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10TH EDITION OF
WORLD CONGRESS ON

INFECTIOUS DISEASES & ONE HEALTH

AND

6TH EDITION OF

INTERNATIONAL VACCINES CONGRESS

05-07 OCTOBER, 2026 | TOKYO, JAPAN

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10TH EDITION OF

World Congress on

INFECTIOUS DISEASES & ONE HEALTH

&

6TH EDITION OF

INTERNATIONAL VACCINES CONGRESS

HYBRID EVENT

05-07

OCTOBER 2026

BOOK OF ABSTRACTS

Index

Keynote Speakers	4
Welcome Messages	6
Table of Contents	11
About Magnus Group	16
Keynote Presentations	18
Oral Presentations	42
Poster Presentations	107

Keynote Speakers

Anant Marathe
Parul Institute of Medical Sciences and Research, Parul University, India

Duccio Medini
BioForge, United States

Francis J Castellino
University of Notre Dame, United States

Jocelyn Jakubik
Apex Pathogen Solutions, United States

K R Aneja
Kurukshetra University, India

Kapil Goel
PGIMER, India

Madhu Khanna
University of Delhi, India

Ranjan Ramasamy
ID-FISH Technology, United States

Reza Nassiri
Michigan State University, United States

Keynote Speakers

Rosane Cuber Guimaraes

Bio-Manguinhos Fiocruz, Brazil

Saurabh Chattopadhyay

University of Kentucky College of Medicine, United States

Sergey V Suchkov

N.D. Zelinskii Institute for Organic Chemistry of the Russian Academy of Sciences, Russian Federation

Yogesh Kumar Gupta

Rukmani Birla Hospital, India

Welcome Message

Anant Marathe

Parul Institute of Medical Sciences and Research, Parul University, India

With immense pleasure and privilege, I welcome all the participants of 10th Edition of

World Congress on Infectious Diseases & One Health

Microbial sciences have undergone a phenomenal renaissance, infectious disease science in particular in last couple of decades. Infectious disease was known as an orphan branch of Medicine for long time.. I remember the quote by William Wordsworth, The child is father of the man. Really the orphan child has become father today with so much of knowledge advancement. In last three decades the landscape of infectious diseases has undergone transformation with great research in molecular technology for precise diagnosis and targeted therapy that resulted into better patient management and clinical outcome. Considering the multidirectional expansion in the field it is difficult to cover complete spectrum of microbiology from basic science to bedside applications, WCID 2026 has tried to cover advances in this field for the audience.

I am sure, everyone will find the topics interesting and hope every one of us takes maximum advantage and enjoy the scientific program.

Welcome Message

Duccio Medini

BioForge, United States

Dear fellow Congress Participants, It is a great pleasure to welcome you to the 6th Edition of the International Vaccines Congress in Tokyo.

Global pandemics, antimicrobial resistance and aging populations are pressing challenges for human health. Vaccinology has the potential to address these challenges, and continues to evolve at remarkable speed, driven by scientific and technological innovation.

From next-generation platforms to new approaches in development, manufacturing, and delivery, these advancements are reshaping how we prevent and respond to disease worldwide.

At the same time, translating innovation into real-world impact requires strong collaboration, equitable access and innovative business models across diverse settings.

This Congress provides a unique opportunity to share knowledge, foster meaningful partnerships, and explore solutions that bridge science and practice on a global scale.

Welcome Message

Sergey V Suchkov

N.D. Zelinskii Institute for Organic Chemistry of the Russian Academy of Sciences, Russian Federation

Dear Colleagues, Partners and Friends,

On behalf of the Organizing Committee, it is my genuine pleasure to address this Welcome Message to the ***6th Edition of International Vaccines Congress (IVC 2026)***, which is scheduled to perform in Oct 05-07 in Tokyo City. The latter representing the multifaceted identity of Japan's capital, conveying a unique fusion of tradition and innovation, illustrating the city's balance of ephemeral beauty and steadfast progress, and attracting international audiences through ancient esthetics with futuristic vitality.

Personalized vaccinomics as the latest trend in global vaccinology represents a new paradigm in vaccine design and development, based on the use of OMICS technologies and bioinformatics-driven support to construct the next-generation vaccines and the expansion of the capabilities in the field of ***Personalized and Precision Medicine (PPM).*** PPM-guided personalized vaccinomics represent a revolutionary frontier in clinical and healthcare practice, unlocking the next era of medical innovation in preventive and prophylactic immunotherapy and harnessing the unique genetic and molecular profile of individuals to elicit targeted immune responses.

Today ***Vaccinomics*** is becoming the strategic mainstream of medical research, disclosing clinically relevant and validate biomarkers of protection and vaccine response heterogeneity, and significantly influences the future of the care based on the in therapeutic vaccine engineering, evidence-based applications and the strategies of biopharma and healthcare bioindustry as well. As the above-mentioned field evolves, leveraging cutting-edge tools such as personalized vaccinomics, AI-driven biodesign, and ex vivo human models will be essential in overcoming the above-mentioned barriers.

This Grand Event is dedicated to the advancement of vaccine research and its pivotal role in shaping a healthier future for all. In this context, the esteemed Conference brings together an extraordinary community of vaccine scientists and promises to be an exceptional

gathering of renowned experts, immunologists, biodesigners and bioengineers, healthcare professionals, policymakers, and bioindustry leaders from around the world, who share a common mission: advancing the science, design-driven bioengineering paradigm and future of immunization, including the necessitation for efficient manufacturing strategies and scaling up novel vaccine platforms.

This Event will provide a dynamic platform for the exchange of knowledge, ideas, and insights into the latest developments in the field of vaccines and immunization. With a focus on collaboration, the Event will also provide opportunities for early-career researchers and colleagues from diverse global regions to engage and contribute. This Event builds on international efforts to understand how vaccines shape health across the lifespan in both sexes - and how that knowledge can guide evidence-based regulation, communication, and policy.

The Program will feature a diverse array of activities, including keynote presentations, oral sessions, plenary talks, young research forums, poster presentations, student forums, technical workshops, symposia, and start-up opportunities.

We are thrilled to extend our warmest invitation to you to join us at the Global and Grand Event, being located at Tokyo as the Tower and Tokyo Skytree integrating the History and Symbolism in Contemporary Japan. We would look forward to welcoming you at the Event as we would come together to explore the future of vaccines and their impact on individualized, population, regional, national, international and planetary global health.

Welcome Message

Yogesh Kumar Gupta

Rukmani Birla Hospital, India

Dear Esteemed Participants,

It gives me immense pleasure to welcome you all to the 10th Edition of the World Congress on Infectious Diseases & One Health (WCID-2026).

It is a privilege to be part of this important global scientific gathering, bringing together experts, clinicians, researchers, academicians, and healthcare professionals from across the world.

Infectious diseases continue to evolve, with antimicrobial resistance, emerging pathogens, and the interconnected health of humans, animals, and the environment presenting significant global challenges. Conferences such as WCID-2026 provide an excellent platform to share knowledge, exchange experiences, discuss innovative approaches, and strengthen collaborations.

I encourage all participants to actively engage in the scientific sessions, interact with fellow professionals, and make the most of this opportunity for learning, networking, and collaboration.

Once again, I warmly welcome you all to WCID-2026. I wish you a stimulating, enriching, and memorable scientific experience.

Thank you, and I look forward to an exciting and productive conference.

Table of Contents

Title: The synergistic effect of using bacteriophages and chitosan nanoparticles against pathogenic bacteria as a novel therapeutic approach
Aghapy Yermans Yakoup, Zewail City for Science and Technology, Egypt 43

Title: Phenotypic characterisation of non tuberculous mycobacterium species isolated from clinical specimens
Anant Prabhakar Marathe, Parul Institute of Medical Sciences and Research, Parul University, India 19

Title: Emerging nanovaccine strategies for enhanced immune targeting and vaccine performance
Aysel Sadayli, A.Y. Axundov Scientific-Research Institute of Medical Prophylaxis, Azerbaijan 45

Title: The largest histamine poisoning outbreak in Brazil: An experience report from a One Health perspective in Fernando de Noronha
Camila Ferro, Fundacao Oswaldo Cruz (Fiocruz), Brazil 108

Title: Socioenvironmental determinants of zoonotic sporotrichosis in vulnerable urban territories: Evaluation of surveillance and veterinary underreporting from a One Health perspective
Camila Ferro, Fundacao Oswaldo Cruz (Fiocruz), Brazil 110

Title: A universal AI design framework and brokerage platform for democratised manufacturing of mRNA therapeutics
Duccio Medini, BioForge, United States 21

Title: The recent outbreak of hantavirus has raised awareness in Europe - Albania is an endemic country for hemorrhagic fever, so vigilance must be high
Ermira Muco, University Hospital Mother Teresa Tirana, Albania 47

Title: Hematologic and inflammatory profiles across different clinical presentations of pediatric brucellosis: A retrospective cohort study
Esra Cakmak Taskin, Kocaeli City Hospital, Turkey 49

Table of Contents

Title: A rare case report: Hepatitis due to Chlamydia trachomatis infection in a 50 year old male patient
Eszter Tothne Karip, Maitland Hospital, Australia 51

Title: Reasons for the applicability of institutional theory approaches to the specific situation of medical care centers in the context of public health
Fabian Renger, St. Elisabeth University of Health and Social Work in Bratislava, Slovakia (Slovak Republic) 53

Title: Molecular crosstalk between the host and pathogen in Streptococcus pyogenes virulence
Francis J. Castellino, University of Notre Dame, United States 23

Title: A novel responsive microneedle platform for reliable drug and vaccine delivery
Huanhuan Li, Queen's University Belfast, United Kingdom 55

Title: Assessment of hematological, hepatic and renal parameters among HIV-infected patients based on duration on antiretroviral therapy
Isaac Bakare, General Hospital Odan, Nigeria 57

Title: Activation of cGAS-STING signaling pathway during HCV infection in human hepatoma cell line, Huh7
Jawed Iqbal, Galgotias University, India 59

Title: From assays to action: Integrating scientific strategy, data analytics, and clinical trial support to accelerate vaccine development
Jocelyn Jakubik, Apex Pathogen Solutions, United States 24

Title: Vaccines for diabetes and associated infections in diabetic patients
K. R. Aneja, Kurukshetra University, India 26

Title: A new universal fever definition and the unscientific nature of the conservative fever definition
K.M.Yacob Kunnathazhath, Independent Researcher, India 61

Title: Should we test and treat the fever triggers or the fever that creates the immune system against the fever triggers?
K.M.Yacob Kunnathazhath, Independent Researcher, India 64

Title: Molecular characterization of nucleoporins–influenza A virus interactions: Potential host-directed therapeutic target
Kajal Sharma, University of Delhi, India 112

Title: Awareness levels and associated factors regarding HIV/AIDS among youth of Red Ribbon Clubs in colleges of Chandigarh, India: A mixed-methods study
Kapil Goel, PGIMER, India 28

Title: Synergistic nebulized therapy for severe viral pneumonia: A biomimetic nano-platform integrating MSC-derived exosomes and interferon-α2b
Liu Yan, Ruijin Hospital, China 66

Table of Contents

Title: Nebulized mesenchymal stem cell-derived exosomes encapsulating interferon-α2b: A synergistic strategy for targeted treatment of severe viral pneumonia
Liu Yan, Ruijin Hospital, China 68

Title: Engineered extracellular vesicles vaccines with conserved peptides induce robust immune defense against influenza virus
Madhu Khanna, University of Delhi, India 30

Title: Assessment of normalization factors in SARS-CoV-2 trends at four treatment plants: Basis for a wastewater surveillance in Mexico City
Martha Elva Mercado Morales, UNAM, Mexico 70

Title: An unprecedented West Nile virus outbreak in Israel (2024): A textbook case for the One Health approach
Michel Bellaiche, Kimron Veterinary Institute, Israel 75

Title: Drone-assisted surveillance of animal diseases: An innovative approach to outbreak response and biosafety
Michel Bellaiche, Kimron Veterinary Institute, Israel 72

Title: Evaluation of biomedical waste management practices and compliance in a tertiary care oncology centre
Minal Poojary, Advanced Centre For Treatment Research & Education In Cancer, India 114

Title: Antimicrobial stewardship in the Middle East, an experience from a tertiary center in Qatar
Omar Imam, Nonaffiliated, Syrian Arab Republic 77

Title: Standardization of lipid identification and quantification in mRNA vaccines: A universal approach via AQbD
Park Jongshik, Ministry of Food and Drug Safety, Korea Republic of 116

Title: Artificial intelligence–driven clinical decision support for differentiating viral and bacterial infections to reduce antibiotic misuse
Pooja Bagdi, Trinity Educational Institute, India 118

Title: Burkholderia cepacia infection outbreak in an oncology set up: Investigation and infection control response
Prasanth Chandrasekhar Bhat, Tata Memorial Centre - ACTREC, India 120

Title: Phase I dose-escalation study of nanobody-armored dendritic cell vaccine (Baize DC) in patients with solid tumors after radical resection
Qing Xu, Shanghai University, China 78

Title: Changing population immunity to COVID-19 in the context of infection, vaccination and emerging SARS-CoV-2 variants
Ranjan Ramasamy, ID-FISH Technology, United States 31

Title: Susceptibility to SARS-CoV-2 infection and nasal air conditioning ability
Ranjan Ramasamy, ID-FISH Technology, United States 80

Table of Contents

Title: Candida auris infections are global health challenge
Reza Nassiri, Michigan State University, United States 32

Title: Health risk among justice-involved youth: A multi-risk, multigroup study
Richard Dembo, University of South Florida, United States 81

Title: Development of a combined Measles-Rubella and Yellow Fever (MR-YF) vaccine for routine immunization in low-and middle-income countries
Rosane Cuber Guimarães, Bio-Manguinhos / Fiocruz, Brazil 34

Title: Opuntia ficus-indica cladode extract as a natural radio modulator: Protection against cisplatin- and radiation-induced DNA damage with potential applications in vaccine and biomedical research
Saloua Sahbani, Taibah University, Saudi Arabia 82

