Hazards, Both Cancerous and Non-Cancerous, Are Related to Consuming Fish Tainted with Heavy Metals from Egypt's Manzala Lake

Manzala Lake was sampled to assess the concentrations and possible ecological risks of heavy metals. The mean heavy metal levels in the muscles of Nile tilapia, Flathead grey mullets and African catfish were 0.01, 0.15 and 0.29 mg/kg, respectively, for mercury; 3.16, 4.25 and 4.74 mg/kg for arsenic; 1.01, 0.87 and 0.95 mg/kg for lead; and 0.05, 0.12 and 0.06 mg/kg for cadmium. The levels of heavy metals exceeded their maximum permissible limits in most samples. The EDIs of some metals were higher than their PTDIs or BMDLs. The THQs and TTHQs from metal intake were >1 for Hg and Cd. In addition, the TCR values of As in all fish species were higher than 1.0×10^{-4} indicating a potential health risks from consumption of fish species which need strict hygienic procedures to prevent fish contamination with heavy metals and ensure that their levels did not exceed the maximum permissible limits.

Biography:

Prof. Sayed-Ahmed was awarded his Ph.D. in Cancer gene-therapy from TIHO, Hanover, Germany. He is working as a Professor at the Department of Infectious Diseases, College of Veterinary Medicine, Mansoura, Egypt. He works at the Department of Clinical Practice, College of Pharmacy, Jazan University, Saudi Arabia. He is an editorial board member, a peer reviewer of several international journals, and a guest editor at the Experimental Pharmacology & Drug Discovery section of Frontiers in Pharmacology. He has a strong research professional with a Doctor of Philosophy in Cancer Biology, Immuno-oncology, and Molecular Biology. He was a Director for (4) research projects funded by the Research Development and, Innovation Authority (RDIA), Ministry of Education in Saudi Arabia, and CO-PI of (1) Research project funded by the Deanship of Graduate Studies and Scientific Research, Jazan University, Saudi Arabia.

Semra Soydam*, Gamze Varan, Buse Türegün Atasoy, Serhat Ünal
Vaccine Institute, Hacettepe University, Ankara, Turkey.

Limitations of BCG and Booster Vaccine Research

Tuberculosis (TB) is an infectious disease that primarily affects the lungs. TB is transmitted from person to person through the air. Individuals with pulmonary TB release *Mycobacterium tuberculosis* bacilli into the air when they cough, sneeze, or spit. Inhaling just a few of these bacilli is enough for a person to become infected. Approximately one-quarter of the world's population is estimated to harbor a latent TB infection. People infected with the tuberculosis bacterium have a lifetime risk of developing active TB disease of about 5–10%. Immune-weakening factors such as **HIV**, **malnutrition**, **diabetes**, or **tobacco use** significantly escalate the risk of disease.

Bacillus Calmette–Guérin (BCG) is the only currently licensed vaccine against tuberculosis and is included in routine vaccination programs in around 180 countries. BCG, a live-attenuated strain of *Mycobacterium bovis* isolated from cattle, has been the sole licensed vaccine to significantly contribute to TB control for over 80 years. It is administered in many countries as part of standard childhood immunization schedules. While BCG is estimated to provide **approximately 80% protection** against TB meningitis and miliary TB in infants and young children, it is **not effective as a therapeutic vaccine** for latent infection. Moreover, its efficacy against **pulmonary TB is limited**, and a second **booster dose** administered during school age has not been shown to confer **additional protection**.TB remains particularly dangerous for individuals infected with **Human Immunodeficiency Virus (HIV)** or those with suppressed immune systems, where **morbidity and mortality rates are exceedingly high**.

According to **WHO**, despite global vaccination efforts, approximately **1.7 million people die from tuberculosis every year**. TB remains among the **top 10 causes of death worldwide** and is the **second leading infectious killer**, only behind **COVID-19** and ahead of **HIV/AIDS**. The emergence of **multidrug-resistant TB (MDR-TB)** and **extensively drug-resistant TB (XDR-TB)**—caused by strains resistant to first-line treatments like **isoniazid** and **rifampicin**—has made treatment of advanced disease increasingly difficult.

In this presentation, we will present an **overview of ongoing booster vaccine development efforts** for the treatment of tuberculosis, followed by a **summary of the research** conducted at the **Hacettepe Vaccine Institute**.

Biography

After graduating from the Department of Biology, Faculty of Science, Anadolu University in 2004, she worked as a Research Assistant at the Department of Biology, Ankara University until 2011, and as an Assistant Professor at Niğde University between 2011 and 2013. Between 2013 and 2019, she worked on the potency analyses of vaccines, blood products, and monoclonal antibodies at the Biotechnological Products Laboratory Unit of the Turkish Medicines and Medical Devices Agency, Ministry of Health. Since 2019, she has been a faculty member in the Department of Vaccine Technology, Vaccine Institute, Hacettepe University. She continues to work on Vaccine Technology, Recombinant Production, Molecular Diagnostic Methods, Biotechnology, and Cell-Based Identity and Potency Analyses.

BaihetinishaTuerdi*, DilixiatiTuerdimaimaiti†, Buzukela Abuduaini†, Shaotao Kang, Jinliang Jiao, Mengchen Li, Wolazihan Madeniyati, Gulisitan Aili, ReyilaTuerhong, AjiguliKulaxi.

Hospital of Xinjiang Medical University, China.

Genome-wide Identification and Functional Analysis of Dysregulated Alternative Splicing Profiles in Sepsis

Background An increasing body of evidence now shows that the long-term mortality of patients with sepsis are associated with various sepsis-related immune cell defects. Alternative splicing (AS), as a sepsis-related immune cell defect, is considered as a potential immunomodulatory therapy target to improve patient outcomes. However, our understanding of the role AS plays in sepsis is currently insufficient. **Aim** This study investigated possible associations between AS and the gene regulatory networks affecting immune cells. We also investigated apoptosis and AS functionality in sepsis pathophysiology.

Methods In this study, we assessed publicly available mRNA-seq data that was obtained from the NCBI GEO dataset (GSE154918), which included a healthy group (HLTY), a mild infection group (INF1), asepsis group (Seps), and a septic shock group (Shock). A total of 79 samples (excluding significant outliers) were identified by a poly-A capture method to generate RNA-seq data. The variable splicing events and highly correlated RNA binding protein (RBP) genes in each group were then systematically analyzed.

Results For the first time, we used systematic RNA-seq analysis of sepsis-related AS and identified 1505 variable AS events that differed significantly (p <= 0.01) across the four groups. In the sepsis group, the genes related to sig nificant AS events, such as, SHISA5 and IFI27, were mostly enriched in the cell apoptosis pathway. Furthermore, we identified differential splicing patterns within each of the four groups. Significant differences in the expression of RNA Binding Protein(RBP) genes were observed between the control group and the sepsis group. RBP gene expression was highly correlated with variant splicing events in sepsis, as determined by co-expression analysis; The expression of DDX24, CBFA2T2, NOP, ILF3, DNMT1, FTO, PPRC1, NOLC1 RBPs were significant reduced in sepsis compared to the healthy group. Finally, we constructed an RBP-AS functional network.

Conclusion Analysis indicated that the RBP-AS functional network serves as a critical post-transcriptional mecha nism that regulates the development of sepsis. AS dysregulation is associated with alterations

in the regulatory gene expression network that is involved in sepsis. Therefore, the RBP-AS expression network could be useful in refining biomarker predictions in the development of new therapeutic targets for the pathogenesis of sepsis.

Biography:

Chief Physician of RICU of First affiliated Hospital of Xinjiang Medical University Dedicated to clinical and basic research in respiratory and critical care medicine. Primary research interests include diagnosis and treatment of sepsis, sepsis-related ARDS, and infection prevention/control of tuberculosis.

Peng Ruan

Department of Gastroenterology, Renmin Hospital of Wuhan University, Wuhan, Hubei, China

Two Fragments of HBV DNA Integrated into chrX: 11009033 and its Genetic Regulation in HepG2.2.15

Hepatitis B virus (HBV) integration into human genome causes hepatocellular carcinoma (HCC). The present study used inverse nested PCR; the full sequence of HBV DNA fragments of the chrX: 111009033 integration site was detected (987 bp), containing two fragments of double-stranded linear DNA with the same orientation (1,744-1,094 and 1,565-1,228 nt). By reverse transcription-quantitative PCR, HBV-cell fusion transcript was observed in HepG2.2.15 cells. The mean copy number of this site in cells with H2O2 treatment (8.73x10-2±1.65x10-2 copies/cell) was significantly higher than that in the cells without H2O2 treatment (3.02x10-2±2.33x10-2copies/cell; P<0.0001). The mean levels of P21-activated kinase 3 (PAK3) were 15.67±5.65 copies/cell in HepG2.2.15 cells with H2O2 treatment, significantly higher than in the cells without H2O2 treatment (11.34±4.58 copies/cell, P=0.0076) and in HepG2 cells (5.92±1.54 copies/cell, P<0.0001). Significant difference of PAK3 levels was also found between HepG2.2.15 cells without H2O2 treatment and HepG2 cells (11.34±4.58 vs. 5.92±1.54 copies/cell, P<0.0001). The average copy numbers of the integration site chrX: 111009033 were positively correlated with the average levels of PAK3 (P=0.0013). The overall trend of PAK3 expression was significantly increased in HepG2.2.15 cells with H2O2 treatment compared with that in HepG2.2.15 cells without H2O2 treatment (37.63±8.16 and 31.38±7.94, P=0.008) and HepG2 cells (21.67±7.88, P<0.0001). In summary, the chrX: 11009033 integration site may originate from primary human hepatocytes, occurrence and clonal expansion of which may upregulate PAK3 expression, which may contribute to hepatocarcinogenesis.

Biography:

Dr. Peng Ruan is an Associate Chief Physician specializing in Gastroenterology at Renmin Hospital of Wuhan University, China. With a Ph.D. in Internal Medicine from Wuhan University, he brings extensive expertise in hepatology. Dr. Ruan's diverse professional journey includes roles as a Resident Physician in General Internal Medicine and ICU, as well as leadership positions in Gastroenterology. He has also served as a Visiting Scholar at INSERM U1052, Université Claude Bernard, Lyon, France. Dr. Ruan's research focus encompasses the study of chimeric protein transcription of HBV integration sites and the detection of intrahepatic HBV cccDNA in chronic hepatitis B patients. His contributions have been supported by grants from the National Natural Science Fund of Hubei Province and the Shiyan Science Technology and Innovation Committee.

Maryam Mohammad Alhashmi
United Arab Emirates University, United Arab Emirates

Genomic Study of High Risk Clones of Enterobacter hormaechei Collected from Tertiary Methods Hospitals in the United Arab Emirates

Enterobacter hormaechei is a significant nosocomial pathogen associated with multi-drug resistance. This study investigates high-risk clones isolated from tertiary care hospitals using whole-genome sequencing (WGS). The findings reveal diverse resistance genes, mobile genetic elements, and virulence factors contributing to its pathogenicity. Comparative genomics identified clonal relationships and novel plasmids driving antimicrobial resistance. These results highlight the urgent need for stringent infection control policies and novel therapeutic approaches to combat *E. hormaechei*-associated infections.

Biography:

Maryam Mohammad is a fifth-year medical student at UAEU who co-authored this research under the mentorship of Professor Musthaq Khan], a specialist in microbiology with a focus on antimicrobial resistance. has published extensively on nosocomial infections and bacterial genomics. Together, they aim to provide insights into combating multi-drug-resistant pathogens, contributing to the global fight against infectious diseases.

Farasat Veisi[1]* and Maryam Khaleghian[2]

[1]Department of Biology, Payame Noor University of Tehran, Qeshm International Campus, Qeshm, Iran.

[2]Department of Biology, Payame Noor University of Tehran, Kish International Campus, Kish, Iran.

Spatio-Temporal Deep Learning for Infectious Disease Forecasting: A Hybrid LSTM-GNN Approach Using Multisource Public Data

Studying the spread of infectious diseases stands as a fundamental worldwide health priority. Traditional statistical models lack sufficient capacity to detect the intricate and dynamic spatial-temporal relationships which affect disease transmission patterns in various geographic areas. Open-access health data availability and deep learning technique development create an immediate need for data-driven frameworks that predict disease outbreaks precisely in both time and space. A new hybrid deep learning model merges Long Short-Term Memory (LSTM) networks and Graph Neural Networks (GNNs) to make predictions about infectious disease transmission across space and time. The model utilizes two datasets from Kaggle which include the “Infectious Disease Prediction” dataset for California county-level disease case counts by disease type and gender across multiple years and the “Infectious Disease 2001–2014” dataset containing comprehensive outbreak data at the state level for different infectious diseases in the United States. The datasets received enhancement through addition of historical weather data including temperature and humidity measurements together with demographic characteristics that included population density and urbanization data. The data instances contain three main components: spatial identifiers (state or county), weekly case count time series and environmental and socioeconomic characteristic data. The model uses the weekly confirmed disease case counts from each region as its prediction output. The proposed methodology implements a spatio-temporal deep learning system which starts with GNN layers that use geographic distance and human mobility pattern adjacency matrices to model regional spatial connections. After spatial embedding processing the LSTM layers analyze the sequential development of disease transmission. The model uses 80-10-10 data split for training and validation and testing while employing cross-validation to achieve both robustness and generalizability. The proposed hybrid model outperforms all baseline models including ARIMA and standalone LSTM and Random Forest algorithms. The model achieved an RMSE of 7.41 which outperformed ARIMA at 12.35 and showed MAE at 5.83 compared to 9.72 for LSTM while obtaining R^2 at 0.89 which surpassed 0.73 from Random Forest. The model demonstrated successful identification of outbreak peaks and precise case surge predictions in dangerous areas during two-week periods. The addition of *environmental and demographic variables resulted in an 11.4% improvement in the accuracy of* predictions. The research presents an innovative approach for disease forecasting through the combination of LSTM and GNN architecture strengths. The proposed model provides a robust tool for early outbreak detection and resource allocation and strategic health intervention planning because it integrates spatial and temporal pattern analysis. Future improvements could be achieved by merging vaccination coverage data with public mobility patterns and international health data for better global application capabilities.

Biography:

Ms. Farasat Veisi is a researcher in Molecular Genetics at the Payame Noor University of Tehran Qeshm International Campus, Iran, specializing in the integration of artificial intelligence (AI) in biomedical research. Her work focuses on disease classification and prediction through machine learning and deep learning algorithms, aiming to enhance diagnostic accuracy and personalized treatment strategies. Her research explores AI-driven predictive modeling in healthcare. Farasat actively participates in international conferences, presenting her findings on the intersection of genetics, AI, and precision medicine. Her expertise spans bioinformatics, statistical modeling, and deep learning architectures such as CNNs, RNNs, and transformer models. Proficient in Python, R, and MATLAB, she applies advanced computational techniques to genomic data analysis and disease risk assessment. Her work is driven by a commitment to bridging genomics and AI, contributing to innovative solutions.

Abdiqadir Omar Mohamed[1]*, Cameron Alexander Lynch[2], Chea Tze Ong[3], Muneeb Khan[4], Mohaned Mohamed[5], M Isuru Hiranya Perera[6], Jason Roberts[7], Aaron Chai[8], Hadeel Hussein[9], Abdal Qadir Zafar[10], Shafiq Rahman[11]

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Necrotizing Fasciitis Outcomes in Diabetic vs Non-Diabetic Patients: A Systematic Review and Meta-Analysis

Necrotizing fasciitis (NF) is a rapidly progressive, life-threatening infection, with the lower limbs being a common site. Diabetes mellitus (DM) is a significant risk factor that influences the progression, outcome, and management of NF. Despite its clinical relevance, comparative data on diabetic versus non-diabetic NF outcomes remain limited. This study aimed to compare mortality, amputation rates, and other key outcomes between diabetic and non-diabetic patients with NF.

A systematic review and meta-analysis were conducted in accordance with PRISMA guidelines. Eligible studies assessed outcomes in diabetic and non-diabetic NF patients. Primary outcome measures included amputation rates, mortality, admission length, debridement frequency, and microbial growth. Secondary outcomes included the Laboratory Risk Indicator for Necrotizing Fasciitis (LRINEC) score and unplanned reoperations. Pooled analyses were performed using OpenMeta[Analyst] software, reporting odds ratios (OR) and mean differences (MD) with 95% confidence intervals.

Nine studies comprising 1,890 patients met the inclusion criteria. Diabetic patients had significantly higher rates of amputation (OR 3.77, 95% CI:3.04–4.68, p<0.001) and polymicrobial infections (OR 2.48, 95% CI:1.48–4.16; p<0.001). Mortality was higher among diabetic patients after sensitivity analysis (OR 1.60, 95% CI:1.09–2.24, p=0.015). No significant differences were observed in the number of debridements or length of admission.

Diabetic patients had significantly higher LRINEC scores (MD 2.02, 95% CI:1.33–2.72; p<0.001).

Diabetic patients with NF experience worse clinical outcomes, including increased amputation, mortality, and polymicrobial infection. These findings highlight DM as a key prognostic factor and underscore necessity for aggressive intervention and risk stratification. Further high-quality prospective studies are needed.

Biography :

Abdiqadir Omar Mohamed is an otolaryngology trainee based in the UK. He graduated from the University of Nottingham Medical School and holds a BSc in Audiology from University College London. He has a special interest in head and neck surgery and continues to actively engage in clinical research.

Ebrahim Abdela Siraj[1]*, Tadele Behulu[2], Sosina Shumye[2], Wondmalem Gebral[2], Beselam Gizachew[2], Adugna Tasew Tebabal[2], AshagrachewTewabe Yayehrad[1], Selamawit Yimer Kebede[3], Gizachew Motbaynor[4], ZenawDebasu Addisu[5]

[1]Department of Pharmaceutics, School of Pharmacy, College of Medicine and Health Science, Bahir Dar University, Bahir Dar Ethiopia.

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[5]Department of Clinical Pharmacy, School of Pharmacy, College of Medicine and Health Science, Bahir Dar University, Bahir Dar Ethiopia

Evaluation of Adherence to Anti-Rabies Vaccination Schedule and Its Predictive Factors at Addis Alem Hospital, Bahir Dar, Ethiopia

Introduction: Rabies is a dangerous viral neglected tropical disease and infects humans, causing big problems for health authorities in Ethiopia. Though PEP is available, still there is insufficient awareness, difficulties of accessing to healthcare and logistics issues still make it hard for some to properly follow the rabies vaccination schedule.

Objective: The primary aim of this study is to measure how properly the anti-rabies vaccine is given and to determine which factors influence the schedule among patients in Addis Alem General Hospital, Bahir Dar.

Method: From June to July 2024, a facility-based cross-sectional study was set up with 190 participants who were initiating rabies vaccination. Data were collected by using planned questionnaires and reviewing charts. To study both adherence rates and their causes, we used descriptive statistics and multivariate logistic regression and considered results significant if $p < 0.05$.

Results: Adherence rates declined significantly across vaccination doses that could be due to several factors such as vaccine hesitancy, misinformation, lack of access to follow-up doses, or diminished perceived risk after the initial dose. While each participant has received the first shot, but fewer received the second and those numbers dropped further for the third and fourth, fifth doses: 97.3%, 95.7% and 94.7%, 93.6% respectively. The majority or 81.6%, displayed good adherence. Significant

factors predicting better adherence were being aged 20–40 years (2.15 times the odds, p = 0.023), having only basic education (2 times the odds, p = 0.027) and residing a short distance (5 kilometers or less) from a healthcare facility (2.49 times the odds, p = 0.042). Concerningly, over 40% of those surveyed recognized that they should have started PEP at least 4 days ago but did not and only 39% knew that an anti-rabies vaccine was available prior to this.

Conclusion: The findings highlight critical gaps in knowledge and timely access to rabies PEP, despite relatively high initial vaccine uptake. Targeted interventions such as public education, decentralized vaccine distribution, and cost-reduction strategies are essential to improving adherence and achieving the WHO's 2030 rabies elimination goal.

Biography

Ebrahim is a Lecturer of Pharmaceutics in the Department of Pharmacy at Bahir Dar University, Ethiopia. He is engaged in multifaceted role as a lecturer, researcher, and community service provider. Since then, he has made significant contributions in teaching, research, community engagement, leadership, and both curricular and extracurricular development at Bahir Dar University. Over the past four years, Ebrahim has contributed to more than 34 research articles in the fields of pharmacy and public health and more than 8 research articles as a Primary Author. Notably, he participated in a collaborative national project led by the World Intellectual Property Organization (WIPO) and the University of Gondar.

Zhiyin Xu[1]*, Jingjing Li[2]， Zhaowen Zhang[1],Dongli Xu[1], Mei Zeng[2,3]

[1] Department of Infectious Diseases Control and Prevention, Minhang District Center for Disease Control and Prevention, Shanghai, China.
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[3]School of Public Health, Key Laboratory of Public Health Safety, Ministry of Education, Fudan University, Shanghai, China.

Dynamic epidemiological changes of Hand, Foot, and Mouth Disease and real-world effectiveness of EV71 Vaccination: a case study in Shanghai (2009-2023)

Background: A significant reduction in hand-foot-mouth disease (HFMD) cases has occurred nationally since the EV71 vaccine was licensed for use in China in 2016.

Objective: To evaluate the effectiveness of EV71 vaccination against HFMD by analyzing the dynamic epidemiological and virological trends before and after its introduction in Minhang District,Shanghai.

Methods: HFMD data from 2009 to 2023 were extracted from the National Notifiable Disease and Virological Surveillance System in Minhang District, Shanghai. EV71 vaccination data were retrieved from the Shanghai Immunization Platform Information System. Epidemiological trends and virological characteristics were compared before and after EV71 vaccine introduction over a 15-year period (2009-2023). A test-negative case-control design was implemented to estimate vaccine effectiveness (VE) against HFMD across seven epidemic seasons (2017-2023).

Results: A total of 73,160 HFMD cases, 361 severe cases, and 3 deaths were reported during 2009-2023. Following EV71 vaccine introduction, significant declines occurred in the HFMD incidence rate (53.1%), case-severity rate (95.2%), and fatality rate (100.0%). The proportion of cases in the 6-10-year age group increased by 105.7%. The predominance of EV71 and CA16 serotypes was replaced by CA6 and CA10 in the post-2017 period. Full-dose immunization coverage remained above 60% during 2019-2023. The overall VE against EV71-associated HFMD was 90.0% (95% CI: 74.8 to 96.0) for the two-dose series and 66.9% (95% CI: -0.7 to 89.1) for one-dose vaccination. For two-dose vaccination, VE was 91.9% against EV71-associated outpatient visits, 87.7% against non-severe hospitalization, and 100% against severe complications. No significant association was observed between EV71 vaccination status

and non-EV71-related illnesses.

Conclusion: HFMD incidence declined substantially following the introduction of EV71 vaccination in Shanghai. Two-dose EV71 vaccination provided effective protection against EV71-associated HFMD. The observed serotype replacement and predominance of non-EV71 pathogens underscores the need for multivalent vaccine development to control HFMD epidemics.

Biography:

Zhiyin Xu has his expertise in evaluation and passion in improving the health and wellbeing. He has been committed to the prevention and control of infectious diseases of children in Shanghai for 15 years, undertaking multiple national, municipal, and district-level key infectious disease prevention and control projects, and participating in research for projects funded by the National Natural Science Foundation of China. His major scholarly background focuses on assessing the epidemiological characteristics, risk factors, disease burden, vaccine efficacy evaluation, and disinfection effectiveness assessment of infectious diseases among children in Shanghai, China. His research encompasses HFMD, enteric infectious diseases, COVID-19, zoonotic diseases, etc.

Jerry Kollie
International Scope Consulting Incorporated (ISCI), Monrovia, Liberia.

Vaccines & their Roles in Preventing Child-hood Diseases.

Immunization is key to primary health care, an indisputable human right, and one of the best health investments money can buy. Vaccines are also critical to the prevention and control of infectious disease outbreaks. They underpin global health security and are a vital tool in the battle against antimicrobial resistance.

Liberia is striving to reach global targets in preventing vaccine preventable diseases due to several factors including but not limited to community misconception of vaccines and refusal of been vaccinated.