Title: Addressing AMR: A scoping review of wastewater treatment measures
Saowalak Rungruang, International Health Policy Program Foundation, Thailand 84

Title: Host brakes on viral inflammation
Saurabh Chattopadhyay, University of Kentucky College of Medicine, United States 36

Title: Personalized and precision medicine (PPM) via biodesign-driven translational applications and upgraded business modeling to secure the human biosafety: The next-step vaccinomics of the future
Sergey V. Suchkov, N.D. Zelinskii Institute for Organic Chemistry of the Russian Academy of Sciences, Russian Federation 37

Title: The promise of nanotechnology in personalized & precision medicine: Nano-driven precision vaccinomics of the future
Sergey V. Suchkov, N.D. Zelinskii Institute for Organic Chemistry of the Russian Academy of Sciences, Russian Federation 86

Title: Carbapenem resistance and carbapenemases in bloodstream Enterobacterales, Busan, South Korea, 2018–2024
Sohyun Park, Busan Metropolitan City Institute of Health and Environment, Korea, Republic of 89

Title: Detection of the rpoB gene of rifampicin-resistant Mycobacterium tuberculosis at the Angré University Hospital in 2024, Ivory Coast
Som Dipielte Estelle Mireille, Angre University Hospital, Cote d'Ivoire 91

Title: Innovation to implementation of owl-natural-biomedicine-vaccination emerge as global perspectives on advancing vaccine-science-technology-global-health impact
Subhas Chandra Datta, Kanchannagar D N Das High School (HS), India 93

Title: Praziquantel for the treatment of preschool-aged children with schistosomiasis: Results of an RCT
Susannah Colt, Brown University, United States 95

Table of Contents

Title: Cloning, expression, and characterisation of Wuchereria bancrofti L1-recombinant filarial protein
Vijay Jagdish Upadhye, Parul University, India 97

Title: Strengthening One Health monitoring and evaluation systems for evidence-informed antimicrobial resistance policies in Thailand
Wanwisa Kaewkhankhaeng, International Health Policy Program Foundation, Thailand 99

Title: Development of multivalent anti-urogenital Chlamydia vaccine
Xiaojian Yao, University of Manitoba, Canada 122

Title: Strategies to reduce antibiotic resistance in urological practice
Yogesh Kumar Gupta, Rukmani Birla Hospital Jaipur, India 40

Title: Context-dependent arbuscular mycorrhizal symbiosis: An integrative review of plant–rhizosphere interactions and microbiome dynamics
Yucheng Lin, Kang Chiao International School Linkou Campus, Taiwan 101

Title: Is functional cure possible in chronic hepatitis B? HBsAg loss in chronic hepatitis B in a real-life cohort: A single-center retrospective study
Zeynep Burçin Yilmaz, Inonu University, Turkey 103

Title: Development of VSV-vector based vaccine against H5N1 avian influenza by targeting both H5N1 hemagglutinin and matrix protein 2
Zhujun Ao, University of Manitoba, Canada 105

About
Magnus Group

About

Magnus Group, a distinguished scientific event organizer, has been at the forefront of fostering knowledge exchange and collaboration since its inception in 2015. With a steadfast commitment to the ethos of Share, receive, grow, Magnus Group has successfully organized over 200 conferences spanning diverse fields, including Healthcare, Medical, Pharmaceutics, Chemistry, Nursing, Agriculture, and Plant Sciences.

The core philosophy of Magnus Group revolves around creating dynamic platforms that facilitate the exchange of cutting-edge research, insights, and innovations within the global scientific community. By bringing together experts, scholars, and professionals from various disciplines, Magnus Group cultivates an environment conducive to intellectual discourse, networking, and interdisciplinary collaboration.

Magnus Group's unwavering dedication to organizing impactful scientific events has positioned it as a key player in the global scientific community. By adhering to the motto of Share, receive, grow, Magnus Group continues to contribute significantly to the advancement of knowledge and the development of innovative solutions in various scientific domains.

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KEYNOTE PRESENTATIONS

Anant Marathe

Department of Microbiology, Parul Institute of Medical Sciences and Research, Parul University, Vadodara, Gujarat, India

Biography: Dr. Anant Marathe studied at Baroda Medical College of M. S. University of Baroda, Gujarat, India. He did his M.Sc. in the 1983, Worked as consultant Microbiologist for several years. Completed Ph.D. from Baroda medical college in Medical Microbiology in the year 2006. He worked with different medical colleges and currently he is working as Professor in department of Microbiology with Parul Institute of medical sciences and Research of Parul University. He is a post-doctoral contributing member of ASM (American Society for Microbiology). He is Reviewer for BMJ case reports and Indian Journal Orthopedic and a member of Editorial Board in IP. Journal of Medical Microbiology and Tropical Diseases. He has published over 15 papers in national as well as International Journals.

Phenotypic characterisation of *non-tuberculous mycobacterium* species isolated from clinical specimens

Background: Non-tuberculous mycobacteria (NTM) are an increasingly recognised cause of pulmonary as well as extrapulmonary infection worldwide. This rising prevalence of NTM, particularly rapidly growing mycobacteria, along with their inherent and acquired drug resistance and species-specific antimicrobial susceptibility patterns, poses major diagnostic and therapeutic challenges, particularly in tuberculosis-endemic regions. Phenotypic characterization and antimicrobial susceptibility profiling remain essential for guiding appropriate clinical management and patient outcome.

Methods: This cross-sectional study comprised a total of 3018 clinical specimens (pulmonary and extrapulmonary) submitted to Microbiology Laboratories. Ziehl-Neelsen (ZN) stain and mycobacterial culture on Bactec MGIT were carried out following decontamination and concentration of specimen. Culture positive isolates were differentiated phenotypically into Mycobacterium tuberculosis complex (MTBC) and NTM. NTM isolates were further characterised to complex/species level using line probe assay (LPA). Antimicrobial susceptibility testing was performed by broth microdilution for clinically relevant antibiotics following CLSI guidelines.

Results: Out of 3018 specimens, 607 (20.11%) were culture positive for mycobacterial growth, of which 125 (20.59%) were identified as NTM. The predominant isolate was M. abscessus complex (77.6%), followed by M. fortuitum complex (18.4%), Mycobacterium spp. (3.2%) and

M. chelonae (0.8%). NTM were most frequently isolated from pus (44%), respiratory samples (28.8%), tissue (17.6%), synovial fluid (8%), and pleural fluid (1.6%). Drug susceptibility testing showed high susceptibility to amikacin (99.2%), tigecycline (85.6%), linezolid (81.6%) and clarithromycin (68.8%). High resistance rates were observed for cotrimoxazole (84%), doxycycline (68%), minocycline (58.4%), ciprofloxacin (52.8%) and moxifloxacin (52.8%).

Conclusion: The study highlights a substantial burden of NTM among culture positive specimens, with dominance of rapidly growing mycobacteria, particularly M. abscessus complex. The observed multidrug resistance underscores the importance of routine NTM identification and phenotypic susceptibility testing for appropriate clinical management. Phenotypic characterisation remains a valuable diagnostic approach, especially in resource-limited settings, while emphasizing the need for molecular confirmation and surveillance to guide effective treatment strategies and improved patient outcomes.

Keywords: Non-Tubercular Mycobacteria (NTM), Prevalence, Multidrug Resistance (MDR), M. abscessus complex, M. fortuitum complex.

Duccio Medini, Phd

Chief Science and Technology Officer, Pitt BioForge, Pittsburgh, PA, USA; Toscana Life Sciences Foundation, Siena, Italy

Biography: Duccio Medini is a scientist and pharmaceutical executive, currently serving as Chief Science and Technology Officer at Pitt BioForge (Pittsburgh, PA) and as Strategic Data Science Director at Toscana Life Sciences Foundation (Siena, Italy).

He designed and led the Wellcome Leap $60M R3: RNA Readiness and Response program, cofunded by CEPI, developing standardized, multi-product, cell-free continuous RNA manufacturing technologies that provide democratized access to diverse biologics and sustainable pandemic response, demonstrated by multiple INDs, and successfully transitioned the program to its second funding cycle, R3 Global.

In executive roles of growing responsibility at Chiron, Novartis and GSK corporations, he led hundreds of data scientists in Vaccines R&D and AI across Europe, US and Asia, holding Research Board, Innovation Board, Clinical Quality Board and Data Governance Board responsibilities.

Working across biological discovery, clinical development and public health, he discovered the pangenome concept co-founding the pangenomics discipline, contributed to the successful registration of four novel vaccines, including the first universal vaccine against serogroup B meningitis, led the Meningococcal Antigen Typing System (MATS) platform worldwide, developed transformative corporate data strategies, authored 70+ publications, books and patents in data science for health, population genomics and mathematical vaccinology.

Prof. Medini received his Ph.D. in Physics from the University of Perugia, Italy, with a residency at the Northeastern University in Boston, MA; is habilitated Full Professor of Molecular Biology; has served in international PhD school committees at the Perugia and Turin Universities in Italy; is honorary member of the Cuban Immunology Society, Fellow of the ISi Foundation, Board member of the WHO mRNA Hub program and of the New Zealand National RNA program, Steering Committee member of the Global Pandemic Prevention & Biodefense Center at Connected OMV; an IMO, ADVAC and UC Berkley alumnus.

A universal AI design framework and brokerage platform for democratised manufacturing of mRNA therapeutics

The growth of mRNA as a general platform for biologics is limited by bespoke manufacturing processes that require adaptation across products and scales.

To overcome this barrier to access and innovation, we developed an AI-driven framework that decouples sequence design from manufacturing, analogous to the universal design principles that revolutionized the semiconductor industry, and a brokerage service giving access to high-quality, multi-product, multi-scale mRNA manufacturing.

We performed large-scale screens with multiple technologies, from batch to continuous flow developed during the R3 program, quantifying the in vitro transcription (IVT) efficiency of one million diverse sequences. We then trained an interpretable deep learning model that accurately predicts manufacturability from sequences alone and learned underlying molecular mechanisms.

This model, deployed on the brokerage service, prospectively improved the IVT yield of a vaccine and a gene-editing therapeutic by over 7.5-fold. Co-optimization for manufacturability and translation efficiency provided improvements over state-of-the-art commercial mRNA products.

Our AI-driven framework and brokerage services establish a universal design paradigm with the promise to democratize and accelerate the development of mRNA medicines, potentially unlocking a new era in biotechnology.

Francis J. Castellino

WM Keck Center for Transgene Research and Department of Chemistry and Biochemistry, University of Notre Dame, USA

Biography: Dr. Francis J. Castellino studied Chemistry as an undergraduate at the University of Scranton (PA) and graduated with a BS in 1964. He then was a NIH graduate fellow graduate student in Biochemistry at the University of Iowa with Robert Barker, where he graduated with a M.S. in 1966 and a Ph.D. in 1968. Following this, he was a NIH postdoctoral fellow at Duke University with Robert L Hill. Dr. Castellino joined the Department of Chemistry and Biochemistry at the University of Notre Dame in 1970, where he remains to this day. He is currently the Kleiderer-Pezold Professor of Biochemistry.

Molecular crosstalk between the host and pathogen in streptococcus pyogenes virulence

The molecular and cellular communication between the host and pathogen is critical to survival of both organisms after Group A Streptcoccus pyogenes (GAS) infection. After attachment and invasion of the pathogen, the human host employs its innate immune system to ward off the bacterium. GAS then rearranges its genome and protein expression according to the properties niche that is invaded. This communication will be discussed in this presentation with emphasis on the humoral innate immune system of the host and the response of the bacterium to avoid its elimination.

Jocelyn Jakubik Ph.D

Apex Pathogen Solutions, LLC, Frederick, Maryland, USA

Biography: Dr. Jocelyn Jakubik, PhD, is Founder and Principal Consultant of Apex Pathogen Solutions, providing strategic scientific consulting to government, pharmaceutical, and biotechnology organizations. With more than 20 years of experience in immunology, vaccine development, assay development, clinical trials, and laboratory quality systems, Jakubik has led programs supporting BARDA-funded research, global disease surveillance, and emerging infectious disease initiatives. Jakubik specializes in assay strategy, translational science, data analysis, program management, and regulatory readiness, helping clients accelerate vaccine and therapeutic development while strengthening scientific rigor, operational efficiency, and clinical trial success.

From assays to action: Integrating scientific strategy, data analytics, and clinical trial support to accelerate vaccine development

The accelerating pace of vaccine innovation requires multidisciplinary expertise spanning assay development, analytical strategy, regulatory readiness, and clinical trial execution. As vaccine platforms continue to evolve, organizations increasingly benefit from scientific partners capable of integrating laboratory science with data-driven decision-making throughout the product development lifecycle.

This presentation highlights a practical consulting framework that supports vaccine and biologic development from preclinical research through late-stage clinical evaluation. Emphasis will be placed on developing fit-for-purpose immunological and molecular assays, establishing analytical strategies that generate high-quality, reproducible data, and translating complex laboratory findings into actionable evidence for clinical and regulatory stakeholders. The discussion will also explore approaches to assay qualification, biomarker evaluation, data interpretation, laboratory quality systems, cross-functional collaboration, and risk mitigation to improve study efficiency and scientific confidence.

Attendees will gain insight into how integrated scientific consulting can strengthen clinical trial readiness, accelerate decision-making, improve data integrity, and support successful collaboration among sponsors, contract research organizations, government agencies, and academic partners. Real-world considerations for emerging infectious diseases, biodefense priorities, and rapidly evolving vaccine technologies will be discussed within the context of modern product development.

Apex Pathogen Solutions partners with pharmaceutical, biotechnology, government, and public health organizations to provide scientific consulting in assay strategy, clinical development support, biosurveillance, laboratory quality, data analysis, program management, and translational science. By combining technical expertise with strategic project leadership, the company helps organizations navigate complex scientific challenges while advancing innovative medical countermeasures from concept to implementation.