Biography

Experienced Public Health Specialist with over 25 years of leadership experience in program management, clinical practice, and public health emergency response;

Expert in Project & Program Development: Adept at designing, managing, and evaluating health programs, with a strong background in resource mobilization and capacity building. Successful track record with organizations such as the World Bank, USAID, WHO, and PACT

Consultancy & Research Leadership: Extensive experience providing strategic consulting and conducting comprehensive assessments to strengthen health systems. Expertise in developing methodologies and recommendations for effective health interventions

Institutional Development & Leadership: Instrumental in founding and leading key health boards and associations, including the Liberia Allied Health Sciences Board and the Global Association of Clinical Officers and Physician Assistants

Robinson Nnaji[1]*, F.Tinuga[2], R. Mutayoba[3], S. Kwayambe[3], S.Warioba[4], R. Ngude[4], Y. Bahati[3], A Ngeni[6], M. Hassan[5], C. Akatobi[1], J. klose[1], P. Chanda[1], S. Sembuche[1],M. Fallah[1], M. Abdulaziz[1], M. Mazyanga, J.Kaseya[1]

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Acceleration of Africa CDC Saving Lives and Livelihoods Covid-19 Vaccination Roll-Out Implementation in the United Republic of Tanzania October to December 2022

Background

Tanzania initially refused COVID-19 vaccinations, questioning their validity. As a result, by January 2022, one year after the WHO approval for the use of the COVID-19 vaccine, only 2.8% of the target population aged 18 and older had been vaccinated nationwide. However, as of September 30, 2022, 11 out of 31 regions achieved 75% coverage, while 20 regions reported poor uptake. To improve COVID-19 vaccination in Tanzania, the Africa CDC Saving Lives and Livelihood Project supported logistics, vaccination, and demand creation starting October 3, 2022, in 11 regions. Ten of these regions are among the poor-performing areas, including Kilimanjaro, which had a high uptake and some non-performing districts. We accelerated our vaccination efforts to meet the goal of vaccinating 100% of the target population by the end of December and planned to integrate COVID-19 vaccination with other health programs starting in January.

Method

We observed the implementation of activities and conducted a desk review of Africa CDC COVID-19 vaccination efforts. We completed initial advocacy, situation analysis, a review of microloans, and pre-implementation workshops. We adopted several innovations, including event-based vaccination, decentralization through devolution, reward-based execution, and pay-for-performance. *Immunization* campaigns utilized fixed and mobile outreach sessions with door-to-door demand creation, supported by collaborative supervision, to reach 3,528,200 individuals in three months with single-dose J&J vaccines.

Results

The Africa CDC SLL vaccinated 4,573,434 individuals, accounting for 130% of our annual target of 3,528,200 in December 2022, just three months post-implementation. The median coverage (range) in the 11 regions pre- and post-acceleration was 55 (36-102) and 111 (82-1380), respectively. Fifty-two percent of people vaccinated were male, with a median age (range) of 42 (18-79).

Biography

Robinson Nnaji has 15 years of experience in public health, including seven years as a supervisor. He has expertise in project management, technical support, One Health implementations, vaccinology, epidemiology, health information systems, surveillance, surveys, and more. He has received training from various organizations and currently serves as the national coordinator in Tanzania for the African Center for Disease Control. He represents the organization in Tanzania. Addressing public health needs and priorities, enhancing partnerships, and contributing to knowledge product development in the Tanzanian health sector.

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17-19 October 2025

POSYERS | DAY 2

Somnath Maitra
Department of General Medicine,Jagannath Gupta Institute of Medical Sciences and Hospital, India.

Variable presentations of dengue fever with diagnostic dilemma:A Case Series

Dengue is a viral fever in humans caused by 4 serotypes of flavivirus.It is spread by the bite of infected *Aedes* mosquitoes.It is associated with multisystem involvement.The case series presented here depicts unusual manifestations of dengue infection with hypoplastic anaemia,hepatitis,pancreatitis and encephalopathy.The cases were diagnosed based on history of dengue with subsequent persistence of pancytopenia,presence of hepatitis,pancreatitis,encephalopathy with serological evidence of dengue ,after ruling out other aetiologies and based on laboratory investigations.

Bone marrow revealed pancytopenia with hypocellular marrow diagnosing hypoplastic anaemia, transaminitis and rise of lipase and amylase enzymes with symptoms diagnosedhepatitis,pancreatitis and finally impairment of consciousness with electroencephalogram diagnosed encephalopathy.

The importance of the case series lies in the fact that atypical manifestations may occur in dengue patients causing diagnostic and treatment dilemma.

Biography

Dr. Somnath Maitra graduated with an M.B.B.S. degree from Calcutta Medical College, Kolkata, under the University of Calcutta in 2004 and earned an M.D. in General Medicine from Calcutta National Medical College and Hospital (CNMCH), Kolkata, affiliated with The West Bengal University of Health Sciences, in 2010. With over 11 years of undergraduate teaching experience, Dr. Somnath Maitra has served as Senior Resident (SR), Resident Medical Officer (RMO), Assistant Professor, and Associate Professor in General Medicine. Currently, Dr.Somnath Maitra has been working as a Professor of Medicine since August 1, 2023. A recognized examiner for M.B.B.S. examinations under WBUHS and a postgraduate teacher in general medicine, Dr. Somnath Maitra has also completed CISP, Revised Basic Course Workshop, AETCOM training, and BCBR training. An accomplished academic, Dr. Somnath Maitra has 36 research papers published in national and international indexed journals and has co-authored the international book *Updates in Dengue Fever* (2014) along with contributing chapters such as “Warfarin Toxicity Management” (2012) and “Updates in Scrub Typhus” (2022). Selected as the editor of three peer-reviewed international journals, Dr. Somnath Maitra is a member of API and IAMCON and has been a speaker at the 3rd Annual Webinar on Orthopedics, Rheumatology, and Musculoskeletal Disorders in Dubai (December 2023). He was also honored with the Academic Excellence Award at PTWCON 2024.

Isheeta Gupta
Washington University in St. Louis, Missouri, U.S.A

The Rise of *Trichophyton indotineae*: A Public Health Threat of Antifungal-Resistant Dermatophytes

Dermatophytoses, commonly known as ringworm, are among the most prevalent superficial fungal infections globally. Recently, a novel strain, *Trichophyton indotineae*, has emerged as a significant dermatological threat due to its resistance to first-line antifungal agents, particularly terbinafine. First identified in India, *T. indotineae* has now been reported in multiple countries, including the United States, prompting global concern. The fungus primarily affects otherwise healthy individuals and is associated with severe, relapsing infections that are often misdiagnosed or inadequately treated, contributing to further transmission.

This literature-based review explores the microbiological characteristics, transmission pathways, clinical manifestations, and resistance mechanisms of *T. indotineae*. It reveals that terbinafine resistance is largely driven by mutations in the squalene epoxidase gene, necessitating a shift to alternative agents such as itraconazole or combination therapies. Public health implications include infection control, surveillance, and antifungal stewardship in both community and clinical settings. This calls for heightened clinical awareness, improved diagnostic protocols, and collaborative global action to curb the spread of this emerging fungal pathogen.

Biography:

Isheeta Gupta is a dual-degree MPH/MSW student at Washington University in St. Louis, with a background in medicine (MBBS) from India. She currently serves as a Graduate Research Assistant at the iCHASM Lab in the Department of Psychiatry and as a Program Support Assistant at HIGH IRI, supporting global infectious disease research. Her interests lie at the intersection of dermatology, infectious diseases, and public health. With experience in clinical rotations, behavioral health research, and academic instruction, she brings a multidisciplinary perspective to emerging public health issues.


Randhir Francis*and Megan Galt*
Guy's and St Thomas' NHS Foundation Trust, United Kingdom

Aggressive Surgical Debridement and Local Use of Antibiotic Loaded Cerament Bone Void Filler in the Management of Calcaneal Osteomyelitis as an Alternative to BBelow-Knee Amputation

Introduction: The incidence of calcaneal osteomyelitis is increasing in tandem with the prevalence of predisposing conditions, such as diabetes and peripheral vascular disease.
Due to the difficulties surrounding calcaneal infection and ulcer management, the usual treatment is often a below-knee amputation.
We at Guy's and St Thomas' Hospital have trialed the combination of surgical debridement with insertion of Cerament bone void filler to deliver antibiotics locally as well as fill dead space.

Objectives: To assess whether or not combining Cerament bone void filler with surgical debridement to treat calcaneal osteomyelitis enables limb salvage.
Methods: A retrospective review of 15 patients over a period of 4 years who underwent calcaneal surgical debridement by a single surgeon and insertion of Cerament containing vancomycin and gentamicin was undertaken.
The patients had been reviewed weekly until improvement was seen by a multidisciplinary team with staff from orthopedics, infectious diseases, podiatry, and diabetes. Negative pressure dressings and podiatry debridement were used in conjunction. The primary goal was to achieve wound closure and avoid recurrence once antibiotics or antifungals were discontinued in order to enable limb salvage.

Results: Of the 15 eligible patients who had the procedure over a 4-year period, three patients' heel ulcers have healed and no longer require antibiotics; 7 have residual ulcers that require Podiatry input but are no longer taking antibiotics and have avoided amputation; 2 have required below-knee amputations; 3 have unfortunately died due to multimorbidity.
In total, 10 out of 15—66% of patients—have avoided below-knee amputation.

Conclusion: A combination of cerament bone void filler with surgery provides an exciting prospect for limb salvage in this difficult-to-manage condition with a salvage rate of 66%.

Biography

Mr. Randhir Francis is a highly skilled trauma and orthopedic surgeon working at Guy's and St. Thomas' NHS Foundation Trust, specializing in foot and ankle surgery. He has a sub-specialty interest in the management of foot osteomyelitis, working closely with the Diabetic Foot Multidisciplinary Team, including infectious diseases, diabetes, and podiatry.

Lyudmila V. Lyubimova[1]*, Evgeniya A. Mikishanina[1,2], Svetlana I. Pavlova[2], Evgeny A. Lyubimov[1]

[1]Federal State Budgetary Institution «Federal Center for Traumatology, Orthopedics and Arthroplasty» of the Ministry of Health of the Russian Federation (Cheboksary), Russia

[2]Federal State Budgetary Educational Institution of Higher Education «Chuvash State University named after I.N. Ulyanov», Cheboksary, Russia

Potential of multiplex PCR in patients with instability of large joint endoprostheses

Relevance: Differential diagnosis between aseptic instability and culture-negative periimplantjoint infection (PJI) presents significant difficulties. Standard microbiological methods have low sensitivity, which dictates the need for the introduction of more accurate molecular-genetic methods.

The aim of the studywas to evaluate the diagnostic efficiency of multiplex real-time PCR for the verification of pathogens and the determination of the tactics of antibacterial therapy in patients with PJI and negative results of microbiological research.

Materials and methods: A prospective single-center study included 151 patients after revision arthroplasty. Based on the ICM criteria (2018), the patients were divided into groups: 1 — aseptic instability (n=108), 2 — PJI with a negative microbiological test result (n=43). In addition, all patients underwent a multiplex PCR test of swabs from implants removed during surgery, using ultrasonic treatment and the BakSkrin UPM and BakResista GLA test systems to identify a wide range of pathogens and antibiotic resistance genes.

Results: Multiplex PCR demonstrated a significant advantage over microbiological testing. In the PJI group, PCR showed a positive result in 79.1% of cases, compared to 37.2% in microbiological testing. ROC analysis confirmed the high diagnostic efficiency of PCR, with a sensitivity of 79%, specificity of 98%, accuracy of 93%, and AUC of 0.889. The Cohen's kappa coefficient (0.812) indicated almost complete agreement between the PCR method and the ICM criteria. In the group of aseptic instability, a false-positive PCR result was recorded in 1.9% of cases. A total of 36 positive PCR results were obtained: the total bacterial mass was detected in 41.7%; *Staphylococcus species* genes were detected in 44.4% (n=16), *Staphylococcus aureus* genes were detected in 16.7% (n=6), and *Streptococcus spp.* - in 5.6% (n=2), *Enterococcus spp.* - in 2.8% (n=1), and *Acinetobacter spp.* - in 2.8% (n=1) of cases. Among the pathogens detected by PCR, gram-positive cocci (*Staphylococcus spp., S. aureus*) dominated; in 5 cases, resistance genes (*mecA, OXA-51*) were detected, which allowed for the adjustment of empirical antibacterial therapy.

Conclusions: Real-time multiplex PCR is a highly informative, rapid, and reliable method for diagnosing culture-negative PJI, which is more sensitive than the microbiological method. The introduction of PCR into the diagnostic algorithm for patients with negative microbiological results allows for the optimization of surgical tactics and the targeted administration of targeted antibacterial therapy, avoiding the unnecessary use of antibiotics in cases of aseptic instability.