Keywords: Vaccine Development, Clinical Trials, Immunoassays, Assay Development, Biomarker Strategy, Translational Science, Laboratory Quality, Data Analytics, Biodefense, Public Health Preparedness, Scientific Consulting.

K. R. Aneja

Kurukshetra University, Kurukshetra (Haryana), India; Sardar Bhagwan Singh University, Dehradun (Uttarakhand), India

Biography: Prof. K.R. Aneja is the recipient of many awards and fellowships, the major ones being President of the Mycological Society of India (2022 Lifetime Achievement Award), Recorder of ISCA, the INSA-Royal Society Academic Exchange Fellowship, Best Citizens of India, Rashtriya Gaurav, the ISWA Lecture Award, Shiksha Rattan Samman, and the 2023 Unnat Bharat Shewa Shree Award. Aneja has served as the Governor's/Chancellor's nominee for teachers' selection at Punjabi University, Patiala, a member of the Research Advisory Committee of the ICAR Weed Research Centre, Jabalpur, and an Expert Member of the ICFRE, Dehradun. Aneja obtained B.Sc., M.Sc. and Ph.D. degrees from Kurukshetra University, Kurukshetra, served the Departments of Botany and Microbiology there for 34 years including 11 years as Professor & Chairman, supervised 23 PhD scholars and over 35 M.Phil. students, and published 181 research papers/reviews/chapters, over 55 abstracts, 16 authored/co-authored books, 5 edited books and 2 manuals. Aneja is an Honorary Professor & Research Advisor at Sardar Bhagwan Singh University, Dehradun (Uttarakhand).

Vaccines for diabetes and associated infections in diabetic patients

Diabetes is a metabolic chronic disease characterized by elevated blood glucose levels over a prolonged period, which occurs either when the pancreas does not produce enough insulin or the human body cannot effectively use the insulin it produces. Worldwide, 590 million people are suffering with diabetes and it is projected to reach 853 million by 2050. It caused an estimated 3.4 million global deaths in the year 2024, representing 9.3% (or 1 in 11) of all-caused global mortality among adults (WHO 2025).

Diabetes causes functional immunosuppression which impairs immune cell function, reduces neutrophil phagocytosis, mainly reducing T-cell function and altering cytokines, thereby weakening the response to infections by fungi, viruses and bacteria. The risk of mycoses increases 1.38-fold in diabetic patients. Candidiasis (oral and vaginal), dermatophytosis (ring worms, onychomycosis) and invasive mycoses (rhino-orbital-cerebral mucormycosis, aspergillosis, cryptococcosis, histoplasmosis and candidemia) are the major mycoses among diabetics. Common superficial mucosal involvement (candidiasis) often serves as an early marker of immune dysregulation, progressing to rapidly progressive, life-threatening deep invasive fungal infections such as mucormycosis, representing a catastrophic sequence of uncontrolled diabetes. There are no vaccines for mycoses. They

can be prevented and treated by maintaining tight glycaemic control, strict hygiene, wearing breathable (cotton) clothes, foot care and antifungal topical or oral medications.

Vaccines for diabetic patients are crucial for preventing serious complications from infections. Major vaccines that cover the most common and dangerous infections in diabetics include: annual flu (influenza) vaccine, Hepatitis-B vaccine, pneumococcal vaccine, shingles (herpes-zoster) vaccine, Tdap vaccine, COVID-19 vaccine, and RSV vaccine.

Significant progress has been made towards developing vaccines to delay or prevent the onset of diabetes entirely. About 11 vaccines based upon five approaches (alum adjuvant-based, protein-based, specific self-antigen based, non-antigen based and other disease-based vaccine) have been developed, which are mostly studied on animal models. The GAD 65 vaccine (Intralymphatic GAD-Alum vaccine, Diamyd®), a specific self-antigen derived vaccine, has been proved to be effective in managing glucose and halting diabetes type-1 progression in patients aged 12-24. This vaccine targets self-reactive T-cells (GAD 65). GAD is a protein fragment located in the insulin-producing β-cells found in the pancreas responsible for destroying islet cells. No vaccine cures diabetes and none has yet been approved for public use.

The diabetes vaccine comes as a remarkable solution in the field of medical science which calls for laying emphasis on continuous research, human trials and innovations to realize such a pioneering remedy for diabetic patients, including searches for vaccines against the fatal mycoses, saving lives of millions of youths in the coming years.

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Biography: Dr. Kapil Goel is Associate Professor of Epidemiology, Community Medicine & School of Public Health, PGIMER, Chandigarh. As a Public Health Expert with an MD in Community Medicine (Manipal University) and EIS training (2012-2014, NCDC-CDC), Goel has 20+ years of public health experience in communicable and non-communicable disease epidemiology, outbreak management, surveillance, COVID-19, vaccinology, maternal-child health, and biostatistics, with 95+ publications, 30+ research projects as PI/Co-PI, and work with WHO, UNICEF, and CDC. A Fellow of the Academy of General Education, Goel mentors India's EIS, WHO-AEP, and ATS-MECOR, and won the 2025 PGIMER Research Day and Outstanding Health Services award.

Awareness levels and associated factors regarding HIV/AIDS among youth of Red Ribbon Clubs in colleges of Chandigarh, India: A mixed-methods study

Background: Youth aged 15–29 years account for nearly one-third of new HIV infections globally. India's National AIDS Control Programme established Red Ribbon Clubs (RRCs) in colleges to build HIV/AIDS awareness, reduce stigma, and promote safe practices among students. Despite widespread implementation, evidence on the actual awareness levels achieved among RRC members, and the factors shaping this awareness, remains scarce. This study assessed HIV/AIDS-related awareness, attitudes, and risk behaviours among RRC youth in Chandigarh and explored the factors and lived experiences underlying them.

Methods: A concurrent, cross-sectional mixed-methods study was conducted across six randomly selected RRC-affiliated colleges in Chandigarh (three women's, three co-educational). A structured, pretested questionnaire based on the National Behavioural Surveillance Survey was administered to 400 RRC members aged 18 years or older, selected by simple random sampling, covering socio-demographics, HIV/AIDS knowledge, attitudes, and risk behaviour. Concurrently, 12 in-depth interviews with RRC leaders/in-charges and 6 focus group discussions with members were conducted and analysed thematically using MAXQDA. Quantitative associations were tested using chi-square/Fisher-Freeman-Halton tests (SPSS v29.0), with significance set at $p<0.05$.

Results: Participants were predominantly female (78.5%) and aged 18–19 years (58%). Awareness of basic transmission routes was high: 96.8% knew HIV/AIDS spreads through sexual contact and shared needles, and 81.5% knew it is preventable. However, critical gaps

persisted: only 29% were aware of PPTCT and ICTC services, 56% knew of testing facilities, and 11.2% incorrectly believed mosquito bites transmit HIV. While 80.8% would accept an HIV-positive family member, 46.5% were unwilling to share food with an HIV-positive person, reflecting residual stigma; only 2.5% reported engaging in risk behaviours. Awareness of transmission routes, PPTCT, and stigma-related attitudes was significantly associated with age, gender, area of residence, duration of RRC membership, and socioeconomic class ($p<0.05$). Qualitatively, leaders described peer influence, workshops, and creative campaigns (rallies, poster-making, cyclothons) as key awareness drivers, while stigma, shyness, and resource limitations emerged as major barriers.

Conclusion: RRC membership was associated with substantial foundational HIV/AIDS awareness, but persistent gaps in service-related knowledge and enduring stigma highlight the need for targeted, peer-led interventions addressing PPTCT/ICTC awareness, myth-busting, and stigma reduction. Strengthening RRC activities through digital engagement, structured feedback mechanisms, and earlier school-level introduction could optimise their contribution to India's youth-focused HIV prevention strategy.

Keywords: HIV/AIDS; Red Ribbon Club; Youth Awareness; Stigma; Mixed-Methods; India

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Biography: Dr. Madhu Khanna has specialized in medical virology and has been passionately committed to the advancement of knowledge and innovation in this field. Khanna's areas of research include the study of the pathogenesis of viruses, antiviral strategies, and vaccine delivery for viruses like influenza, dengue, Chikungunya and SARS-CoV-2, and has provided essential diagnostic services during major pandemics such as COVID-19 and influenza under ICMR. Additionally, the Department of Health Research, Government of India, designated the institute as a Viral Research and Diagnostics Laboratory for managing epidemics and national calamities. Khanna has received several national and international awards and is a member of the Indian Virological Society and the National Academy of Medical Sciences, India.

Engineered extracellular vesicles vaccines with conserved peptides induce robust immune defense against influenza virus

Influenza viruses are known to cause respiratory illnesses that often lead to mortality and morbidity in humans worldwide. Currently available vaccines predominantly target highly variable surface glycoproteins, thereby reducing the protective efficacy of the vaccine over time due to continuous antigenic drift and occasional shift. Subsequently, seasonal vaccine needs to be reformulated frequently to provide protective efficacy against emerging strains. Therefore, there is a need to design a vaccine candidate that focuses on conserved viral antigens such as nucleoprotein (NP) that will provide long-term immunity, obviating the need for frequent updates of vaccine. Extracellular vesicles have emerged as promising nanocarriers for antigen delivery due to their biocompatibility and robust uptake by antigen-presenting cells. Our study focuses on the role of engineered EVs in effectively eliciting cellular immune responses in influenza virus infection. Further, characterization of EVs was performed by western blotting for exosomal markers (CD9 and CD63), dynamic light scattering (DLS), and transmission electron microscopy (TEM). A highly conserved peptide of NP of influenza virus was selected as an antigenic target and analyzed in vitro. The vaccine candidate was loaded into EVs isolated from HEK293T cells and delivered to experimental cells, which generated a significant immune response with increased levels of IL-17 and other cytokines. The immunogenic potential of engineered EVs was further evaluated in vivo to confirm the proof of concept. This study provided a robust immune response and may serve as an effective strategy for next-generation vaccines against influenza virus and other pathogens.

Ranjan Ramasamy

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Biography: Ranjan Ramasamy obtained a BA and PhD from the University of Cambridge, UK, and has held academic appointments in the UK and abroad including Australia, Sri Lanka and the USA. Ramasamy was Chairman of the National Science Foundation of Sri Lanka and held Professorial appointments in Biochemistry, Immunology and Life Sciences, was a member of the Board of Governors of the International Centre for Genetic Engineering and Biotechnology (ICGEB), and a member of the Committee for Scientific Planning and Review (CSPR) of the International Council for Science (ICSU) for several years, with 300 publications pertaining to Biochemistry, Immunology and Infectious Diseases.

Changing population immunity to COVID-19 in the context of infection, vaccination and emerging SARS-CoV-2 variants

The changing state of protective immunity to COVID-19 in the global population during the time since COVID-19's origin in 2019 is analysed in the context of the (i) circulation of SARS-CoV-2 in the population, (ii) widespread use of different types of COVID-19 vaccines beginning in December 2020 and continuing to the present time, and (iii) ongoing evolution of SARS-CoV-2 to produce mutant viruses with greater infectivity, replication rate, evasion of immunity and transmissibility. The outlook, and possible vaccine strategies, for the future control of COVID-19 are also examined. The continuing generation of new SARS-CoV-2 variants, and the rapid global spread of the more fit variants, also highlights the need to continue the worldwide effort to sequence viral genomes and determine virological characteristics of the variants. Appropriate monitoring of emerging SARS-CoV-2 variants in animals also seems essential.

Reza Nassiri

Departments of Clinical Pharmacology/Toxicology and Community Medicine, Michigan State University, East Lansing, Michigan, USA

Biography: Prof. Dr. Reza Nassiri is a former Dean of Global Health at MSU, East Lansing, Michigan, USA, and a former Director of the Institute of International Health at MSU. Nassiri is a French-trained hematologist -with training in clinical pharmacology and has expertise in Global Health/One Health, Infectious Diseases, and Antibiotic Resistance, and is currently a professor of clinical pharmacology at MSU. Nassiri is on the editorial board of four medical journals and has written extensively about antibiotic resistance and COVID-19.

Candida auris infections are a global health challenge

The CDC classifies C. auris as an urgent antimicrobial resistance threat, the highest level of concern due to its resistance to multiple antifungal drugs and the ease of transmission in healthcare settings. The WHO places it in the critical priority group of fungal pathogens. C. auris has five recognized clades worldwide classified as South Asian, East Asian, African, and South American. Clade V was recently discovered in Singapore and Bangladesh and has a close genetic relationship to Clade IV but represents a distinct lineage. C. auris' spread in the U.S. has been alarming, with the number of clinical cases increasing markedly since its first reported cases in 2016. Since 2023, there have been well over 4,000 cases. C. auris is known for its multidrug resistance profile and can cause severe and often life-threatening infection. The fungus spreads easily in healthcare facilities and primarily affects people who are already immunocompromised or have co-morbid conditions. Worldwide, this fungal pathogen is rapidly emerging across six continents and over 60 countries, with outbreaks particularly concentrated in hospitals and healthcare facilities, making it a serious global epidemic concern. It should be noted a C. auris case was first reported in 2009 by Japanese investigators, though retrospective samples show it existed as early as 1996 in South Korea. C. auris infections present with nonspecific symptoms and vary depending on the site of infection, most often involving the bloodstream, wounds, or ears. Interestingly, in Western Europe, Spain currently has the highest number of reported cases of C. auris with nearly 2,000 cases between 2013 and 2023. Colombia has also reported more than 2,000 cases and has a high incidence of C. auris candidemia, while South Africa, India, and the US (particularly NY and NJ) are experiencing significant numbers of cases. It seems for many

countries, sustained hospital outbreaks, gaps in infection control, and robust surveillance that detects more cases are the main challenging gaps. Once established in the healthcare facilities, the fungus is extremely difficult to eradicate from their environments. Many patients are colonized without symptoms, but invasive infections can be severe, risking mortality. Usually candidemia presents with fever, chills, hypotension, tachycardia, or sepsis-like symptoms often indistinguishable from other causes of sepsis. C. auris otitis presents with pain, pressure, or fullness in the ear. Other sites include urinary tract, respiratory tract, and intra-abdominal infections, though less common.