Biography:

Lyudmila V. Lyubimova is a clinical pharmacologist, a general practitioner with 21 years of experience, a postgraduate student, and a candidate for a medical degree. Her main area of expertise is the clinical management of patients with traumatology and orthopedics after surgical treatment of limb joints. Her research interests include infectious and vascular complications of endoprosthetics of large limb joints. She has conducted 10 local clinical studies on relevant issues. She regularly presents scientific reports at Russian specialized conferences, including those with international participation. Published 36 scientific papers. ORCID 0000-0002-5750-4459.

Ying Ma*,Dan Zhao, Juan Li, Xiaomei Li, Zhiqiang Cao, Wei Yao, Jiang Wu, Luodan Suo

Beijing Center for Disease Prevention and Control, Beijing Research Center for Respiratory Infectious Diseases, China

Effectiveness of Vaccination Against Covid 19 Related Hospitalization in Elderly Adults Aged 80 Years and Over During the Period of Omicron Circulation in Beijing, China: A Retrospective Cohort Study Using Linked Regional Healthcare Data

Background:A large wave of COVID-19 caused by SARS-CoV-2 Omicron subvariants began in Beijing in early December 2022. We evaluated the COVID-19 vaccine effectiveness (VE) in mitigating the risk of COVID-19-related hospitalization during the epidemic.

Methods: We conducted a retrospective cohort study linking regional healthcare data and vaccination registry routinely collected in Beijing. All electronical medical records on COVID-19 related hospital discharges of the elderly inpatients aged 80 years and over during November 2022 and February 2023 were included in the study. Poisson regressions were used to estimate incidence risk ratio (IRR) of COVID-19 related-hospitalization or death. VE was calculated as 1 minus IRR ×100%.

Results: A total of 53,789 individuals aged 80 and above were included, 30531 individuals were in the vaccine group (56.76%) and 23258 individuals in the unvaccinated group (43.24%). 17916 (33.31%) were diagnosed with COVID-19. The analysis revealed that the VE of booster vaccination in preventing COVID-19-related hospital, severe/critical COVID-19 and in-hospital death were 63.5% (95%CI: 59.8%–66.9%), 66.9% (95%CI: 60.1%–72.6%) and 79.4% (95%CI: 77.0%–81.5%), the VE of primary series were 56.0% (95%CI:51.4%–60.2%), 66.8% (95%CI:59.0%–73.0%) and 66.4% (95%CI: 63.0%–69.5%).

Conclusion: Booster vaccination significantly reduced the risk of COVID-19-related hospitalization, critical illness or in-hospital deaths in the elderly inpatients during an Omicron dominant period. Offering booster dose and regularly monitoring the coverage and VE of COVID-19 vaccines remains the main stay for mitigating impacts of upcoming epidemics.

Biography:

Ma Ying is a public health professional at the Beijing Center for Disease Control and Prevention, focusing on the research field of vaccine - preventable diseases. She participates in the research on the protective effect of COVID - 19 vaccines on the elderly. By analyzing the real - world data of vaccinated elderly people, she clarifies the protective effects of the vaccines against severe illness and hospitalization. Dedicated to safeguarding vulnerable groups, she now shares the research results to optimize the immunization strategies for the elderly population and help enhance this group's resilience in responding to the epidemic.

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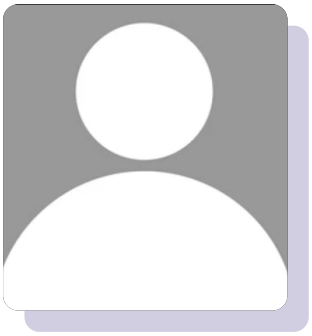
ORAL SESSION 01 | DAY 3



Jianying Xiao*, Mark Daben Javate Libardo, Fred Racine, Jing Xiao, Cheryl Callahan, Ioan Petrescu, Lorraine Hernandez, Eberhard Durr, Michael Citron

Merck & Co Inc, Rahway, USA.

Establishing an NTHi Viral Co Infection Cotton Rat Model

Bacteria-induced acute otitis media (AOM) is primarily characterized by eustachian tube dysfunction that occurs during an acute viral upper respiratory tract infection. AOM remains the most common condition leading to antibiotic prescriptions in young children. While mice and other rodent models have been utilized for AOM research, they often exhibit rapid clearance of the associated human-specific bacteria. In this study, we describe a viral/bacterial co-infection model using the cotton rat. Our data demonstrate that a co-infection strategy, initiated with a respiratory viral infection followed by bacterial colonization with non-typeable Haemophilus influenzae (NTHi),results in prolonged colonization in the nasopharynx. This colonization persists for several weeks, closely mimicking the patterns observed in humans. Establishing this model allows for the evaluation of both prophylactic and therapeutic interventions for AOM. Furthermore, this model may be further explored as a disease model in the ear, contributing valuable insights into the pathophysiology and treatment of AOM.

Biography

Jianying Xiao is affiliated with Merck & Co., Inc., based in Rahway, USA

Taghrid S. El-Mahdy[1,2]*, Amr Tarek[1], Ali A. Ahmed[3], Salah Abdalla[3]

[1]Department of Microbiology and Immunology, Faculty of Pharmacy, Modern University for Technology and Information, Cairo, Egypt

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[3]Department of Microbiology and Immunology, Faculty of Pharmacy, University of Suez Canal, Ismailia, Egypt

Association between virulence and resistance genes of Uropathogenic Escherichia coli isolated from non-hospitalized patients in Egypt

Background: One of the most prevalent microbiological conditions that can affect people of any age is urinary tract infection (UTI). Uro-pathogenic Escherichia coli (UPEC) is the primary cause of UTIs worldwide and is a major health and life-threatening threat. Therefore, our objective is to analyze the antibiotic resistance pattern of UPEC in Egypt on nonhospitalized patients and investigate the significant associations between genes encoding virulence factors and antibiotic resistance in UPEC isolates.

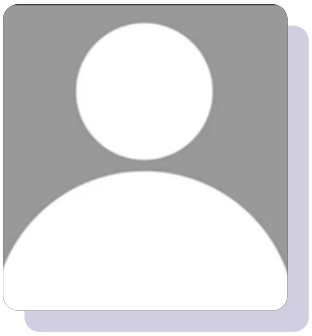
Methods: The DL Microbial ID/AST system® was used for the identification and antimicrobial minimum inhibitory concentration (MIC) determinations of 100 E. coli isolates. A total of 49 E. coli isolates were subjected to PCR to identify resistance and virulence genes. The data collected was analyzed statistically using the Chi-square test, and the strength of the relationship was determined using the Phi coefficient. Page 2 of 3

Results: E. coli showed resistance rates of 48% for cefoxitin and 72–74% for other cephalosporins (cefazoline, cefepime, cefuroxime, and ceftazidime). Carbapenems (imipenem, ertapenem, meropenem) showed the highest susceptibilities against tested strains (7–10% resistance rates), while resistance against aminoglycosides (amikacin, gentamicin) was 4% and 21%, respectively. Sulfamethoxazole/trimethoprim had 58% resistance, while nitrofurantoin had only 3% resistance. Among virulence genes, fimH was the most prevalent (91.8%), while sfa was the least detected (20.4%). Resistance genes showed blaCTXM had the highest occurrence (59.1%), and blaNDM was the lowest (12.2%). sfa and hlyA had significant associations with non-Extended-spectrum beta-lactamases (ESBL), non-Multi drug resistance, and quinolone-sensitive isolates, while traT was associated with ESBL isolates. papC significantly coexisted with hlyA but rarely with blaNDM.. Similarly, sfa significantly coexisted with hlyA but infrequently with traT, blaCTXM, and blaOXA. Minimal significant coexistence was seen between hlyA and blaTEM. blaOXA significantly coexisted with blaCTXM and blaNDM.

Conclusion: The relationship between certain virulence genes and antimicrobial resistance underscores the importance of tailored regional studies, as E. coli's response to antibiotics can either diminish or heighten its virulence. Improper antibiotic use in Egypt potentially shapes the frequency of less virulent, yet resistant, strains.

Biography:

Prof. Taghrid S. El-Mahdy is a member of Dept. of Microbiology and Immunology, Faculty of Pharmacy, Helwan University, Egypt. She was a Head of Microbiolgy and Immunology Dept. in the Faculty of Pharmacy, Modern University for Technology and Information, Egypt and in the Faculty of Pharmacy, Ahram Canadian University (ACU), Egypt. She was also an Ex-Vice Dean Academic Affairs-Female Section, College of Clinical Pharmacy, King Faisal University, Saudi Arabia. Prof. El-Mahdy achieved her PhD in Biomedical Sciences, Bradford University, UK jointly with Helwan University, Egypt. She got two postdoc grants, Fulbright Postdoc fellowship in the College of Medicine, Creighton University, USA and Postdoc in the College of Pharmacy, Université de Reims Champagne-Ardenne, France funded by STDF/IFE. She has more than 30 publications, 4 Genbank accession numbers. Her research interests include medical molecular bacteriology, genetic basis of bacterial antibiotic resistance and bacterial typing.



Fang Yuan[1,2]*, Wan Erya[1,2], Li Yuanyuan[1], Yang Limin[1], Zhou Xiaonong[1,2], Zhang Yi[1,2,]

[1]National Institute of Parasitic Diseases, Chinese Center for Disease Control and Prevention (Chinese Center for Tropical Diseases Research); NHC Key Laboratory of Parasite and Vector Biology; WHO Collaborating Center for Tropical Diseases; National Center for International Research on Tropical Diseases; Shanghai,China
[2]School of Global Health, Chinese Center for Tropical Diseases Research, Shanghai Jiao Tong University School of Medicine; Shanghai, China

Cross-Species Transmission of Avian Coronaviruses: Unveiling Spillover Dynamics from Migratory Birds to Poultry at the Wildlife-Domestic Interface

Emerging zoonotic diseases, especially coronaviruses (CoVs), pose significant public health risks, with migratory birds as key reservoirs. This study investigates CoV spillover at the wildlife-domestic interface, focusing on the seasonal and annual fluctuations of avian CoVs in migratory birds at Chongming, China. Samples collected from migratory birds during 2023-2024 showed seasonal variation in CoV prevalence, with Charadriiformes having a 22.29% positivity rate in autumn 2023, and Anseriformes showing 85.71% in winter 2023, decreasing to 10.53% in 2024. Phylogenetic analysis identified Gamma-CoVs as DuCoV_NL3, with high genetic similarity to poultry strains, indicating cross-species transmission. Environmental contamination in wetland habitats facilitated CoV transmission, with migratory birds acting as dispersers. Delta-CoV was detected less frequently but showed diversity in migratory birds and environmental samples. This study provides the first empirical evidence of pathogen spillover from migratory birds to poultry, with environmental contamination playing a key role. The findings emphasize the importance of enhanced surveillance of wildlife-poultry interactions and the need for a One Health approach to prevent zoonotic spillover and mitigate risks.

Biography:

Dr. Fang Yuan is an associate researcher of National Institute of Parasitic Diseases, ChinaCDC, adjunct faculty member of School of Global Health, Shanghai Jiao Tong University School of Medicine, a professional member of the Tropical Diseases Committee of Chinese Endemic Disease Association. She is mainly engaged in reverse etiology of vector-borne diseases, genomic tracing, transmission risk assessment, and control strategy research. She also interests in transmission mechanism of flavivirus, virus cross-species transmission. As the first author, she has published more than 30 SCI papers on Advances in Parasitology, Infectious diseases of Poverty, Frontier in Cellular and Infection Microbiology.

Alex Dower
Creating Freedom, United Kingdom.

Acting for Health': A Participatory Theatre Methodology for Behaviour Change in Infectious Disease Control

Background:

Sustainable infectious disease control often fails due to social, cultural, and behavioural barriers, even when effective biomedical interventions exist. Conventional health education can struggle to create deep, lasting change. Acting for Health is a participatory theatre methodology designed to address these challenges by engaging communities in co-created, culturally relevant role-play and storytelling, fostering learning, ownership, exploration, dialogue, and practical behaviour change.

Methods:

The approach draws on principles of active listening, co-creation, and community agency & empowerment, incorporating participants' lived experiences to explore barriers, beliefs, and solutions. Using tools and exercises from theatre modalities The Science of Acting and Forum Theatre as well as the RANAS (Risk, Attitude, Norms, Ability, Self-regulation) framework, workshops typically run over five days with diverse local stakeholders — from at-risk occupational groups to health workers, community leaders, mothers and youth.

Sessions culminate in performances for wider audiences, which can be adapted into films for extended reach. Participants are supported to become "community champions" who continue peer education beyond the workshop period.

Case Study:

In the WISER project on schistosomiasis control in Tanzania and Ethiopia, this methodology was integrated with disease awareness and capacity-building activities. Quantitative and qualitative evaluation demonstrated significant improvements in knowledge and prevention behaviours, including increased uptake of preventive chemotherapy, latrine construction, and safe water practices.

Six months later, post-intervention surveys measured changes in knowledge, attitudes, and behaviours. Qualitative data were gathered via focus groups and key informant interviews.

Results:

In Tanzania, preventive chemotherapy uptake increased from 56% to 73% in men and from 43% to 50% in women; latrine construction rose from 10% to 41%. In Ethiopia, selection of safe sanitation as a prevention method rose from 63% to 90%. Participants exposed to theatre or film were significantly more likely to report behavioural change (83–92%) compared with those unexposed (61%). Qualitative findings indicated reduced stigma, increased dialogue, and stronger advocacy for safe water access.

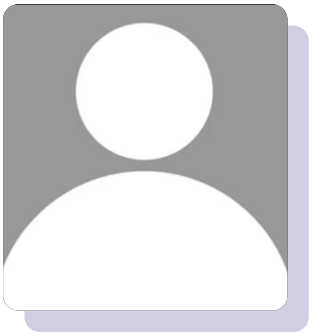
Theatre-based participatory engagement proved effective in shifting entrenched norms, reducing stigma, and mobilising communities to adopt protective behaviours. The approach's adaptability makes it applicable to a wide range of infectious diseases, particularly those where transmission is embedded in social practice

Conclusion:

Acting for Health offers a scalable, low-cost methodology for integrating behaviour change and community engagement into infectious disease prevention strategies. Its combination of imagination work, cultural resonance, creative communication, participatory design, and stakeholder ownership complements biomedical interventions offering a replicable strategy for integrated control of neglected tropical and other water-related infectious diseases.

Biography

Alex Dower is an actor, director, and creative project leader specialising in socially driven theatre and film. Founder of Creating Freedom and Acting for Health, he has led international projects in Africa, Russia, Lebanon and the UK, working with marginalised communities including prisoners, refugees, people with disabilities, and those affected by mental health challenges. An expert in The Science of Acting, Alex co-developed the innovative theatre-based behaviour change approach used in schistosomiasis control projects in Tanzania and Ethiopia. His work combines creative storytelling with participatory methods to foster health awareness, behaviour change, and community resilience.



Kaiqi Yang*, Xiaoxue Wang, Zihan Qin, Wei Jiang, Rui Gong, Xinyuan Liu, Peng Li, Shutian Zhang, Xiujing Sun, Jiugang Song

Department of Gastroenterology, Beijing Friendship Hospital, Capital Medical University, National Clinical Research Center for Digestive Diseases, State Key Laboratory of Digestive Health, Beijing Digestive Disease Center, Beijing Key Laboratory for Precancerous Lesion of Digestive Diseases, China.

Regional and Gender Disparities in Tobacco-Related Esophageal Cancer: Insights from the Global Burden of Disease Study

Background: Tobacco-related esophageal cancer (TREC) is a significant public health concern, with rising incidence and mortality rates globally. Understanding the epidemiological characteristics of TREC is crucial for developing targeted prevention strategies.

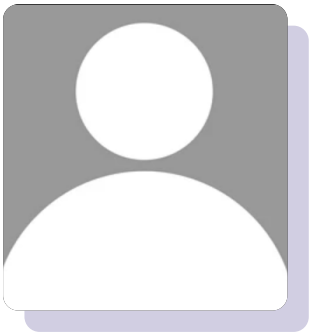
Methods: This study utilized data from the Global Burden of Disease (GBD) 2021 to analyze the epidemiological features of TREC, focusing on mortality rates, disability-adjusted life years (DALYs), and other relevant indicators across different regions, and genders. Decomposition analysis was performed to identify the main factors influencing changes in TREC burden, including population growth, aging, and epidemiological changes.

Results: From 1990 to 2021, global deaths due to TREC increased from 143,332.8 to 219,185.3, while the age-standardized death rate (ASDR) decreased from 3.6 to 2.5 per 100,000 persons. The rise in TREC burden was primarily attributed to population growth (154.62%) and aging (39.75%). DALYs associated with TREC rose from 3,844,095.6 to 5,136,277, with a notable decline in age-standardized DALYs rate (AS DALYs R) from 93.3 to 58.5 per 100,000 persons. Significant regional and gender disparities were observed, with males experiencing a higher burden.

Conclusion: The findings highlight the need for targeted public health interventions to address the rising burden of TREC, particularly in regions with high smoking rates. While population growth and aging are key contributors, improvements in public health policies have the potential to mitigate TREC burden in certain areas. Further research is necessary to explore additional factors influencing TREC epidemiology.

Biography:

Kaiqi Yang is a promising researcher in gastroenterology at Capital Medical University in Beijing. Kaiqi has published several impactful papers in prestigious journals including *Gastroenterology* and *Ecotoxicology and Environmental Safety*, focusing on topics ranging from epidemiology of gastrointestinal disorder to air pollution's health impacts. Their research excellence has been recognized with numerous accolades including the National Scholarship and an Outstanding Oral Presentation Award at the Asia Pacific Digestive Week. Kaiqiis skilled in data analysis using R and SPSS and has contributed to groundbreaking research on electromagnetic navigation colonoscopy technology and clinical trials investigating folic acid's efficacy in atrophic gastritis treatment.



Arezoo Esmaeili

Department of Biology, Branch Damghan, Azad University, Iran

The Correlation between Human Papillomavirus (HPV) Infection and Epidermodysplasia Verruciformis (EV) Disorder: A Systematic Review and Meta-Analyses

Background and Objective: Epidermodysplasia verruciformis (EV) is a rare genetic disorder characterized by abnormal susceptibility to various types of human papillomavirus (HPV), leading to widespread verrucous lesions and an increased risk of skin malignancies. The correlation between HPV infection and EV is crucial for developing effective management and preventive strategies. This meta-analysis aimed to clarify the association between HPV infection and the incidence and severity of EV, provide insight into the specific HPV types involved, and their clinical outcomes.

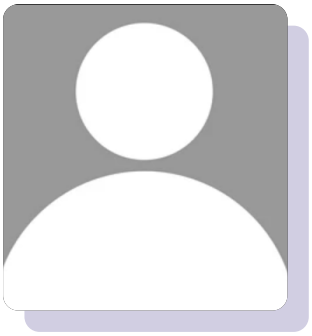
Methods: A comprehensive search of relevant literature in multiple databases (Web of Science, PubMed, and Scopus) was conducted for studies published up to March 2025. The inclusion criteria focused on studies reporting on patients with EV and their HPV status. Data on HPV types, prevalence, and clinical outcomes were also extracted. Moreover, a random-effects meta-analysis was performed to determine the pooled prevalence of HPV infection among EV patients.

Results: A total of 25 studies were included in the final analysis, including 1200 patients diagnosed with EV. This meta-analysis demonstrated a pooled HPV prevalence of 85% among EV patients, with HPV types 5, 8, and 17 being most frequently detected. The odds of developing keratinocyte carcinoma were significantly higher in HPV-positive EV patients compared with HPV-negative individuals (OR = 3.45, 95% confidence interval (CI [1.76-6.76], $P < 0.001$).

Conclusion: This meta-analysis revealed a strong correlation between HPV infection and the development of epidermodysplasia vesiculiformis. The findings indicated the importance of HPV vaccination and regular skin surveillance in patients at risk for EV to reduce the risk of skin malignancies.

Biography

Arezoo Esmaeili is affiliated with the Department of Biology, Damghan Branch, Azad University, Iran.



Moudy Bin Saleh* and Robert Hirt
Bioscience institute, medical school, Newcastle university, United Kingdom

Investigating the Effects of Short-Chain Fatty Acids on Caco-2 Cell Barrier Function with Microsporidia E. cuniculi and E. intestinalis Infection

Microsporidia are obligate intracellular parasites associated with gastrointestinal disorders, including inflammatory bowel disease (IBD). Short-chain fatty acids (SCFAs), key microbial metabolites, play a crucial role in maintaining gut epithelial integrity and modulating immune responses. This study examines the effects of SCFAs on Microsporidia-infected CACO-2 cells grown on transwell filters, focusing on infection severity, barrier function, and cell viability.

CACO-2 cells were cultured on transwell inserts to establish a differentiated intestinal epithelial monolayer. Infection severity was assessed by collecting media from the apical and basolateral compartments, and spore quantification using a hemocytometer. Transepithelial electrical resistance (TEER) was measured to evaluate barrier integrity, while paracellular permeability was assessed using fluorescent tracer molecules. Cell viability was determined to assess cytotoxic effects of infection and SCFA treatment.

Our results indicate that SCFAs significantly mitigate the impact of Microsporidia infection on CACO-2 cells. SCFA-treated cells exhibited higher TEER values, indicating improved barrier integrity, and reduced paracellular permeability, suggesting enhanced tight junction function. Additionally, SCFAs increased cell viability and decreased spore burden compared to untreated infected controls. These findings suggest that SCFAs may play a protective role in reducing Microsporidia-induced epithelial damage, potentially influencing disease progression in IBD patients. Further research is needed to elucidate the molecular mechanisms by which SCFAs modulate hostpathogen interactions and to explore their therapeutic potential in Microsporidia-associated infections.

Biography:

Moudy Bin Saleh a PhD student at Newcastle University. My research focuses on understanding the impact of Microsporidia on epithelial cells in the presence of short-chain fatty acids (SCFAs) and how this interaction may contribute to inflammatory bowel disease (IBD). I am particularly interested in hostmicrobe interactions, molecular microbiology, and gut health. My work involves molecular techniques such as PCR and eDNA analysis to detect and study Microsporidia in IBD patients. Through my research, I aim to uncover new insights into the role of Microsporidia in gut inflammation and disease progression.

Maryam Khaleghian*[1] and Farasat Veisi[2]

1Department of Biology, Payame Noor University of Tehran, Kish International Campus, Kish, Iran.
2Department of Biology, Payame Noor University of Tehran, Qeshm International Campus, Qeshm, Iran.

A Deep Learning-Based Framework for Predicting Infectious Disease Outbreaks Using Temporal and Demographic Data

The continuous occurrence of infectious disease outbreaks proves the necessity for precise and immediate forecasting methods to tackle global health challenges. The traditional surveillance systems use past data for analysis, but they do not have predictive features which restrict their capacity for early response preparation. This study develops a deep learning system which combines temporal and demographic data to make predictions about infectious disease outbreaks. The integration of time series and demographic data provides the model with improved predictive capabilities for public health monitoring. The study analyses two publicly available datasets from Kaggle which are titled “Infectious Disease Cases Data” and “Infectious Disease Prediction”. The main target variable measures confirmed infectious disease cases that occur daily or weekly. The analysis depends on input data which includes past disease cases combined with date information along with seasonal indicators together with demographic elements like population density and age group distribution and gender ratio and geographical region. External environmental data about temperature and humidity can be integrated as optional features to enhance model context understanding. The proposed approach uses a hybrid deep learning framework which includes Long Short-Term Memory (LSTM) networks and an attention mechanism. The temporal input stream runs through LSTM layers to extract time-dependent patterns which combine with a dense layer to process static demographic features. A subsequent attention mechanism processes the temporal data to determine which time steps hold the most significance. The predictive model combines output from both branches to produce its final predictions. The assessment of model performance compares against three traditional forecasting methods: ARIMA, Random Forest and XGBoost. The experimental findings show that the proposed model demonstrates strong predictive performance along with universal applicability. The model demonstrates performance metrics of RMSE at 13.42 and MAE at 9.81 and an R^2 score of 0.91 during multiple cross-validation experiments. The model achieves a binary classification accuracy rate of 94.7% when it is used for outbreak risk prediction through a defined threshold classification. The attention visualization results show that the most influential factors for prediction include recent seven days case values and regional population density thus demonstrating the model’s practical and interpretive value. The study presents an original solution to predict infectious disease outbreaks by merging temporal patterns and demographic variables through a clear deep learning framework. LSTM integration with attention mechanisms produces precise forecasting outcomes and improves outbreak driver understanding. This method shows strong potential for deployment as an early warning system that enables data-driven public health decisions at the right time.