The core pathophysiologic features of C. auris include its ability to colonize skin and hospital environments, resist antifungal drugs, evade immune defenses, and cause invasive bloodstream infections in vulnerable patients. The fungus has evolved an extraordinary ability to form multilayer biofilms and to resist both antifungal drugs and hospital cleaning protocols. Fungal biofilms can block penetration of antifungal drugs, especially azoles and echinocandins. The extracellular matrix acts like a shield, trapping and neutralizing drugs before they reach fungal cells. Biofilms allow the fungal pathogen to survive for weeks on surfaces, resisting standard disinfectants. This type of persistence seems to be a major reason for outbreaks that are hard to control once the fungus enters a healthcare setting. Clinical isolates show enhanced adherence due to amplification of adhesin genes such as ALS4, which increases surface colonization and biofilm capacity. In addition, a newly identified adhesin, Scf1, is critical for biofilm formation on skin and devices, highlighting potential therapeutic targets. The clinical impacts are concerning worldwide; one of the urgent concerns is that biofilm-associated resistance leads to high treatment failure rates and frequent relapses. Recent studies show about 90% of isolates are resistant to at least one antifungal drug. About 30% are resistant to two or more drug classes. Rare strains show pan-resistant patterns to azoles, echinocandins and amphotericin B. Mutations in ERG11 (azole target) and FKS1 (echinocandin target) reduce drug binding. Alterations in sterol biosynthesis pathways confer amphotericin B resistance. Mortality rates for invasive C. auris infections remain 30–60%, especially in critically ill patients. The current guidelines for management of C. auris infections emphasize echinocandins as the 1st-line therapy and mandatory reporting to public health authorities. For adults & children ≥ 2 months, anidulafungin, caspofungin, or micafungin are recommended as the initial treatment. For infants < 2 months, amphotericin B deoxycholate (1 mg/kg daily) is recommended. If echinocandin resistance is suspected or confirmed, switch to liposomal amphotericin B (5 mg/kg daily). For management of pan-resistant strains, consider investigational antifungals (e.g., fosmanogepix, ibrexafungerp) under expanded access programs.

Rosane Cuber Guimaraes*, Noemi Rovaris Gardinali, Iaralice Medeiros de Souza, Hugo Garcia Tonioli Defendi

Bio-Manguinhos, Fundacao Oswaldo Cruz (Fiocruz), Rio de Janeiro, Brazil

Biography: Rosane Cuber Guimaraes is the General Director of Bio-Manguinhos/Fiocruz, with over two decades of experience in vaccine development, production, and regulatory affairs. Guimarães coordinated the national rollout of the COVID-19 vaccine in partnership with AstraZeneca and enhanced Yellow Fever vaccine supply for national and international programs. Dr. Guimarães holds a PhD from Fiocruz and combines academic excellence with industrial leadership in global immunization.

Development of a combined Measles-Rubella and Yellow Fever (MR-YF) vaccine for routine immunization in low- and middle-income countries

Routine immunization programs in low- and middle-income countries (LMICs) face persistent programmatic challenges, including the need for multiple injections per visit and operational constraints inherent to resource-limited settings. Measles-Rubella (MR) and Yellow Fever (YF) vaccines are currently administered separately in many countries, creating logistical burden and reducing overall coverage efficiency. To address this structural demand for more efficient vaccine delivery, Bio-Manguinhos/Fiocruz, with support from the Gates Foundation, is developing a combined MR-YF vaccine designed as a single-shot solution for routine immunization programs targeting infants above nine months of age in LMIC and Gavi-eligible countries.

The MR-YF combination vaccine is a lyophilized, multi-dose presentation administered subcutaneously, formulated to be non-inferior to existing standalone MR and YF vaccines while eliciting a strong and durable immune response. The product is designed for compatibility with existing immunization schedules and for affordability, scalability, and programmatic fit. Bio-Manguinhos brings proven end-to-end capability as an established producer of both YF and MR vaccines, with extensive egg-based and live-attenuated vaccine expertise, large-scale production experience, a track record of LMIC supply, and ongoing engagement with Gavi and PAHO, supporting a low execution risk profile with strong potential for global supply.

The development pathway encompasses formulation development, lyophilization cycle optimization, and stability assessment. To date, twelve MR-YF batches have been produced

across two candidate formulations, demonstrating stable potency under accelerated conditions up to 180 days, with formulation selection completed. Preclinical studies in the BALB/c mouse model have been finalized, evaluating protection via an intracerebral yellow fever challenge model and humoral and cellular immunogenicity (PRNT, ELISA, ELISPOT), alongside assessment of immune interference among vaccine components. Results demonstrated strong protection and survival following YF challenge, with final interpretation pending completion of the full immunogenicity dataset. Complementary studies in a hamster model, using a viscerotropic YF challenge, are ongoing and expected to conclude by September 2026, further characterizing safety, immunogenicity, and protection. A planned study in non-human primates (Rhesus macaques) will evaluate safety, viral interference, and immune response characterization using standalone and combined vaccine groups under a 45-day dosing interval, without a challenge component.

A clinical development plan has been drafted for studies in Brazil, comprising a Phase I randomized, double-blind, active-controlled trial in healthy adults (18–49 years) under a two-dose, 60-day interval regimen, followed by a Phase II/III randomized, multicenter, non-inferiority trial with blinded laboratory assessment in infants aged 9 and 11 months, also under a two-dose, 60-day interval schedule.

The commercial roadmap outlines key milestones toward licensure and deployment, including engagement with WHO SAGE and Gavi, regulatory submissions to ANVISA and WHO Prequalification, and projected vaccine launch, supported by ongoing COGS assessment and business case development. Collectively, these efforts position the MR-YF combination vaccine as a timely and strategic evolution of existing immunization programs, with the potential to simplify vaccination schedules, reduce the number of injections per visit, and improve overall coverage and efficiency in LMIC settings.

Saurabh Chattopadhyay

University of Kentucky College of Medicine, United States

Biography: Saurabh Chattopadhyay, Ph.D., is an Associate Professor in the Department of Microbiology, Immunology, and Molecular Genetics at the University of Kentucky College of Medicine. Saurabh's research investigates how viral pathogens interface with innate immune signaling pathways, with a particular focus on interferon-regulated mechanisms that shape antiviral defense and inflammatory responses. Saurabh's laboratory has been funded by the National Institutes of Health, the Ohio Department of Health, the Centers for Disease Control and Prevention, and the American Heart Association. Dr. Chattopadhyay earned his doctoral degree in Biotechnology from the Indian Institute of Technology Delhi and completed postdoctoral training in Virology at the Cleveland Clinic. Before joining the University of Kentucky, Saurabh was a faculty member at the University of Toledo College of Medicine.

Host brakes on viral inflammation

The interferon (IFN) system is a critical first-line defense against viral infection, orchestrating antiviral programs while shaping early inflammatory responses. Although inflammation is essential for pathogen control, dysregulated cytokine production is a major driver of morbidity and mortality in severe viral diseases. Our work investigates how specific components of the IFN signaling network modulate this balance between antiviral immunity and pathological inflammation. Through integrated studies in primary cells and mouse models of respiratory viral infection, we have uncovered previously unrecognized host mechanisms that actively restrain excessive cytokine responses without compromising antiviral protection. These pathways delineate a host-intrinsic brake on inflammation and reveal potential therapeutic targets for mitigating cytokine-driven immunopathology in acute respiratory infections

Sergey Suchkov[1-14*], Roger D. Kamm[15], Gregory A Poland[19], Shawn Murphy[16,17], Kristen Dahlgren[20], Hyunseung Kong[21], Michele Mussap[22], Holland Cheng[18]

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Biography: Sergey Suchkov was born in Astrakhan, Russia, into a family of medical doctors. In 1980, Suchkov graduated from Astrakhan State Medical University with an MD, earned a PhD in 1985 as a student of the I.M. Sechenov Moscow Medical Academy and Institute of Medical Enzymology, and a Doctor of Science degree in 2001 at the National Institute of Immunology, Russia. From 1989 to 1995, Suchkov was Head of the Laboratory of Clinical Immunology at the Helmholtz Eye Research Institute in Moscow, and from 1995 to 2004 Chair of the Department of Clinical Immunology at the Moscow Clinical Research Institute (MONIKI). From 1993 to 1996, Suchkov was Secretary-in-Chief of the Editorial Board of Biomedical Science, an international journal published jointly by the USSR Academy of Sciences and the Royal Society of Chemistry, UK. Dr. Sergey Suchkov, MD, PhD, is affiliated with the N.D. Zelinskii Institute for Organic Chemistry of the Russian Academy of Sciences (Moscow), the China Hong Kong Innovation International Business Association (Hong Kong) and InMedStar (Russia), and is a member of numerous scientific bodies including the Russian Academy of Natural Sciences, the New York Academy of Sciences, the American Chemical Society, the American Heart Association, the Association for Medical Education in Europe (AMEE), the EPMA, ARVO, ISER, and the Personalized Medicine Coalition, and serves as Secretary General of the United Cultural Convention (UCC), Cambridge, UK.

Personalized and Precision Medicine (PPM) *via* biodesign-driven translational applications and upgraded business modeling to secure the human biosafety: The next-step vaccinomics of the future

A new systems approach to diseased states and wellness results in a new branch in the healthcare services, namely, personalized and precision medicine (PPM). To achieve the implementation of the PPM concept, it is necessary to create a fundamentally new strategy based upon the subclinical recognition of biomarkers of hidden abnormalities long before the disease clinically manifests itself.

Each decision-maker values the impact of their decision to use PPM on their own budget and well-being, which may not necessarily be optimal for society as a whole. It would be extremely useful to integrate data harvesting from different databanks for applications such as prediction and personalization of further treatment to thus provide more tailored measures for the patients, resulting in improved patient outcomes, reduced adverse events, and more cost-effective use of the latest health care resources including diagnostic (companion), preventive and therapeutic (targeted molecular and cellular) resources.

In this connection, the field of PPM-based vaccinology remains empirical in many respects but combines next-generation diagnostics with state-of-the-art manufacturing to create a herd-specific, custom vaccine to help physicians prevent disease. PPM-based vaccinology focuses on continuous improvement in herd health by seeking solutions for ongoing and emerging disease challenges. The new field of vaccinomics provides models that permit global profiling of the innate, humoral, and cellular immune responses integrated at systems biology, PPM and translational medicine levels. This knowledge is being utilized to better understand the following: identifying who is at risk for which infections; the level of risk that exists regarding poor immunogenicity and/or serious adverse events; and the type or dose of vaccine needed to fully protect an individual.

PPM and systems vaccinology are becoming a valuable tool in vaccine development whilst prompting application of systems vaccinology for investigating complex pathogens or oncogenes to produce vaccines of the next-step generation. These promising changes call

for the inclusion of systems vaccinology as early as possible in the vaccine development chain to better understand why some vaccines work and others do not. This will enable efficiency of vaccine development proportionally in the design phase and will lead to improved vaccine evaluation in early phases, thereby reducing time and costs. Meanwhile, a lack of medical guidelines has been identified by responders as the predominant barrier for PPM adoption, indicating a need for the development of best practices and guidelines to support the implementation of PPM. This is the reason for developing global scientific, clinical, social, and educational projects in the area of PPM to elicit the content of the new branch.

Keywords: Personalized & Precision Medicine, Biomarkers, Targets, Nanoparticles, Nanocarriers, Vaccinomics, Nanovaccines, Nanobiomedicine, Nanotechnologies.

Yogesh Kumar Gupta

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Biography: Dr. Yogesh Kumar Gupta completed his MBBS from SMS Medical College, Jaipur, and MD in Microbiology from SP Medical College, Bikaner, along with specialized training in critical care (IDCC) and infection control. His key areas of interest include hospital infection control, antimicrobial stewardship, laboratory quality management, and healthcare accreditation. He is a Principal Assessor for NABH, a Technical Assessor for NABL, and actively contributes to setting infection prevention standards. He is also the Founder of the Rajasthan State Chapter of the Indian Association of Medical Microbiologists and currently serves as an Executive Member of its national body.

Strategies to reduce antibiotic resistance in urological practice

Background: Antibiotic resistance has emerged as a major challenge in urological practice due to the high prevalence of urinary tract infections (UTIs), frequent antimicrobial exposure, increasing use of invasive urological procedures, and the growing burden of multidrug-resistant (MDR) organisms. Empirical overuse of broad-spectrum antibiotics and inappropriate prophylaxis have further accelerated antimicrobial resistance (AMR), compromising treatment outcomes and increasing healthcare costs.

Objectives: This presentation aims to discuss practical, evidence-based strategies to reduce antibiotic resistance in urology through antimicrobial stewardship, optimized diagnostic approaches, and infection prevention measures.

Content: The session will review current resistance trends among common uropathogens and identify key drivers of AMR in outpatient and inpatient urological practice. Emphasis will be placed on appropriate microbiological investigations, culture-guided therapy, rapid diagnostic techniques, local antibiogram-guided empirical treatment, and timely de-escalation or discontinuation of antibiotics. Best practices for perioperative antimicrobial prophylaxis, management of asymptomatic bacteriuria, catheter-associated urinary tract infection (CAUTI) prevention, and infection control interventions will be discussed. The role of multidisciplinary antimicrobial stewardship programs involving urologists, microbiologists, infectious disease physicians, pharmacists, and infection prevention teams will be highlighted. Emerging strategies, including biomarker-guided antibiotic therapy, surveillance of resistance patterns, and clinician education, will also be explored.

Conclusion: Reducing antibiotic resistance in urological practice requires a multifaceted approach that integrates antimicrobial stewardship, evidence-based prescribing, accurate microbiological diagnosis, infection prevention, and continuous surveillance. Adoption of these strategies can preserve antibiotic effectiveness, improve patient outcomes, reduce healthcare costs, and contribute to global efforts to combat antimicrobial resistance.