Biography:

Ms. Maryam Khaleghian is a researcher in Molecular Genetics at Payame Noor University of Tehran, Kish International Campus, Iran, specializing in the application of artificial intelligence (AI) in biomedical research. Her work focuses on disease classification and prediction using machine learning and deep learning techniques. She has contributed to advancing precision medicine through AI-driven models. Maryam actively participates in international conferences, presenting AI-driven solutions for genetic disorders, disease risk assessment, and predictive analytics in healthcare. She has Under Review Papers in peer-reviewed journals and collaborates on multidisciplinary projects bridging genomics and AI. Her expertise includes bioinformatics, statistical modeling, and deep learning architecture like CNNs, RNNs, and transformer models. Proficient in Python, R, and MATLAB, she applies these tools for genomic data analysis and predictive modeling. Dedicated to innovation in biomedical AI, she continues expanding her research through academic collaborations and advanced training programs.

Muhammad Ali Abdullah Shah*, Muhammad Faheem, Ayesha Riaz
Chairman, Department of Parasitology and Microbiology. PMAS Arid Agriculture University, Rawalpindi. Pakistan

Identification and molecular characterization of gene etmic-2 of*Eimeria tenella*as a potential DNA vaccine candidate

Avian coccidiosis is the intestinal disease of poultry. It is caused by the infection of Eimeria species. It has a devastating effect on the poultry industry worldwide. Two species Eimeria tenella and Eimeria maxima cause severe losses in the poultry industry. Eimeria tenella is used as a model species to understand the Eimeria species. In all Apicomplexan parasites, microneme is used to host cell invasion. Microneme protein 2 in Eimeria tenella (EtMic-2) has an important role in parasite adhesion to the host cell to initiate the invasion process. Ten gut samples of broiler chickens were collected randomly from infected chickens. All caecal material was homogenized and RNA extracted by using Trizol reagent then cDNA was formed with the help of enzyme reverse transcriptase. The gene EtMic-2 that encodes the Micronemes-2 protein was isolated by using gene-specific primers. PCR was used to obtain a large number of copies of that particular gene and sequence them. The sequence gene of EtMic-2 was compared with the available gene of Etmic-2 in GenBank affirm similarity of the nucleotide sequence were 98 and 97% respectively. The purpose of this study to sequence the gene EtMic-2 also investigated for mutation and studied the phylogenetic relationship. Etmic-2 gene is possible choice for new vaccine against E.tenella infection in chickens.

Biography:

Dr. Muhammad Ali A. shah completed his PhD from Nanjing Agricultural University, China with specialization in DNA vaccines. He has completed his Post Doctorate with distinction from Biomedical Engineering at School of Biological Sciences & Medical Engineering, Southeast University, China. During the Post Doctorate studies he had an opportunity to work with legend like Prof He Nongye. He worked on different possibilities of application of nanoparticles with drug delivery. There are almost 70 publications at his credit, which have been cited in 5, 00 plus publications by other research groups throughout the world. He has co-authored a couple of books as well and Editor of a couple of journals from The Science Publishers. He is the recipient of 6 international R & D grants funded from Higher Education Commission, China Science Foundations, and Jiangsu Science Fund etc. He is regular receipt of Research Productivity award from Pakistan Council of Science and Technology. Currently he is working as Professor/Chairman, in Arid Agriculture University. His current research interests include immuno-therapeutics especially DNA vaccination and Nano vaccines against Infectious agents and their delivery.

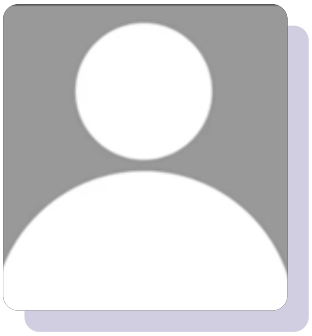
Garima Joshi*, Gulistan Parveen, Asuru Tejaswar Rao, Prasenjit Guchhait
Regional Centre for Biotechnology, NCR Biotech Science Cluster, Faridabad, Haryana, India.

Promising Therapeutic Intervention: Dietary Supplementation with αKGReduces Pulmonary Fibrosis and ARDS Pathogenesis in SARS-CoV-2-Infected Mice

Our recent study elucidates the protective role of alpha-ketoglutarate (αKG) in suppressing thrombosis and inflammation in mice. This effect is mediated through augmentation of prolyl hydroxylase 2 (PHD2) activity, leading to inhibition of AKT phosphorylation and HIF1-α stabilization. Recently, we described that dietary αKG supplementation attenuated lung inflammation and improved the mice survivability against SARS-CoV-2 infection. We further investigated the therapeutic potential of αKG in ameliorating pulmonary inflammation and fibrosis in SARS-CoV-2-induced acute respiratory distress syndrome (ARDS) in mice. Mice with acute infection developed pulmonary fibrosis, leading to ARDS pathophysiology limiting O_2 levels. We describe that supplementation with 1% αKG till 15 days post-infection (DPI) significantly reduced SARS-CoV-2 infection, and decreased inflammation and fibrosis markers like surfactant proteins B and C in the lungs and thus helped to restore the limiting O_2 levels. SARS-CoV-2 induced epithelial to mesenchymal transition (EMT) in the lung tissues. Notably, αKG supplementation effectively inhibited the EMT and rescued lung fibrosis by suppressing P-AKT and TGF-β, reduced ZEB-1 and vimentin, and rescued EMT. Our findings thus underscore the promising therapeutic potential of αKG in treating lung fibrosis in SARS-CoV-2-induced ARDS-like conditions.

Biography:

I'm Garima Joshi, a Ph.D. scholar at the Regional Centre for Biotechnology (RCB). As a senior research fellow, my research focuses on combating post-acute COVID-19 complications, especially pulmonary inflammation and fibrosis, through alpha-ketoglutarate supplementation. To drive this forward, I've developed a unique SARS-CoV-2-induced ARDS mice model, enabling new insights. With four publications—three research articles and a review—I'm committed to advancing science and sharing findings. I actively engage in scientific conferences, including the IUBMB RNA virus meeting (2022) and a human microbiome conference with a next-generation sequencing workshop (2023). These events have enriched my research perspective and facilitated valuable professional connections



Fahad Alreshoodi
Designation:Executive Department of Reference Laboratories, Research and Laboratories, Saudi Food and Drug Authority (SFDA), Saudi Arabia

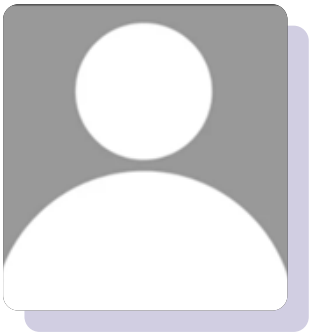
Antimicrobial Resistance and Genomic Characterization of Salmonella Enterica Isolates from Chicken Meat in Saudi Arabia

Introduction

Over the past decades, the increase of multidrug-resistant (MDR) forms of Salmonella in food-producing animals has progressively become a serious risk worldwide (1). This is likely due to the widespread and long term use of common antimicrobials in poultry and animal husbandry for therapeutics, prophylaxis and growth promotion 2 Although Salmonella is a major cause of human foodborne illnesses worldwide, little is known about its phenotypic and genotypic characteristics in food sources in Saudi Arabia Therefore, this study investigated genotypic and phenotypic antimicrobial resistance profiles, phylogenic relatedness, plasmid and virulence composition of 39 Salmonella enterica strains isolated from chicken meat samples using whole genome sequencing (WGS) technology.

Biography

Fahad Alreshoodi is an Executive Department of Reference Laboratories, Research and Laboratories, Saudi Food and Drug Authority (SFDA), Saudi Arabia



Maryam Jamil*, Sana Zafar, Tehmina Bibi, Parveen Akhtar Buttar, Bushra Shal, Kifayatullah Shah, Fakhar ud Din, Eun Kyoung Seo, Salman Khan
Pharmacological Sciences Research Lab, Department of Pharmacy, Faculty of Biological Sciences, Quaid-i-Azam University, Pakistan

Suppression of TLR4/NF-κB Signaling by Kaurenoic Acid in a Mice Model of Monosodium Urate Crystals-Induced Acute Gout

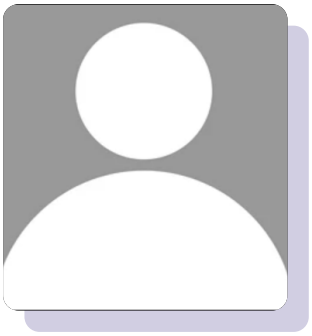
Aim: The aim of the current study was to investigate the potential therapeutic effect of kaurenoic acid (KA) against Monosodium Urate Crystals (MSU)-induced acute gout by downregulation of NF-κB signaling pathway, mitigating inflammation and oxidative stress. KA potentially targeted NF-κB pathway activation and provided comprehensive insights through multiple approaches. This was accomplished by advanced analytical techniques. This methodology highlighted the efficacy of KA in acute gout attacks offering new approach for gout management.
Methods: In-vivo model of acute gout was established in BALB/c mice. Anti-inflammatory and urate-lowering potential was determined through pain behavioral evaluation, biochemical analysis, histological and immuno histochemical assays, radiological assessments, Fourier Transform Infrared (FTIR) analysis, and computational analysis.
Results: The paw edema, joint thickness, and the frequency and duration of acute gout flare-ups were all significantly ($p < 0.001$) decreased by the administration of KA. A considerable reversal of inflammation and deterioration was observed in the KA-treated groups in X-ray examination. The FTIR spectroscopy indicated the changes in the molecular makeup of tissues, and modifications of biomolecules including proteins, lipids, and carbohydrates. Histopathological changes showed marked ($p < 0.001$) improvements in cellular structure of the paw, and inflammatory cell infiltration in the treatment groups. Trichrome staining revealed suppressed collagen deposition, inflammation, and tissue repair in the paw. In paw tissues, the KA therapy up- regulated IκB α expression while down-regulating toll-like receptor 4 (TLR4), nuclear factor- kappa B (NF-κB), inducible nitric oxide synthase (iNOS), and cyclooxygenase-2 (COX-2) expression. On the other hand, KA therapy greatly increased antioxidants and decreased oxidative

stress indicators significantly ($p < 0.001$). According to Evans's blue permeability analysis, results showed that the treatment groups' vascular permeability was intensely reduced in comparison to the diseased group. Molecular docking studies indicated that KA appeared to have a high tendency to bind to protein targets. KA was associated with the drop in the cytokines such as tumor necrosis factor-alpha (TNF α) and interleukin-1beta (IL-1β).
Conclusion: In conclusion, this study highlighted the potential therapeutic effect of KA in alleviating MSU-induced gout by suppressing the NF-κB signaling pathway. The anti- inflammatory and antioxidant activity was demonstrated by behavioral studies and advanced biochemical evaluations including blood analysis and

oxido-nitrosative stress markers. Histopathological analysis, including H&E staining, immunohistochemistry, and Masson Trichrome staining, revealed tissue preservation, while FTIR and X-ray revealed structural improvements. Molecular docking verified strong binding affinity to NF-κB-related targets, verifying its mechanistic.

Biography

Maryam Jamil is currently serving as a Lecturer in Pharmacology at Allied College of Health Sciences, Multan, Pakistan, and has also worked as a Research Assistant at Quaid-i-Azam University, Islamabad. She holds a Pharm.D and an MPhil in Pharmacology, with research expertise in inflammation, pain, neuroprotection, and natural product pharmacology. As the first author of this study, she contributed to conceptualization, experimental design, data curation, and manuscript preparation. She has published multiple research articles in peer-reviewed journals and is passionate about investigating bioactive compounds to develop novel, safe, and effective therapies for chronic and inflammatory diseases.



Dlamini S[123]*, Ismail F[3], Tshabane C[3], Zwane T[12], Joseph L[3], Shabalala A[3], Vally O.S[3], Moultrie H[3]

[1] School of Public Health, Faculty of Health Sciences, University of the Witwatersrand, Johannesburg, South Africa

[2] South African Field Epidemiology Training Programme, National Institute for Communicable Diseases, a Division of the National Health Laboratory Service, Johannesburg, South Africa

[3] National Institute for Communicable Diseases Centre for Tuberculosis, Division of the National Health Laboratory Service, Johannesburg, South Africa

Characteristics Of Recurrent Individuals with Tuberculosis and Factors Associated with Unsuccessful Treatment Outcomes, South Africa, 2019–2023

Introduction: Tuberculosis (TB) remains the second leading cause of death from a single infectious agent globally. Recurrent TB episodes, defined as individualsConclusion: In conclusion, this study highlighted the potential therapeutic effect of KA in alleviating MSU-induced gout by suppressing the NF-κB signaling pathway. The anti- inflammatory and antioxidant activity was demonstrated by behavioral studies and advanced biochemical evaluations including blood analysis and

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Ahad Al Balushi[1]*, A. Al Wahaibi[2], A. Al Rashdi[3], A. Al Jardani[3], N. Al Balushi[3], I. Al Wahaibi[3], A. Al Maani[4]

[1]Oman Medical Specialty Board - Muscat (Oman).
[2]Ministry of Health - Muscat (Oman).
[3]Central Public Health Laboratories - Muscat (Oman).
[4]Ministry of Health - Muscat (Oman).

The epidemiology of brucellosis in Oman: a seven-year retrospective analysis (2017-2023)

Background: Brucellosis is a zoonotic disease with a significant impact on Middle Eastern countries, including Oman. Its diagnosis is challenging due to non-specific symptoms and difficulty in interpreting serological test results. This study aims to understand the epidemiology and clinical presentation of human brucellosis in Oman, and to assess the performance of brucellosis screening tests.

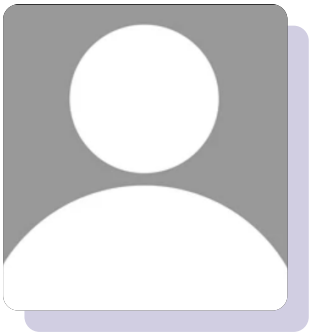
Methods: A retrospective cross-sectional study, conducted among patients diagnosed with brucellosis in Oman over seven years (2017–2023), using two datasets: the first included all notified cases reported to the Ministry of Health from 2017 to 2023, providing a comprehensive epidemiological profile, while the second focused on laboratory-confirmed cases from Central Public Health Laboratories and Sultan Qaboos Hospital in Salalah, comparing the cases between the northern and southern governorates of Oman. Data were analysed for trends and demographic relationships, with comparative analyses of the symptoms and diagnostic performance between the two governorates (i.e., endemic and non-endemic). Data were analysed using R project software.

Results: Among 3,383 cases, 77.2% were from the southern governorate (Dhofar) and 22.8% from northern regions. Males were predominantly affected. The 30-39 age group had the highest incidence in both regions, with young children (0-9 years) also significantly affected in Dhofar. Fever (82.3% in the south, 64% in the north) and body aches (64% vs. 52.1%) were the most common symptoms. Complications such as spondylodiscitis were more frequent in the north (14.8%) than in the south (5.4%). Diagnostic accuracy varied significantly, with serological test performance dependent on regional prevalence and cutoff thresholds.

Conclusions: The study revealed significant regional and demographic differences in brucellosis cases. These findings highlight the importance of ongoing surveillance, tailored diagnostic strategies, and targeted public health interventions to improve brucellosis management in endemic and non-endemic areas.

Biography:

Dr. Ahad Al Balushi, a medical microbiology resident at the Oman Medical Specialty Board (OMSB), is the primary investigator for this study. Interested in infectious diseases, epidemiological studies and rare zoonotic diseases. Has a publication on sexually transmitted diseases.



Christian Dondonan*, Alexander Von Roenn, Japjit Serai,Robert Gemayel, Elizabeth Brooks

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Non-typhoidal Salmonella Presenting as Bilateral Cellulitis and Bacteremia in a Diabetic Patient

Non-typhoidal salmonella typically presents acutely with gastrointestinal distress. Rarely, these infections can present extra-intestinally, likely secondary to gut translocation. It is exceedingly rare however for them to manifest with cellulitis, especially in a bilateral distribution.A 35-year-old male with past medical history of diffuse adiposity, essential hypertension, neuropathy, and depression presented to the ED for evaluation of sudden onset, bilateral, lower extremity swelling, pain, and redness. The patient first appreciated these symptoms upon awakening 2 days prior, accompanied by night sweats. He mentions having burned his right medial lower leg on a motorcycle exhaust pipe a week prior but reported appropriate healing to the burn thus far. Of note, the patient owns a corn snake and was diagnosed with diabetes during this admission. He was ultimately found to have diffuse cellulitis of his bilateral lower extremities with subsequent blood cultures yielding a diagnosis of bacteremia secondary to salmonellosis.A very small subsection of patients with confirmed salmonella infection develop bacteremia. Cellulitis is also an uncommon presentation for salmonellosis. Given this patient's recent burn wound and his exposure to reptiles; in conjunction with uncontrolled diabetes, we suspect the bacteria seeded the patient's bloodstream via the burn wound and was able to proliferate given his somewhat immunodeficient state. There remains the possibility that this patient, who claims rigorous adherence to hygienic handling of his reptile, was already a carrier of salmonella and that his burgeoning diabetes hampered his immune system to the point the bacteria was able to flourish and cause tissue breakdown in the dependent portions of his body.

Biography:

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Latent Tuberculosis Management in Liver Transplant Recipients: Insights from a Retrospective Analysis

Objective: This retrospective cross-sectional study aimed to investigate latent tuberculosis infection (LTBI) management in liver transplant recipients, assessing the impact of isoniazid prophylaxis and patient outcomes.

Methods: Data from liver transplant recipients (2013-2021) at Montaseriyeh Hospital, Mashhad, were analyzed. Inclusion criteria comprised patients with a positive tuberculin skin test (PPD) or interferon-gamma release assay (IGRA) in either the donor or recipient (n=30). Demographic, clinical, and laboratory information, including the duration of isoniazid use, liver enzyme levels, and patient outcomes, was collected. Statistical analyses included descriptive statistics, non-parametric tests, and logistic regression.

Results: Thirty liver transplant recipients received isoniazid prophylaxis (up to 9 months). Isoniazid usage duration and liver enzyme levels distribution were non-normal. The distribution of isoniazid use duration and liver enzyme levels did not follow a normal distribution. No significant increase was found in liver enzyme levels (serum glutamic oxaloacetic transaminase (SGOT), and serum glutamate pyruvate transaminase (SGPT)) across different intervals. When examining each variable separately, higher SGOT and SGPT levels at the end of the first month after isoniazid consumption were significantly associated with increased mortality risk. The duration of isoniazid use and liver enzyme levels in subsequent months did not exhibit a significant relationship with patient survival.

Conclusions: Managing LTBI in liver transplant recipients presents challenges in isoniazid prophylaxis and predicting outcomes. Elevated SGOT and SGPT levels at the end of the first month after isoniazid consumption were associated with increased mortality risk. Further research is required for optimizing LTBI management in this patient population.

Biography: My name is Rozita Khodashahi, and I am an Infectious Disease Specialist and Associate Professor at Mashhad University of Medical Sciences. I also serve as the Research Deputy at the Transplant Hospital and General Imam Reza Hospital, as well as the Head of the Clinical Research and Development Unit at Imam Reza Hospital, Faculty of Medicine, Mashhad University of Medical Sciences. I have published 56 articles in my field. My professional areas of expertise include immunocompromised patients, solid organ transplantation (SOT), bone marrow transplantation (BMT), all types of transplant patients, hematologic malignancies, and cancers.

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A Changing Epidemiology of Typhoid Fever: Pre- and Post-COVID-19 Trends in India with Emerging XDR cases

Introduction: Typhoid fever, a systemic febrile illness caused by *Salmonella* Typhi (*S.* Typhi) has a complex history ofongoing adaptation and progressive build-up of resistance to commonly used antibiotics. Since the XDR (resistant to chloramphenicol, trimethoprim-sulfamethoxazole, ampicillin, fluoroquinolones, and third-generation cephalosporins) typhoid fever outbreak in Sindh, Pakistan, cases from different part of the world have been reported but no XDR case has been reported from India until now. To better understand the seasonal dynamics in India to aid the evaluation of disease surveillance and control efforts we analyse the typhoid data from 2017 to 2024.
Overall, the data was divided in two groups: pre-COVID-19 (2017-2019) and post COVID-19 (2020-2024) which also includes the isolation of one XDR Salmonella Typhi in 2023.

Methods: All the culture positive enteric fever cases during 2017–2024 presenting to our hospital were included in the study. Antimicrobial susceptibility was done against amoxicillin, chloramphenicol, cotrimoxazole, ciprofloxacin, levofloxacin, ofloxacin, pefloxacin, ceftriaxone and azithromycin as per corresponding CLSI guidelines for each year.

Whole-genome sequencing (WGS):WGS was carried outfor molecular characterization of XDR isolate with paired-end2 x 150 bp reads on Illumina MiSeq (Illumina, USA) employing v2 and v3 chemistry.

Results: Total isolation of blood culture positive typhoidal Salmonella was 596 during the study period (2017-2024). Out of which Salmonella Paratyphi A was 117 followed by 479 Salmonella Typhi.

Pre-COVID 19 - Fluoroquinolones (CIP, LEV, OFL) show notable non susceptibility which is 14–20% followed by 74–89% intermediate susceptibility and exhibiting only 2–6% susceptibility.
While ceftriaxone and cefixime showed complete susceptibility, azithromycin resistance was observed in 2% isolates. Resistance to chloramphenicol, cotrimoxazole and ampicillin (MDR) was recorded in 2-3% isolates.

Post-COVID 19-Fluoroquinolones (CIP, LEV, OFL) shows increase in non-susceptibility which is 28–52%followed by 69–44% intermediate susceptibility and exhibiting only 3–4%susceptibility.
In case of ceftriaxone and cefixime marginal resistance starts appearing with the isolation of XDR

Salmonella Typhi while azithromycinresistance was observed in 2% Salmonella Paratyphi A. In case of Salmonella Typhi, though there was increased MIC but it was completely sensitive. Resistance to chloramphenicol, cotrimoxazole and ampicillin (MDR) was again observed in 2-3% isolates.

WGS analysis- Genomic analysis revealed this isolate belongs to H58 lineage 1 (genotype 4.3.1.1). It carried mutations in gyrBS464F, aac6-Ib-cr and qnrB gene responsible for resistance to ciprofloxacin and other fluoroquinolones, blaCTX-M-15_23; blaOXA-1; blaTEM-1D for ampicillin resistance, blaCTX-M-15_23 for cephalosporin resistance, catA1 for chloramphenicol resistance, dfrA1; dfrA7; sul1; sul2 for trimethoprim sulfamethoxazole resistance. The presence of IncR plasmid was also observed. The genomic analysis revealed a resistance pattern consistent with XDR, aligning with the outbreak reported in Pakistan. Interestingly, the strain displayed a new lineage, distinct from known XDR isolates in Pakistan.

Conclusion: These results support the fact that ceftriaxone-resistance in India is evolving independently. Azithromycin remains the available treatment option for XDR. *S.* Typhi since most isolates in India are currently susceptible to azithromycin with only occasional reports indicating an increase in MIC.

Biography:

Working as a Professor in the Department of Microbiology, AIIMS, New Delhi. Academic activity includes teaching UG (MBBS) and Post Graduate Medical (MD), DM (Infectious Disease) Students and guiding PhD students. Research activities involve understanding host-pathogen relationships and molecular epidemiology of Streptococcus pneumoniae, Haemophilus influenzae, and Neisseria *meningitidis*. Interest also involves understanding HIV immunology. Had been involved in vaccine development of rotavirus vaccine for India,which led to the development, licensing, and finally implementation of rotavirus vaccine (Rotaract) based on AIIMS neonatal rotavirus 116E, currently a part of the expanded program of immunization for children in India

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Ceftriaxone in the Management of Community-Acquired Pneumonia: A Multicentre, Retrospective, Real-World Evidence Study

Introduction: Ceftriaxone has long been a cornerstone in the management ofcommunity-acquired pneumonia (CAP), a major global health concern. However, real-world evidence on its effectiveness and safety in the Indian population remains limited. This study assessed clinical effectiveness and safety of ceftriaxone in the treatment of CAP across diverse healthcare settings in India.

Methods: This multicentre, retrospective, real-world study analyzed medical records of patients with CAP who received ceftriaxone in both outpatient (OPD) and inpatient (IPD) settings. Data on patient demographics, clinical presentation, diagnosis, and treatment details were collected at baseline and a follow-up visit. The primary efficacy endpoints included clinical and microbiological cure rates, while safety was evaluated based on adverse event monitoring.