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ORAL PRESENTATIONS

Aghapy Yermans Yakoup

Center for Microbiology and Phage Therapy, Zewail City of Science and Technology, Giza, Egypt

The synergistic effect of using bacteriophages and chitosan nanoparticles against pathogenic bacteria as a novel therapeutic approach

Public health and environmental security are seriously at risk due to the growing contamination of pathogenic microorganisms. Therefore, effective antimicrobials are urgently needed. In our study, the antimicrobial effects of three types of nanoparticles were investigated with phage. The biosynthesis of nanoparticles was confirmed based on the color change and shapes, which tended to be mono-dispersed with a spherical shape with a size range of 20-35 nm for Ag-CS-NPs, 15-30 nm for Phage-CS-NPs (Ph-CS-NPs), and 5-35 nm for Propolis-CS-NPs (Pro-CS-NPs). Nanoparticles displayed peaks between 380-420 nm, 335-380 nm, and below 335 nm for Ag-CS-NPs, Pro-CS-NPs, and Ph-CS-NPs, respectively. Throughout the three synthesized nanoparticles, Ag-CS-NPs represented a higher antibacterial effect in combination with phages. It showed MIC against S. sciuri, S. Typhimurium, and P. aeruginosa between 31.2 and 62.2 Confirm unit: pg/mL vs ug/mL (MIC/MBC values suggest ug/mL). and MBC at 500, 62.5, and 31.2 Confirm unit: pg/mL vs ug/mL (MIC/MBC values suggest ug/mL), respectively, while in combination with phages showed MIC at 62.2, 31.2, and 15.6 Confirm unit: pg/mL vs ug/mL (MIC/MBC values suggest ug/mL). respectively, and MBC at 125, 62.2, and 15.6 Confirm unit: pg/mL vs ug/mL (MIC/MBC values suggest ug/mL), respectively. Furthermore, a significant killing efficiency was observed with 16.5-30.1 Confirm unit: pg/mL vs ug/mL (MIC/MBC values suggest ug/mL). of Ag-CS-NPs combined with phages. In conclusion, Ag-CS-NPs with phages present potential bactericidal and inhibitory effects against Gram-positive and Gram-negative bacteria, as well as against the production of biofilms.

Biography

Aghapy Yermans Yakoup is a graduate, batch 2023, with a biomedical sciences major (BMS) (medical sciences concentration) from Zewail City for Science, Technology, and Innovation. In addition, she worked as a Junior Researcher Assistant (jRA) in the Center for Microbiology and Phage Therapy (CMP) in Zewail City for Science, Technology, and Innovation from Fall 2021 until Summer 2023. Currently she is working as an R&D specialist in Pharmaplast company. She is interested in finding new solutions to get rid of multi-drug-resistant bacteria and inventing new compounds that can be alternatives to antibiotics. Also, she is interested in the medical microbiology field. In the future, Aghapy Yermans Yakoup is planning to enroll in a Ph.D. program that aims to find new applicable solutions for infectious diseases in different body systems like the nervous system and cardiovascular system.

Aysel Sadayli
V.Y. Axundov Scientific-Research Institute of Medical Prophylaxis, Baku, Azerbaijan

Emerging nanovaccine strategies for enhanced immune targeting and vaccine performance

The rapid evolution of vaccine science has accelerated interest in nanotechnology-based strategies aimed at improving immune precision, vaccine stability, and translational performance. Nanovaccines have emerged as versatile platforms capable of addressing critical limitations of traditional vaccine approaches by enabling controlled antigen delivery, enhanced cellular uptake, and modulation of innate and adaptive immune responses. This review explores emerging nanovaccine strategies with a focus on their role in optimizing immune targeting and overall vaccine performance.

Recent advances in nanocarrier design, including lipid nanoparticles, polymer-based systems, virus-like particles, and hybrid nanostructures, are discussed with emphasis on how physicochemical characteristics such as particle size, surface functionalization, and antigen loading influence immune activation pathways. Integration of nanotechnology with modern vaccine modalities, including mRNA, recombinant protein, and peptide-based vaccines, demonstrates significant potential to enhance immunogenicity while minimizing dose requirements and adverse effects.

In addition to technological progress, this review addresses key translational challenges associated with nanovaccine development, including large-scale manufacturing, formulation stability, safety profiling, and regulatory considerations. Strategies to improve reproducibility, standardization, and clinical scalability are highlighted as essential components for successful implementation. Bridging experimental innovation with real-world vaccine deployment remains a central challenge for next-generation vaccine technologies.

Overall, nanovaccine strategies represent a promising direction for the future of vaccine development, offering adaptable solutions for infectious disease prevention and pandemic preparedness. Continued interdisciplinary collaboration between immunology, nanotechnology, and biotechnology will be critical to fully realize their potential within global vaccination programs.

Biography

Aysel Sadayli works as a scientific researcher at the V.Y. Axundov Scientific-Research Institute of Medical Prophylaxis. Aysel's scientific interests include vaccine technologies, nanovaccine platforms, and biotechnology. Aysel is particularly interested in next-generation vaccine development and translational aspects. Aysel has participated as a speaker (oral presenter) in one international scientific conference, and Aysel follows review-based research in the fields of vaccinology and preventive medicine.

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The recent outbreak of *hantavirus* has raised awareness in Europe — Albania is an endemic country for hemorrhagic fever, so vigilance must be high

A tourist trip to Ushuaia, Argentina, the southernmost city in the world, ended like a horror movie. The outbreak of a highly dangerous virus, such as the hantavirus, drew widespread attention across Europe. On board were 149 people of 23 different nationalities, including citizens from nine EU/EEA member states like Belgium, France, Germany, Greece, Spain etc. This extensive media coverage sparked not only fear but also a desire to learn and discover more. The hantavirus is not new to us because Albania is known to be an endemic area for it. In Albania, the primary causative agent is the Dobrava-Belgrade virus (DOBV). The main reservoir in our country is the yellow-necked mouse Apodemus flavicollis. Our country offers ecological and climatic conditions that are highly conducive to the virus's circulation in nature, as they favor the presence of various rodent species that harbor hantaviruses. It is a small, mountainous country—largely defined by mountains and hills—and is rich in forests. The infection manifests in two distinct medical syndromes: Hantavirus Pulmonary Syndrome and Hemorrhagic Fever with Renal Syndrome. These conditions are well-known among medical professionals. The first case of HFRS caused by the Dobrava virus in Albania was diagnosed in 1985, and another 31 cases were diagnosed in the two years that followed. The prestigious medical journal The Lancet documented the study conducted by Albanian physicians at the time. Global climate change is altering the seasonality of Dobrava virus infections, making year-round infections possible.

Conclusion: Hantaviruses are not really a new and unknown threat to Albania. They are indeed infrequent infections but they carry global risks. The best possible epidemiological knowledge as well as the identification of their endemic areas is the task of public health. Only in this way can the risk of human infection be significantly reduced.

Keywords: Hantavirus, Albania, Dobrava Virus, Public Health.

Biography

Dr. Ermira Muco studied medicine at the University of Tirana, Albania, and graduated in 1998. In 2007, Muco received the title of specialist in Infectious and Sexually Transmitted Diseases for the treatment of patients in the Infectious Diseases Service and Emergency at QSUT 'Mother Teresa', and received a PhD degree in 2016 at the same institution. The main areas of scientific interest include zoonotic diseases, emerging infections, epidemiology, viral infections, epidemic diseases, tropical diseases, and HIV/AIDS infection. Muco is a co-author or first author in international congresses held in various regional, European and world countries, as well as in articles published within Albania or in journals indexed in PubMed and Scopus.

Esra Cakmak Taskin
Kocaeli City Hospital, Pediatric Infectious Diseases, Kocaeli, Turkiye

Hematologic and inflammatory profiles across different clinical presentations of pediatric brucellosis: A retrospective cohort study

Background: Pediatric brucellosis has heterogeneous clinical presentations, while laboratory features of relapse and chronic disease remain poorly characterized. We aimed to compare hematologic, inflammatory, serological, and microbiological findings across presentations.

Methods: This retrospective cohort included 97 children with acute (n=52), subacute (n=14), chronic (n=14), relapse (n=9), or asymptomatic brucellosis identified through household screening (n=8), diagnosed at a center in eastern Türkiye between April 2021 and January 2023. Hematologic indices, erythrocyte sedimentation rate (ESR), C-reactive protein (CRP), serological tests, and blood cultures were compared using non-parametric methods. Exploratory receiver operating characteristic (ROC) analysis evaluated total lymphocyte count (TLC) for distinguishing relapse from chronic disease.

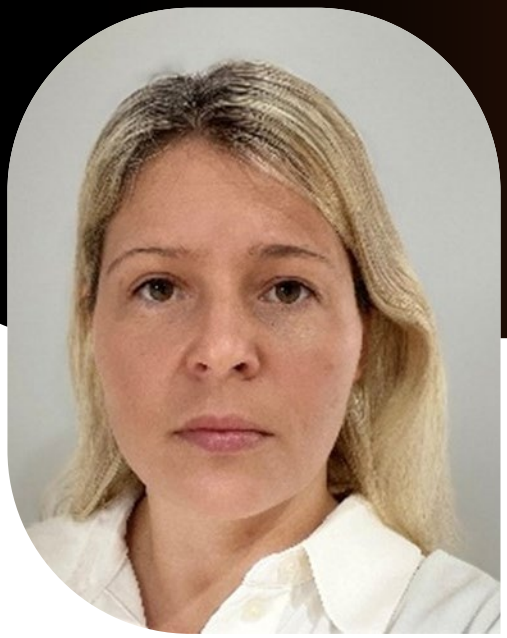
Results: Significant differences were observed for TLC (p=0.016), ESR (p<0.001), CRP (p<0.001), neutrophil-to-lymphocyte ratio (NLR; p=0.030), and platelet-to-lymphocyte ratio (PLR; p=0.023). Acute disease showed the highest ESR and CRP levels, whereas chronic disease had higher NLR and PLR values. TLC was highest in relapse (3480/µL) compared with chronic disease (2250/µL). Brucella IgM concentrations (p=0.016) and blood culture positivity (p=0.018) differed, whereas SAT, Coombs agglutination, Rose Bengal, and Brucella IgG did not. Exploratory ROC analysis suggested a discriminatory signal of TLC for relapse versus chronic disease (AUC=0.857; 95% CI, 0.691–1.000; p=0.005).

Conclusion: Hematologic and inflammatory parameters show different patterns across pediatric brucellosis presentations. Higher TLC in relapse is hypothesis-generating and should not be considered a relapse marker. Prospective multicenter validation is needed.

Keywords: Pediatric Brucellosis, Relapse, Total Lymphocyte Count, Inflammatory Markers, NLR, PLR.

Biography

Dr. Cakmak Taskın studied Medicine at Istanbul University, Cerrahpasa Medical Faculty, Turkiye, and graduated in 2011 in seventh place, became a pediatric specialist in 2016, and completed pediatric infection specialist training at Ankara University Faculty of Medicine in 2020. Cakmak Taskın currently works at Kocaeli City Hospital as a pediatric infection specialist and has published more than 15 research articles in SCI(E) journals.



Eszter Tothne Karip[1*], Calista Spiro[2]

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A rare case report: Hepatitis due to *Chlamydia trachomatis* infection in a 50-year-old male patient

We would like to present a rare case of hepatitis with Fitz-Hugh-Curtis syndrome caused by *Chlamydia trachomatis* infection in a middle-aged man.

Perihepatitis or Fitz-Hugh-Curtis syndrome is a well-known complication of Pelvic Inflammatory Disease in female patients, but it has only been described in a handful of cases in male patients. It is normally characterized by right upper quadrant pain caused by string-like adhesions between the liver capsule and parietal peritoneum. Hepatitis, on the other hand, has never been reported due to Chlamydia infection.

The patient presented with a three-day history of right upper quadrant pain and mildly deranged LFTs. US and CT images revealed a thickened gallbladder wall with small calculi and a slightly heterogenous mildly fatty liver; therefore, a decision was made to take him to theatre for laparoscopic cholecystectomy. During surgery it became evident that the whole liver was inflamed with purulent exudate and adhesions were noted between the liver capsule and the parietal peritoneum. We decided – after intraoperative consults with Gastroenterology and a fellow General Surgeon – not to proceed with the planned operation.

His viral screen confirmed *Chlamydia trachomatis* infection via PCR testing, he was treated with a course of Doxycycline and Metronidazole, and his symptoms settled with the above management.

Biography

Dr. Eszter Tothne Karip completed a Medical Degree in Budapest, Hungary, and has since worked in various hospitals across Ireland, the United Kingdom and Australia throughout different specialities including Intensive Care, General Surgery, Trauma & Orthopaedics, Orthogeriatrics and Medicine. Tothne Karip is currently working as a surgical registrar at Maitland Hospital.

Fabian Renger*, Attila Czirfusz
St. Elisabeth University of Health and Social Work in Bratislava, Slovak Republic

Reasons for the applicability of institutional theory approaches to the specific situation of medical care centers in the context of public health

Introduction: Since their authorization in 2004, Medical Care Centers (Medizinische Versorgungszentren, MVZs) have become an integral component of both the outpatient and inpatient healthcare sectors in Germany. They were introduced to improve interdisciplinary collaboration, strengthen continuity of care, and enhance the efficiency of healthcare delivery. Over the past two decades, MVZs have evolved into a significant organizational form within the German healthcare system, increasingly influencing the provision and coordination of medical services.

Subject of Study: While the legislature's original objectives have largely been achieved, the rapid expansion and structural transformation of MVZs have generated new economic, organizational, and regulatory challenges. These developments require further scientific analysis and appropriate regulatory responses to ensure sustainable healthcare delivery.

Objectives: This study aims to contribute to the theoretical and practical understanding of MVZs by applying established concepts from institutional economics. The research seeks to demonstrate the relevance of economic theories for analyzing organizational structures, governance mechanisms, and decision-making processes within MVZs.

Methodology: The study employs a conceptual and theoretical approach, examining the transaction cost approach and principal-agent theory as key analytical frameworks. These theories are applied to the institutional and organizational characteristics of MVZs in Germany to assess their explanatory potential regarding contractual relationships, coordination mechanisms, and incentive structures.

Results: The findings indicate that both the transaction cost approach and principal-agent theory are well suited to analyzing MVZs as economically oriented healthcare organizations. These theoretical perspectives provide valuable insights into governance, efficiency, information asymmetries, and the management of complex stakeholder relationships within integrated healthcare settings.

Conclusions and Recommendations for Public Health: By integrating concepts from business administration and institutional economics with healthcare research, this study expands the theoretical foundation for analyzing MVZs. The results contribute to a better understanding of their organizational dynamics and provide a basis for future research and evidence-based health policy decisions aimed at improving efficiency, quality of care, and long-term sustainability within the German healthcare system.

Keywords: Medical Care Centers (MVZs), Institutional Economics, Transaction Cost Economics, Principal-Agent Theory, Healthcare Management, Healthcare Economics, Public Health.

Biography

PD Dr. Fabian Renger is a German scholar in health sciences and business administration whose research focuses on healthcare management, institutional economics, and the organization of Medical Care Centers (MVZs). Renger earned a Ph.D. in Health Sciences and completed a habilitation at St. Elizabeth University. With extensive professional experience in healthcare management, Renger's work bridges economic theory and healthcare practice, emphasizing governance, efficiency, and sustainable healthcare delivery within the German healthcare system.

Huanhuan Li*, Ryan Donnelly
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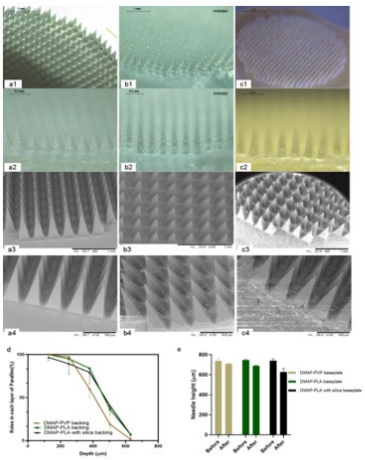
A novel responsive microneedle platform for reliable drug and vaccine delivery

Introduction: Driven by rising demand for minimally invasive healthcare, ageing populations and at-home treatment options, microneedles (MNs) offer a compelling alternative to injections, particularly for vaccines and chronic therapies. However, commercial adoption has been hindered by usability challenges, specifically the absence of clear visual indicators for correct patch application and removal. Addressing this gap is critical to unlocking their full potential in clinical and consumer markets, enhancing patient confidence, therapeutic accuracy and regulatory approval. To address this, we have developed an innovative, responsive microneedle platform featuring a built-in colour-change feedback mechanism.

Results: The final optimised MNs demonstrated well-defined geometries, consistent microneedle heights, and precisely controlled interspacing, attributed to the uniform micro-mould design. These features enabled effective insertion into Parafilm®M models, with height reduction upon compression remaining below 20% (Figure 1).



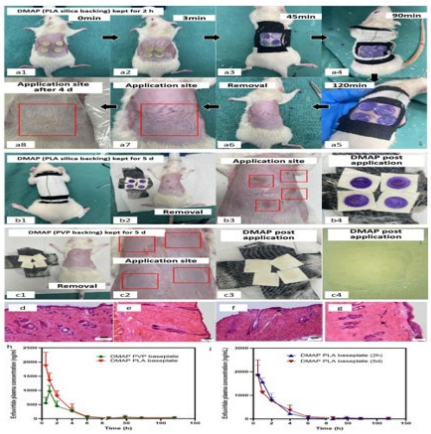


Figure 1: Morphology and insertion ability of microneedles.
Figure 2: *In vivo* pharmacokinetic results.

The MNs integrated with visual feedback indicators showed a rapid colour transition from yellow to green within 3 minutes post-insertion on rat skin, triggered by microneedle hydration from interstitial fluid. This was followed by a shift to purple within 2 hours, indicating complete microneedle dissolution and confirming successful drug delivery. In vivo pharmacokinetic studies in Sprague Dawley rats revealed that the PLA-silica MN achieved a peak plasma concentration (C_{max}) of 1864 ± 480 ng/mL at 0.5 hours, while the PVP-baseplate MN reached a C_{max} of 973 ± 200 ng/mL at 1 hour. Both systems demonstrated good biocompatibility with no signs of irritation or adverse reactions (Figure 2).

Conclusion: This study presents a responsive microneedle platform for painless, reliable transdermal delivery of enfuvirtide. The PLA–silica system provides a colour-change feedback mechanism for accurate dosing and easy removal while maintaining safety and biocompatibility. With tunable release and a user-friendly application, it offers a promising, scalable solution for next-generation peptide and vaccine delivery.

Biography

Huanhuan Li is a Research Fellow specialising in transdermal peptide delivery using microneedles, dedicated to enhancing the user experience with this innovative technology.

Isaac Bakare
General Hospital Odan, Lagos, Nigeria

Assessment of hematological, hepatic and renal parameters among HIV-infected patients based on duration on antiretroviral therapy

Background: HIV and antiretroviral therapy (ART) can significantly impact hematological, hepatic and renal functions, although the effects are complex and influenced by factors including type of drugs, duration of therapy and patients' underlying conditions. However, the influence of ART duration on these laboratory markers remains underexplored.

Aim: The aim of this study was to evaluate and compare the hematological, hepatic and renal parameters among HIV-infected patients based on the ART duration.

Methods: This study employed a cross-sectional design and was conducted from January to December 2025 among 100 HIV-infected patients attending General Hospital Odan, Lagos State, Nigeria. Demographic data and ART duration were recorded. Laboratory assessment such as full blood count, liver function tests and renal function markers and electrolytes were carried out. Descriptive statistics were used to summarize the means and standard deviations while trend and correlation analyses examined the associations between laboratory parameters and ART duration.

Results: The prevalence of laboratory abnormalities such as anemia, leucopenia, thrombocytopenia, elevated liver enzymes and renal impairment were 49%, 99%, 5%, 90% and 35% respectively. Trend analysis showed that laboratory abnormalities were more pronounced in early to mid-term ART durations (13–36 months) with partial stabilization in long-term therapy (>48 months). Mean RBC increased from 3.37 $\times 10^9$/µL (≤12 months) to 3.83 $\times 10^9$/µL (>60 months), hemoglobin from 11.83 g/dL to 12.90 g/dL, and platelets from 178 $\times 10^3$/

μL to 226 ×103/μL. Liver enzymes were elevated in early and mid-term ART but stabilized in long-term therapy. Renal parameters showed slight mid-term increases (urea 3.25–6.54 mmol/L; creatinine 72–135 μmol/L) with normalization in long-term therapy. Correlation analysis revealed significant positive association between ART duration and some laboratory parameters like RBC count ($r = 0.336$, $p = 0.001$), MCH ($r = 0.261$, $p = 0.009$), MCHC ($r = 0.257$, $p = 0.010$), eosinophils ($r = 0.283$, $p = 0.004$), basophils ($r = 0.223$, $p = 0.026$), and platelet count ($r = 0.221$, $p = 0.027$).

Conclusion: Antiretroviral therapy duration is associated with progressive recovery of the hematological indices while hepatic and renal functions remain vulnerable. Regular monitoring of laboratory parameters is recommended to guide clinical interventions, optimize patient care and minimize complications.

Keywords: HIV, Antiretroviral Therapy, Liver Function, Renal Function, Hematology, Laboratory Abnormalities.

Biography

Bakare Isaac Ayodeji is a Medical Laboratory Scientist and emerging biomedical researcher whose work focuses on infectious diseases, laboratory diagnostics and environmental health. He trained at Lead City University, Nigeria, and has experience in haematology, clinical chemistry, microbiology, immunology and molecular diagnostics. His research interests include HIV, tuberculosis, antimicrobial resistance and environmental contaminants, with a commitment to translating laboratory findings into evidence that improves clinical practice and public health. He has authored multiple peer-reviewed publications and actively contributes to interdisciplinary biomedical research.

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Activation of cGAS-STING signaling pathway during HCV infection in human hepatoma cell line, Huh7

Hepatitis C virus (HCV) is a major global health issue, infecting over 170 million people worldwide and leading to severe liver diseases, including fibrosis, cirrhosis and eventually hepatocellular carcinoma (HCC). The ability of HCV to persist and cause chronic infection is partly due to its evasion of the host's innate immune responses, particularly those mediated by the RIG-I-MAVS pathway, which is critical for the antiviral defense system. Many studies have shown the crucial role of genome sensing of DNA viruses by cyclic GMP-AMP synthase (cGAS) followed by cGAMP production and activation of downstream effector STING (stimulator of interferon genes) to induce IFN-β; however, it is not understood in RNA viruses, especially in HCV infection. In this study, we explored for the first time the mechanism of the cGAS-STING pathway in HCV-infected human hepatoma cells, specifically using the JFH-1 strain of HCV (genotype 2a). We observed that cGAS expression is significantly upregulated during the early HCV infection, leading to the production of the second messenger cyclic GMP-AMP (cGAMP), which in turn activates STING. This activation results in the significant induction of type I interferon responses, particularly interferon-β (IFN-β), which is essential for mounting an effective antiviral response. Moreover, knockdown experiments targeting cGAS, STING and RIG-I revealed that these proteins play a crucial role in suppressing HCV replication, underscoring their potential as therapeutic targets. These findings provide valuable insights into the molecular mechanisms of the cGAS-STING pathway in mediating the innate immune response against HCV. Understanding this pathway's role in the immune defense against HCV opens up new possibilities for therapeutic strategies aimed at enhancing the host's antiviral immunity and potentially developing new treatments for chronic HCV infection.

Biography

Dr. Jawed Iqbal is Professor at the School of Biosciences and Technology, Galgotias University, India. Iqbal holds a PhD in Biochemistry from Aligarh Muslim University and has extensive research experience in virology, molecular genetics, immunology, and recombinant DNA technology, and previously served as a Ramalingaswami Fellow at Jamia Millia Islamia and as Senior Research Associate at Rosalind Franklin University, USA. Iqbal's research focuses on host–virus interactions, HCV biology, innate antiviral signaling, CRISPR-based diagnostics, and viral genome sensing, with 32 publications, five book chapters, one edited book, two patents, three research grants, and three PhD scholars supervised.

K.M.Yacob Kunnathazhath
Marma Health Centre, Kaloor, Kochi, Kerala, India

A new universal fever definition and the unscientific nature of the conservative fever definition

No medical textbook tells us what the purpose of fever is. Without knowing this, no one in the world can define, test, or treat fever. The current definition, testing, and treatment of fever, which is constructed without knowing what the purpose of fever is, has no scientific basis. There is no uniform definition or test for fever alone.

What are the shortcomings of the current fever definition?

The current definition of fever is usually only an elevated body temperature above 100.4°F (38°C). Different types of fever definitions can be seen in medical books. It is against modern science to give different definitions for one thing (fever).

An elevated core body temperature of more than 38.0°C is not a scientific definition. Elevating the temperature is an action like walking and sitting. The definition of fever does not include anything that occurs only when there is a fever. A single criterion for a definition is not found in the current definition of fever.

Correct definition, basis for research: For a topic to have a basis for research, there must be a proper definition of that topic and a test based on this definition. Not only do many existing fever definitions lack even the basic qualifications for a definition, but testing and treatment based on these fever definitions do not exist. Fever cannot be recreated according to current fever definitions. An important criterion for deciding whether something is true in modern science is that it can be reproduced.

You cannot create a fever with hot objects. So far, fever research has tested and treated fever by creating hyperthermia, the opposite of fever. Many research studies use hot objects or

heating materials, such as electric bulbs and prostaglandin E2, to induce fever in laboratory animals such as rats and rabbits. Fever is determined by observing the rise in temperature in these animals using a thermometer. It is not a fever-measuring device. Little did they know that what these researchers were producing and testing was not fever, but hyperthermia. The fundamental fallacy of fever begins here, is reflected in the definition of fever, and continues in diagnosis and treatment. Even Stone Age humans did not use similar science or technology.

The definition of fever is the basis of fever: If the definition of fever is wrong, the diagnosis and treatment based on it will be wrong. In modern science, no one can make a true definition, diagnosis, or treatment of fever without knowing the basics of fever. If made, it would be fundamentally against modern science. The seriousness and danger of the definition of fever are recognized when the diagnosis and treatment of fever are not based on the current definition of fever. The current definition of fever has nothing to do with modern science.
What is the need for a universal fever definition?

Both warm-blooded and cold-blooded animals, including humans, mammals, birds, and reptiles, experience fever. Even brainless creatures can experience fever. Therefore, fever is a universal phenomenon. A universal phenomenon requires a universal definition. When infected, cold-blooded animals will actively seek out warmer environments, such as by soaking up sunlight or moving into warm water, to increase their body temperature. This behavior is similar to the fever response in warm-blooded animals. When a fever occurs, both warm-blooded and cold-blooded animals, including humans, prefer higher temperatures to reduce inflammation and increase blood flow.

What are the criteria for a universal fever definition?

A universal fever definition should be able to scientifically evaluate, differentiate, concisely describe, and easily understand fever. A correct definition of fever can be made by knowing what triggers fever, what substances are produced during fever, who causes fever, why fever occurs, and what processes occur in the body during fever, and why. The only things that trigger fever in any organism are substances that lower body temperature, increase inflammation, and decrease blood flow. Fever in any organism serves the general goals of increasing body temperature, reducing inflammation, and increasing blood flow. A universal fever definition should include the triggers of fever and the purpose of fever.

Yacob's Universal Fever Definition: Fever is the body's defense mechanism against the triggers of fever (inflammation).

If essential blood flow to organs is reduced due to increased inflammation, fever is an adaptive and sensible action by the immune system to reduce inflammation and increase essential blood flow to maintain the organ or system as the body's self-defense mechanism. To this end, our immune system usually generates more heat than normal and prevents body heat from leaving the body.