Results: This study included 1,799 patients, with a mean age of 38.67 ± 17.6 years, of whom 70% were male. The largest proportion of patients (38.5%) belonged to the 18–40 age group, followed by 34% in the 41–60 age bracket. Among the total cohort, 1,150 individuals were treated with ceftriaxone as inpatients. *Streptococcus pneumoniae* was the most commonly identified pathogen, followed by *Staphylococcus aureus, Klebsiella pneumoniae*, and *Haemophilus influenzae*. The majority of patients (56.67%) received an intravenous dose of 1 g ceftriaxone twice daily, with an average treatment duration of five days (46.8%). A clinical cure was achieved in 72.4% of cases, while 27.4% of patients experienced symptomatic relief. Adverse reactions were uncommon, with only four patients reporting mild side effects such as nausea, vomiting, and urinary disturbances.

Conclusion: This study reaffirms the efficacy and safety of ceftriaxone in treating CAP in India, demonstrating high clinical cure rates with minimal adverse effects. Its continued use remains valuable, particularly in resource-constrained settings where access to effective treatment options is essential.

Biography:

After completing MBBS and MD Pharmacology from Seth GS Medical College & KEM Hospital, Mumbai, my professional career began as a Medical Advisor with Ferring Pharmaceuticals. Being involved in pre-clinical and clinical studies during academics, I represented India in an ethics conference in Nagasaki, Japan. Thereafter, I gained experience as a Scientific Writer with Cactus Communications, Mumbai. I've worked as a Medical Monitor for several global clinical trials with IQVIA, India as a part of data science, safety, and regulatory team. Overall, >6 years of experience in various portfolios and therapy areas. Currently, I'm associated with the Medical Affairs department of Alkem Laboratories in Mumbai and handle the infectious diseases, gastroenterology, and gynaecology therapy areas.

Zhujiazi Zhang[1]*, Qing Wang[2], Qi Zhu[3], Shuang Bai[1], Yang Liu[2], Jia Ren[4], Xin Xu[3], Jiangwen Que, Jingbin Pan[1], Li Lu[1], Luodan Suo[1], Xiaodong Sun[4], Ying Zhang[5], Jiang Wu[1]

[1]Department of Immunization and Prevention, Beijing Center for Disease Prevention and Control, China.
[2]Department of Immunization and Prevention, Chongqing Municipal Center for Disease Control and Prevention, China.
[3]Department of Immunization and Prevention, Guangdong Provincial Center for Disease Control and Prevention, China.
[4]Department of Immunization and Prevention, Shanghai Municipal Center for Disease Control and Prevention, China.
[5]Department of Immunization and Prevention, Tianjin Center for Disease Control and Prevention, China.

Seroepidemiology of Pertussis Immunity in Five Provinces of China: A Population-Based, Cross-Sectional Study

This study aimed to evaluate the seroprevalence of Bordetella pertussis and persistence of antibodies following vaccination. We recruited 6060 healthy subjects from five provinces of China during 2017–2018. Serum IgG antibodies against pertussis toxin (anti-PT IgG) and filamentous hemagglutinin (anti-FHA IgG), and serum IgA antibodies against pertussis toxin (anti-PT IgA) were measured by ELISA. Geometric mean concentration (GMC), seropositivity rate, and recent infection rate were calculated. Among 0–6 years-olds, the anti-PT IgG, anti-PT IgA, and anti-FHA IgG GMCs were 6.4 IU/ml (95% CI 6.1–6.8), 2.8 IU/ml (95% CI 2.7–2.8), and 13.3 IU/ml (95% CI 12.4–14.2), respectively. The anti-PT IgG GMC increased in accordance with the primary vaccination series (4–6 months) and the toddler booster (18–24 months), but declined thereafter through to age 5 years [4.7 IU/ml (95% CI 4.2–5.4)]. The seropositivity rate of pertussis in >6 year-olds was 9.0% (95% CI 8.1–9.9) and the recent infection rate was 3.3% (95% CI, 2.7–3.8). Recent infection rate began to increase from 6 years of age, with peaks at 9, 20, 40, and ≥60 years of age. The anti-PT IgG GMCs of children aged 0–6 years who were vaccinated with DTaP, DTaP-IPV//PRP□T, and DTaP-Hib were 5.9 IU/ml (95% CI 5.6–6.3), 20.7 IU/ml (95% CI 15.6–27.8), and 11.7 IU/ml (95% CI 7.5–18.1) ($p < .001$), respectively ($p < .001$). Pertussis vaccination improves anti-PT IgG levels, however these wane soon after vaccination. Sero-estimated recent infec-tion rates appear to increase from school age into adolescence and adulthood. Pertussis vaccine boosters should be considered in these age groups.

Biography:

I am the department of immunization and preventiondeputy director of the Beijing Center for Disease Control and Prevention. I have been deeply involved in vaccine-preventable infectious diseases surveillance and control for many years, including

poliomyelitis, measles and pertussis. As a member of the National Health Emergency Team, I contributed to the epidemic prevention and control of significant infectious diseases outbreaks, including poliomyelitis, H1N1, COVID-19, and plague, while also played a key role in ensuring health security for various major events, such as the centenary of the Communist Party, National Day celebrations, domestic and international sports events, and international conferences.My primary research focus lies in evidence-based vaccine immunization strategies, providing critical evidence support and scientific basis to inform government decisions on immunization strategies, technical plans, and disease prevention measures.

Bahar Nayeri Fasaei

Department of Microbiology and Immunology, Faculty of Veterinary Medicine, University of Tehran, Iran

Thymus daenensis and Satureja hortensis essential oils inhibit biofilm formation and quorum sensing of Escherichia coli O157:H7

Bahar Nayeri Fasaei

Enterohemorrhagic Escherichia coli (EHEC) is a highly pathogenic strain leading to hemorrhagic colitis and to the hemolytic-uremic syndrome (HUS) in humans. EHEC is able to form biofilms on various biotic and abiotic surfaces, such as, on plants, stainless steel, glass, and polymers. In the present study we aimed to investigate the antibacterial, anti-biofilm and quorum sensing (QS) inhibitory potential of Thymus daenensis and Satureja hortensis essential oils (EOs) against E. coli O157:H7.

The plant EOs were extracted by hydrodistillation and their compounds were analyzed by gas chromatography-mass spectrometry (GC-MS). The antibacterial and anti-biofilm potential of the tested EOs were determined by microdilution broth and microtiter-plate (MtP) tests, respectively. The QS inhibitory (QSI) potential of T.daenensis and S. hortensis EOs was examined by inhibition of motility (swimming and swarming) at sub-MIC levels and determination of the expressions of two QS-system-related genes (luxS and pfs) at sub-MIC concentrations.

Based on microdilution broth, the MICs for T. daenensis and S. hortensis EOs against EHEC were 3.12 and 6.25 µg.ml-1, respectively. In addition, the MtP test showed a significant ($p < 0.05$) inhibitory and disruptive effects of both tested EOs on EHEC biofilm formation at MIC/2 (1.56 µg.ml-1 for T. daenensis; 3.12 µg.ml-1 for S. hortensis) and MIC/4 (0.78 µg.ml-1 forT. daenensis; 1.56 µg.ml-1 for S. hortensis) concentrations. Real time PCR showed a significant down-regulation of luxS and pfs following treatment with MIC/2 concentrations of both tested EOs.

Accordingly, the present study highlighted the acceptable antibacterial, anti-biofilm and anti-QS potential of T. daenensis and S. hortensis EOs against E. coli O157:H7.

Biography :

I am Bahar Nayeri Fasaei associated professor in faculty of veterinary medicine, Tehran university.I am so interested to participate in the uropeancongress.I have worked in Tehran university for 15 years.

Nisrina Nur Fatiha[1]*, Qonita Jayanti Wijayatno[1], Khansa Anindya[1], Dian Kesumapramudya Nurputra[2]

[1]Department of Child Health, Faculty of Medicine, Public Health, and Nursing, Gadjah Mada University, Indonesia

[2]Sardjito General Hospital, Indonesia

The Evaluation of MXA Protein as a Diagnostic Biomarker in Paediatric Bacterial and Viral Meningitis

Introduction: Bacterial and viral meningitis remain leading causes of paediatric mortality in Indonesia, with an incidence of 1,000 cases per 100,000 live births and a case fatality rate of up to 25%. Prompt initiation of antibacterial therapy is crucial to reduce disease burden and severity. However, this requires rapid and accurate differentiation between bacterial and viral aetiologies. Current diagnostic methods are often non-specific and time-consuming. The MXA protein is a recognised component of the antiviral defence system and a proposed serum biomarker for viral infections. However, its presence in other clinically relevant sample types, specifically cerebrospinal fluid, and plasma, during bacterial meningitis is not well characterised, representing a significant diagnostic gap.

Objective: This study aims to characterise the presence of the MXA protein in both bacterial and viral meningitis to evaluate its specificity. The primary objectives are to: 1) determine the presence of MXA protein in cerebrospinal fluid (CSF) and peripheral blood mononuclear cells (PBMCs) of patients with bacterial and viral meningitis, and 2) compare its relative concentration and abundance between these sample types and infection aetiologies.

Methods:CSF samples were analysed directly. Paired blood samples were processed using Ficoll-Hypaque density gradient centrifugation to isolate PBMCs. Total protein was extracted from PBMCs using a lysis buffer, and its concentration was quantified via Bradford assay. Qualitative detection of MXA protein in both CSF and PBMC protein extracts was performed using Western Blot analysis.

Results: MXA protein was detected in both CSF and PBMC-derived samples from patients with confirmed bacterial and viral meningitis, as indicated by distinct bands on Western Blot. However, the protein concentration as measured by Bradford assay and relative abundance as indicated by the band intensity varied considerably across samples and did not follow a consistent pattern specific to either the sample type (CSF vs. PBMC) or the infection aetiology (bacterial vs. viral).

Conclusion: These findings demonstrate that MXA protein is present not only in viral infections, as previously established, but also in bacterial meningitis. Its detectable presence in both CSF and PBMCs suggests it is not a specific biomarker for viral meningitis in these clinical samples. This challenges the existing paradigm and underscores the need for further investigation to interpret the clinical significance of MXA expression. Future research with quantitative assays and larger cohorts is essential to define its role in host immune response and its potential implications for diagnostic strategy.

Biography

Nisrina Nur Fatiha, MD, MSc, is a medical doctor and genetic researcher. She earned her medical degree from Universitas Gadjah Mada and her Master's in Genomic Medicine from the University of Oxford. Currently, she is a Research Assistant at the Department of Child Health, Universitas Gadjah Mada, where she develops molecular diagnostic and treatment pipelines for various paediatric disorders. With experience in translational research and clinical practice, she is dedicated to advancing evidence-based, genomic medicine to improve child health outcomes in Indonesia, with a strong commitment to ethical and patient-centred care.

Rozita Khodashahi
Transplant Research Center, Clinical Research Institute, Mashhad University of Medical Sciences, Iran

Latent Tuberculosis Management in Liver Transplant Recipients: Insights from a Retrospective Analysis

Objective

This retrospective cross-sectional study aimed to investigate latent tuberculosis infection (LTBI) management in liver transplant recipients, assessing the impact of isoniazid prophylaxis and patient outcomes.

Methods

Data from liver transplant recipients (2013-2021) at Montaseriyeh Hospital, Mashhad, were analyzed. Inclusion criteria comprised patients with a positive tuberculin skin test (PPD) or interferon-gamma release assay (IGRA) in either the donor or recipient (n=30). Demographic, clinical, and laboratory information, including the duration of isoniazid use, liver enzyme levels, and patient outcomes, was collected. Statistical analyses included descriptive statistics, non-parametric tests, and logistic regression.

Results

Thirty liver transplant recipients received isoniazid prophylaxis (up to 9 months). Isoniazid usage duration and liver enzyme levels distribution were non-normal. The distribution of isoniazid use duration and liver enzyme levels did not follow a normal distribution. No significant increase was found in liver enzyme levels (serum glutamic oxaloacetic transaminase (SGOT), and serum glutamate pyruvate transaminase (SGPT)) across different intervals. When examining each variable separately, higher SGOT and SGPT levels at the end of the first month after isoniazid consumption were significantly associated with increased mortality risk. The duration of isoniazid use and liver enzyme levels in subsequent months did not exhibit a significant relationship with patient survival.

Conclusions

Managing LTBI in liver transplant recipients presents challenges in isoniazid prophylaxis and predicting outcomes. Elevated SGOT and SGPT levels at the end of the first month after isoniazid consumption were associated with increased mortality risk. Further research is required for optimizing LTBI management in this patient population.

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