The answer to any question about fever can be found in this definition of fever.

The new universal fever definition can scientifically assess, differentiate, concisely describe, and facilitate easy understanding of fever. Fever can be recreated according to the new universal fever definition.

Biography

K.M.Yacob Kunnathazhath is a practicing physician in the field of healthcare in Kerala, India, for the last 37 years, with a strong interest in basic research spanning fever, inflammation and back pain. He is a writer who has printed and published ten books on these subjects, written hundreds of articles in various magazines, and published 15 articles on fever in various journals. Following scientific studies, Yacob has developed 8000 affirmative cross-checking questions that can explain all queries related to fever.

K.M.Yacob Kunnathazhath
Marma Health Centre, kaloor, Kochi, Kerala, India

Should we test and treat the fever triggers or the fever that creates the immune system against the fever triggers?

Fever is one of the least knowledgeable topics in modern science.

Looking at medical journals and medical books, modern science does not even know the basic facts about fever.

Modern science does not know what the purpose of fever is, what fever is, what to do to get a fever, how to diagnose it, and how to treat it because of a lack of precise definition.

What are the triggers of fever? What are they?

Fever triggers are substances and their actions that trigger the immune system to induce fever. These substances reduce heat, increase inflammation, and reduce blood flow.

Fever triggers include water below body temperature, soft drinks, ice cream, weather, medications including paracetamol2 that reduce body heat and increase inflammation, etc. Decreased blood flow due to severe inflammation is the sole trigger for fever. Any substance that is cooling or reducing temperature (antipyretic) is a fever stimulant because it increases inflammation and reduces blood flow. Antipyretics are the only substances needed to induce fever in any organism. By using antipyretics in anyone, anyone can reduce the body's heat energy and cause inflammation and fever within a few hours.

The causes of fever triggers, the triggers of fever, and the substances produced by the immune system fight against the triggers of fever, their functions are not the same, and they are opposite to each other. Fever triggers caused by external factors are always harmful to the body, but a fever that builds immunity against it is always beneficial to the body. Fever is the body's defense mechanism against the triggers (inflammation) of fever.

The current definition of fever does not mention any fever-triggering substances. Therefore, fever triggers are not included in fever testing or treatment. Rather than identifying and eliminating the triggers of fever, today's definition, testing, and treatment focus on identifying and eliminating the substances the immune system produces to fight against the triggers of fever. Today's fever treatment destroys the substances that create immunity against the triggers of fever and increase the triggers of fever.

In addition, today fever is diagnosed and treated as hyperthermia, the opposite of fever. Eliminating fever, which creates immunity against fever stimuli, and treating fever as hyperthermia will increase morbidity and mortality. It is not a treatment according to any scientific law in the world today, but a murder attempt. The treatment of fever triggers is to reduce fever triggers. The only solution against fever triggers is to increase blood flow and reduce inflammation. This is an immutable scientific fact. The basic elements necessary for a scientific treatment are not provided in fever treatment. Fever should be checked and treated, not for the fever, but for its triggers. The only solution against fever triggers is to increase blood flow and reduce inflammation. This is an immutable scientific fact.

Keywords: Fever triggers, inflammation, immune system, prostaglandins, oxygen consumption.

Biography

K.M.Yacob Kunnathazhath is a practicing physician in the field of healthcare in Kerala, India, for the last 37 years, with a strong interest in basic research spanning fever, inflammation and back pain. He is a writer who has printed and published ten books on these subjects, written hundreds of articles in various magazines, and published 15 articles on fever in various journals. Following scientific studies, Yacob has developed 8000 affirmative cross-checking questions that can explain all queries related to fever.

JiaoJing Chen, Shan Wang, Liu Yan*

Ruijin Hospital Affiliated to Shanghai Jiao Tong University School of Medicine, Shanghai, China

Synergistic nebulized therapy for severe viral pneumonia: A biomimetic nano-platform integrating MSCderived exosomes and interferon-α2b

Background: Severe viral pneumonias, particularly those caused by influenza A virus, respiratory syncytial virus (RSV), and emerging coronaviruses, continue to pose formidable challenges to global public health. While Interferon-alpha (IFN-α) remains a cornerstone of antiviral therapy due to its potent induction of antiviral states in host cells, its clinical utility via traditional delivery routes is severely constrained. Systemic administration often triggers significant adverse effects, including bone marrow suppression and neurotoxicity. Conversely, direct nebulized inhalation of naked IFN-α proteins is hindered by rapid proteolytic degradation in the lung microenvironment, poor retention in deep alveolar tissues, and loss of bioactivity during the high-shear nebulization process. There is an urgent clinical need for a delivery system that ensures both stability and localized therapeutic concentration.

Methods: In this study, we developed Exo-Aero α, a translational biomimetic nano-platform designed to overcome these barriers. Mesenchymal stem cell-derived exosomes (MSC-Exos) were isolated from P3-generation cells via ultracentrifugation and characterized as the primary delivery vehicle. Recombinant human IFN-α2b was encapsulated into the MSC-Exos using a proprietary physical-chemical loading and micro-extrusion protocol, optimizing the Target-Treat-Repair trinity logic. To facilitate large-scale distribution and clinical application, the formulation was engineered into a stable lyophilized powder using a specialized vacuum-freeze-drying process (10Pa/-50°C). The physicochemical properties, including particle size distribution (NTA), morphology (TEM), and post-nebulization bioactivity, were rigorously validated. Therapeutic efficacy was evaluated in a murine model subjected to a lethal-dose H1N1 viral challenge.

Results: The Exo-Aero α platform exhibited a highly uniform and stable particle size of 85.2 ± 21.6 nm, optimized for deep lung penetration. Post-nebulization analysis confirmed that the exosomal lipid bilayer provided robust physical shielding, maintaining over 95% of IFN-α2b biological activity. In vivo results demonstrated that the synergistic Exo-Aero α group achieved a remarkable 100% survival rate against lethal-dose H1N1 infection, significantly outperforming the IFN-α2b monotherapy group (32% survival) and the MSC-Exos group (60% survival). Mechanistic investigations revealed a profound 1+1>2 synergistic effect: IFN-α2b effectively suppressed viral replication via the JAK-STAT signaling pathway, while the MSC-Exos functioned as a potent immunomodulator, suppressing the pro-inflammatory cytokine storm and promoting the regeneration of damaged alveolar epithelial cells.

Biography

Dr. Yan Liu, PhD, is a Senior Engineer at the National Center for Translational Medicine, Ruijin Hospital. Specializing in biopharmaceutical R&D and clinical translation, Liu has led several National Major New Drug Discovery Projects, securing two Class I IND approvals and 13 patents. Liu's research focuses on anti-infective mechanisms, with landmark publications on TFF2-Interferon synergy in The Lancet EClinicalMedicine. With 16 peer-reviewed papers, Liu currently develops exosome-based delivery platforms for severe respiratory diseases, leveraging expertise in molecular pharmacology and regulatory science to bridge the gap between laboratory innovation and clinical application.

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Nebulized mesenchymal stem cell-derived exosomes encapsulating interferon-α2b: A synergistic strategy for targeted treatment of severe viral pneumonia

Background: Severe viral pneumonias (e.g., influenza, RSV) lack effective localized treatments. While Interferon-α (IFN-α) is a potent antiviral, its clinical utility via inhalation is limited by rapid degradation, poor lung retention, and systemic toxicity. We developed Exo-Aero α, a novel translational platform using mesenchymal stem cell-derived exosomes (MSC-Exos) as bio-nanocarriers to enhance IFN-α2b delivery and provide synergistic lung repair.

Methods: MSC-Exos were harvested from P3-generation stem cells and loaded with IFN-α2b (100-200 IU/mL) via a proprietary physical-chemical loading process. The formulation was stabilized through a specialized lyophilization technique (10 Pa/-50°C). Physicochemical properties, including particle size (NTA) and bioactivity retention, were validated. In vivo efficacy was tested in a lethal-dose H1N1 influenza mouse model using a precision nebulization system.

Results: The Exo-Aero α formulation maintained a stable particle size of 86.2 ± 21.6 nm with over 95% bioactivity retention post-nebulization. In the lethal viral challenge model, the synergistic group achieved a 100% survival rate, significantly outperforming IFN-α2b monotherapy (32%) and MSC-Exos alone (60%). Mechanism studies revealed a 1+1>2 effect: IFN-α2b suppressed viral replication via the JAK-STAT pathway, while MSC-Exos modulated the pulmonary immune microenvironment, suppressed the cytokine storm, and promoted alveolar epithelial regeneration. Preliminary safety assessments in pilot translational studies support its high biocompatibility.

Conclusion: Exo-Aero α successfully addresses the stability and targeted delivery hurdles of biological drugs for respiratory infections. By integrating potent antiviral action with endogenous tissue repair, this Trinity platform provides a promising, scalable candidate for the clinical management of severe viral pneumonia and acute lung injury.

Biography

Dr. Yan Liu, PhD, is a Senior Engineer at the National Center for Translational Medicine, Ruijin Hospital. Specializing in biopharmaceutical R&D and clinical translation, Liu has led several National Major New Drug Discovery Projects, securing two Class I IND approvals and 13 patents. Liu's research focuses on anti-infective mechanisms, with landmark publications on TFF2-Interferon synergy in The Lancet EClinicalMedicine. With 16 peer-reviewed papers, Liu currently develops exosome-based delivery platforms for severe respiratory diseases, leveraging expertise in molecular pharmacology and regulatory science to bridge the gap between laboratory innovation and clinical application.

Martha Mercado[1*], Rene Arredondo[1], Mario Santana[2], Jorge Velasco[3], Yolanda Lopez-Vidal[1]

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Assessment of normalization factors in SARS-CoV-2 trends at four treatment plants: Basis for a wastewater surveillance in Mexico City

Background: The potential of wastewater-based epidemiology (WBE) as a surveillance and early warning tool for the COVID-19 outbreak and antimicrobial resistance has been demonstrated in numerous publications.

Since WBE is an emerging research area, connecting wastewater data to clinical surveillance remains challenging. To gain a better understanding of this phenomenon, we tested whether normalizing SARS-CoV-2 concentrations using biomarkers that measure the relative human fecal contribution could improve analysis to calculating trends of community infection. This study also aimed to assess the necessary conditions to establish a COVID-19 monitoring system in Mexico (one of the places with the highest number of cases in the world during the pandemic) and to develop a predictive model that generates quantitative estimates of the infected population through SARS-CoV-2 loads in wastewater.

Method: Long-term monitoring of SARS-CoV-2 in wastewaters of Mexico City was conducted at four wastewater plant treatments (WWTPs): the biggest WWTP in Latin America (Atotonilco, 2020-2023), the first- and second-largest WWTPs in Mexico City, and the flagship University campus treatment plant (2024) at UNAM. Concentrations of SARS-CoV-2 RNA were quantified by RT-qPCR, along with three fecal virus normalizers: Pepper mild mottle virus (PMMoV), F-specific RNA phages of human genogroup III (FRNAG-III) and Human adenoviruses serotype 41 (HAdV-F41). Linear regression analysis and cross-correlation analysis between viral genome copies and confirmed case data were performed.

Results: The three fecal normalizers included in this study (PMMoV, FRNAG-III, and HAdV-F41) were detected in all samples, regardless of the season. As expected, wastewater tracking showed HAdV-F41 genome copies peaked at different time points from COVID-19, while the other normalizers (PMMoV and FRNAG-III) remained without seasonal variation and decreased titers during the rainy season (by fifty and thirty percent respectively) due to dilution. Incorporating flow rate improves the correlation between fecal normalizer concentration data and the estimated population served by each WWTP; however, flow-normalized SARS-CoV-2 wastewater concentrations did not produce a strong correlation with COVID-19 cases (R^2 = 0.2-0.5). Our assessment shows that utilizing flow normalization, along with fecal indicators, to normalize SARS-CoV-2 wastewater concentrations yields stronger correlations between SARS-CoV-2 wastewater concentrations and COVID-19 cases (r=0.78-0.92).

Conclusions: The strongest correlation with reported COVID-19 cases was provided by SARS-CoV-2 wastewater concentrations normalized by flow plus fecal normalizer, with FRNA-GIII showing the highest Pearson coefficient (0.92), a viable alternative to PMMoV, which is subject to regional dietary variability. The outcomes of this study provide a basis for improving public health decision-making regarding SARS-CoV-2 circulation in Mexico.

Biography

Martha Mercado graduated with a degree in pharmaceutical chemistry from the Faculty of Chemistry, UNAM, completed a master's degree at the Faculty of Medicine specializing in proteomics and microbiology, and is currently pursuing doctoral studies focusing on molecular biology and statistical data analysis.

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Drone-assisted surveillance of animal diseases: An innovative approach to outbreak response and biosafety

Introduction: The increasing complexity of animal disease outbreaks highlights the need for innovative, rapid, and safe approaches to field surveillance. Following a major outbreak of Lumpy Skin Disease (LSD) in Israel, the potential use of drones to support disease surveillance was explored. The aim was to assess whether drones could assist in locating affected animals and herds, monitoring infected premises, and identifying previously undetected free-ranging herds in remote or difficult-to-access areas.

Materials and Methods: The Israeli Veterinary Services operate a DJI Inspire 2 multi-rotor drone weighing less than 4 kg. During an LSD outbreak, the drone was deployed to locate clinically affected animals within known infected herds and survey large open areas for previously undetected herds. High-resolution photographs and videos were obtained for animal counting, identification, clinical assessment, and epidemiological surveillance. The potential application of drone-assisted surveillance to other infectious animal diseases was also evaluated.

Results: Drone-assisted surveillance proved particularly useful for locating and monitoring herds in remote, hidden, or difficult-to-access areas. Large areas could be scanned rapidly, reducing the time required for field searches. Physical obstacles such as water bodies, difficult terrain, dense vegetation, and steep or inaccessible areas could be readily overcome. The technology was particularly valuable when surveying potentially hazardous areas, including locations affected by land mines.

Drone deployment also reduced occupational exposure of veterinary personnel to environmental and biological hazards, including extreme weather, dust and air pollution, as well as potential encounters with aggressive animals, snakes, and arthropods.

High-quality aerial images facilitated animal counting and identification, providing a useful tool for herd census and quarantine surveillance. This enabled verification of animal numbers and helped assess whether animals had potentially escaped movement restrictions. Drone surveillance was also useful where cooperation from herd owners was limited.

No significant disturbance, stress, or fear was observed among the animals during drone operation. Clinically affected animals could be readily identified within herds, while camera zoom enabled close examination of visible lesions, including assessment of lesion characteristics and apparent age. In some cases, insects present on affected animals could also be identified. Individual animals could be recognized through ear tags or tattoos.

Discussion and Conclusion: Drone technology offers several potential advantages for animal disease surveillance, including rapid herd location, clinical screening, animal counting, individual identification, and remote monitoring of affected premises.

An important additional benefit is its potential contribution to biosafety and biosecurity during infectious disease outbreaks. For highly contagious diseases such as Foot-and-Mouth Disease (FMD) and Peste des Petits Ruminants (PPR), remote aerial surveillance could reduce the need for veterinary personnel to enter potentially infected premises, thereby minimizing occupational exposure and the risk of mechanical transmission between farms.

Drones may therefore serve as a valuable complementary tool for epidemiological surveillance and outbreak investigation. Limitations include regulatory requirements, licensing and permits, limited battery endurance, weather dependency, and the need for trained operators. Further studies are warranted to evaluate the diagnostic sensitivity of drone-assisted surveillance and its integration into routine animal disease surveillance and One Health preparedness and outbreak response systems.

Figure 1. Beef cattle with LSD, found with a drone.

Biography

Dr. Michel Bellaiche is Deputy Director of the Kimron Veterinary Institute, Israeli Veterinary Services and Animal Health (VSAH), and Head of the Department of Epidemiology at the Kimron Veterinary Institute. Bellaiche serves as OIE focal point for animal disease notification, Training Focal Point to the EuFMD (FAO), and Editor of the yearly report of the Israeli Veterinary Services, dealing with emerging and reoccurring diseases in Israel including Lumpy Skin Disease, Epizootic Haemorrhagic Disease, Highly Pathogenic Avian Influenza, Rabies, Bovine Tuberculosis, Classical Swine Fever, Brucellosis and West Nile Fever.

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An unprecedented West Nile Virus outbreak in Israel (2024): A textbook case for the one health approach

Background: West Nile Virus (WNV) is a well-established flavivirus endemic to Israel, maintained in an enzootic cycle between Culex spp. mosquitoes and avian reservoirs, with humans and equines serving as incidental dead-end hosts. While approximately 80% of human infections remain asymptomatic, the virus can cause severe neurological illness and fatalities. In June 2024, central Israel experienced an unprecedented surge in WNV activity, presenting significant deviations from historical baselines in morbidity, mortality, and positivity rates in both humans and birds, in addition to WNV infected mosquitoes' diagnosis.

Methods & Inter-Sectoral Surveillance: A synchronized, multi-agency One Health investigation was launched involving public health, environmental, and veterinary sectors. The Ministry of Health monitored human clinical data. Concurrently, the Pest Control Division of the Ministry of Environmental Protection carried out intensive vector trapping, while mosquito pool testing was routinely performed by the Medical Entomology Laboratory and the Central Virology Laboratory (Ministry of Health). To amplify avian surveillance, the Veterinary Services launched a public reporting campaign via a dedicated mobile application (Bird Button), integrated with municipal 106 hotlines. Local authorities and the Nature and Parks Authority facilitated the collection of wild bird carcasses for cost-free laboratory diagnostic testing at the Central Kimron Veterinary Institute, Ministry of Agriculture.

Results: The 2024 summer season culminated in 930 confirmed human cases, resulting in 73 deaths, predominantly affecting individuals over the age of 60. The outbreak was characterized by unusually intense viral circulation, reflected in high positivity rates in humans, birds, and mosquito pools. Simultaneously, massive wild bird mortality was recorded, with 319/1047 birds testing positive for WNV, including 221 hooded crows (Corvus cornix) and 33 domestic pigeons (Columba livia), exhibiting severe neurological signs or death between mid-June and the end of September 2024. The hooded crow is the most common bird species found in close proximity to humans in Israel, and its susceptibility to West Nile virus is substantially higher than that of other synanthropic bird species, outweighing differences in relative abundance. Commercial poultry sectors remained symptomatically unaffected due to geographical segregation and low susceptibility of chickens.

Environmental trapping successfully isolated WNV-positive mosquito pools across central Israel. An environmental root-cause analysis identified a critical infrastructure failure at a wastewater treatment plant in Ramat HaSharon (Central district) which served as an extensive breeding habitat for the mosquito vectors Culex perexiguus and Culex pipiens, likely driving regional viral amplification and spillover.

Conclusion & One Health Significance: The 2024 WNV outbreak underscores the critical intersection of failing environmental infrastructure, vector proliferation, wildlife sentinels, and human vulnerability. This crisis highlights that human health cannot be safeguarded and cannot be isolated from environmental risks management and wildlife monitoring. The deployment of cross-sectoral tools—such as citizen avian reporting, free veterinary diagnostics, and targeted environmental investigations—demonstrates the operational necessity of the One Health framework in predicting, detecting, and mitigating vector-borne zoonotic threats.

Tight multidisciplinary cooperation and coordination among all relevant governmental ministries enabled the rapid implementation of surveillance and response activities throughout the outbreak, and very likely contributed to reducing human morbidity and mortality.

Keywords: West Nile Virus, One Health, Vector-Borne Outbreak, Enzootic Surveillance, Environmental Infrastructure, Citizen Reporting.

Biography

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Omar Imam
Ministry of Public Health, Syrian Arab Republic

Antimicrobial stewardship in the Middle East: An experience from a tertiary center in Qatar

Antimicrobial stewardship is one of the most challenging issues in the 21st century. The author aims to present a personal experience from one of the best funded pediatric hospitals in the Middle East, outlining strategies used including communication with physicians and hard stop policies, outcomes, published research on the topic from Sidra, and a personal outlook on the future of antimicrobial stewardship.

Having relocated to Syria, the author will also try to contrast the situation between one of the richest countries in the Middle East and a country fresh out of a civil war, and explain challenges to antimicrobial stewardship implementation in Syria.

Biography

Omar Imam trained as a pediatric infectious disease specialist in Qatar and worked as a physician in Qatar for 10 years. Imam has published research in the area of antimicrobial stewardship and case reports on unusual infections, is a member of the International Society of Travel Health, and is interested in the use of affordable molecular diagnostics in pediatric infectious diseases. Imam currently works as a volunteer in the Ministry of Public Health in Syria as part of the outbreak response team.

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Phase I dose-escalation study of nanobody-armored dendritic cell vaccine (Baize DC) in patients with solid tumors after radical resection

Background and Objective: Conventional dendritic cell (DC) vaccines face limitations including immunosuppressive lymph node microenvironment and low tumor antigen immunogenicity. In an early investigator-initiated trial (IIT), a total of 805 post-surgical patients treated with a DC2.0 plus vaccine demonstrated 98.6% grade 1 adverse events, 54.8% T cell response rate, and 96.0% 1-year recurrence-free survival (RFS). Baize DC is an upgraded next-generation vaccine candidate (SHC1001) derived from DC2.0 plus, employing a proprietary technology enabling DCs to secrete PD-1/CTLA-4 antibodies and load four antigens including P53 and KRAS. This phase I dose-escalation study (NCT07479667) was initiated to evaluate its safety, impact on MRD (ctDNA), bispecific antibody pharmacokinetics, and antigen-specific T cell responses in patients after radical resection.

Methods: Eight patients were enrolled in this dose-escalation study after R0/R1 resection and had completed adjuvant chemotherapy. Tumor types included colorectal cancer (n=2), gastric cancer (n=2), and pancreatic cancer (n=4). Baize DCs were administered as a single subcutaneous injection at four dose levels: 1.5×107 (n=3), 4.5×10^7 (n=3), 9.0×10^7 (n=1), and 1.8×10^8 cells/dose (n=1). The primary endpoint was safety; secondary endpoints included bispecific antibody pharmacokinetics, T cell responses, and MRD monitoring (ctDNA).

Results: All 8 patients received a single dose of Baize DC vaccine candidate injection.

(1) Safety: Adverse events occurred in only 2 patients (dry mouth, hyperhidrosis), both at grade 1. No higher grades (≥2) were observed with treatment-related adverse events.

(2) MRD Monitoring: Of the first 4 evaluable patients, two were MRD-positive and two were MRD-negative at baseline. Both MRD-positive patients had pancreatic cancer (one from dose Level 2, one from dose Level 4). Post-injection, both patients showed favorable ctDNA dynamics: the Level 2 patient demonstrated continuous VAF decline, and the Level 4 patient converted to MRD-negative. Among MRD-negative patients, one transiently became ctDNA-positive at 2 months but reverted at 3 months, while the other maintained ctDNA-negative status throughout.

(3) Bispecific Antibody Pharmacokinetics: Plasma concentrations peaked at Day 2 in all 4 evaluable patients, ranging from 20.50 to 43.67 pg/mL vs ug/mL, with no dose-dependent relationship observed.

(4) Antigen-Specific T Cell Responses: Three of 4 evaluable patients (75%) showed positive ELISPOT responses. At Day 14, JL0102 responded to multiple antigens (SI: KRAS 57.6, P53 58.9, TERT 30.8), and JL0103 showed P53 response (SI 12.9). At Day 21, JL0101 exhibited P53 response (SI 23.5). JL0104 remained negative.

Conclusion: SHC1001, a nanobody-armored Baize DC vaccine candidate, achieved excellent safety (no adverse event grade ≥2) and promising immunogenicity and MRD dynamics. The vaccine enhances immunogenicity through autocrine checkpoint antibodies and mRNA antigen loading. Notably, both MRD-positive pancreatic cancer patients showed marked ctDNA decline post-vaccination. Given the high post-surgical recurrence rate of pancreatic cancer and these encouraging signals, future efforts will prioritize enrolling more pancreatic cancer patients in a planned Phase II study.

Biography

Prof. Qing Xu, MD, PhD, is Vice President and Director of Medical Oncology at Shanghai Mengchao Cancer Hospital, Shanghai University, and Chief Expert of Oncology at Shanghai Tenth People's Hospital, Tongji University. Xu is a doctoral supervisor and Shanghai Pujiang Talent, specializing in tumor immunotherapy, targeted therapy, and comprehensive treatment of solid malignancies, and has published nearly 100 SCI papers in leading journals including Science Advances, Oncogene, and Signal Transduction and Targeted Therapy (STTT). Xu serves as Vice President of the China Medical Education Association and Vice Chairman of the China Medicinal Biotechnology Association.

Ranjan Ramasamy

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Susceptibility to SARS-CoV-2 infection and nasal air conditioning ability

The nasal cavity has an important physiological role in warming and humidifying inspired air before it enters the nasopharynx and trachea. This process has been termed nasal air conditioning. Nasal structures vary geographically, and have been correlated with the varying needs for nasal air conditioning in cold and dry climates at one extreme and warm and humid climates at the other. Morbidity and mortality from COVID-19 during the pre-vaccination phase of the pandemic was reported to be greater in persons of tropical descent in temperate zone countries and was attributed to differential nasal air conditioning ability influencing protective immune responses in the upper respiratory tract to SARS-CoV-2. Supportive scientific evidence, and the implications for controlling respiratory viral infections and our understanding of human evolution, are discussed.

Biography

Ranjan Ramasamy obtained a BA and PhD from the University of Cambridge, UK, and has held academic appointments in the UK and abroad including Australia, Sri Lanka and the USA. Ramasamy was Chairman of the National Science Foundation of Sri Lanka and held Professorial appointments in Biochemistry, Immunology and Life Sciences, was a member of the Board of Governors of the International Centre for Genetic Engineering and Biotechnology (ICGEB), and a member of the Committee for Scientific Planning and Review (CSPR) of the International Council for Science (ICSU) for several years, with 300 publications pertaining to Biochemistry, Immunology and Infectious Diseases.

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Health risk among justice involved youth: A multi-risk, multigroup study

Youth involved in the juvenile justice system remain a significantly underserved population at markedly elevated risk for multiple problems, including traumatizing experiences, substance misuse, mental health, and sexually transmitted diseases. A trauma informed focus is needed to identify and address the elevated health risks of these youth, especially health risk differences between female and male youth. The present study examined the heterogeneity in traumatic and at-risk health experiences in a sample of newly arrested adolescents. Analysis identified four latent class subgroups of male and female youth with overlapping and distinctive risk factors. Conclusions are drawn in regard to differences in court response to male and female arrested youth, the importance of using biomarkers in health screening of arrested youth, and the need for health risk assessment at post-arrest processing facilities.

Biography

Richard Dembo, Ph.D., is a Professor of Criminology at the University of South Florida in Tampa. Dembo is also an American Association for the Advancement of Science (AAAS) Fellow and a Fellow at the Mississippi State University Social Science Research Center, with a long-term interest in developing, implementing, and evaluating intervention programs for at-risk and high-risk youth.

Saloua Kouass Sahbani

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Opuntia ficus-indica cladode extract as a natural radio modulator: Protection against cisplatin- and radiation-induced DNA damage with potential applications in vaccine and biomedical research

Background: DNA damage induced by ionizing radiation and chemotherapeutic agents remains a major limitation in biomedical applications, including cancer therapy and vaccine development. Natural compounds with antioxidant properties may provide effective protection against oxidative DNA damage while preserving therapeutic efficacy. This study investigated the radiomodulatory activity of Opuntia ficus-indica cladode extract (CCE) against cisplatin- and gamma radiation-induced DNA damage.

Methods: Plasmid pGEM-3Zf(–) DNA was treated with cisplatin in the presence or absence of CCE and exposed to γ-radiation. DNA damage was quantified by agarose gel electrophoresis and lesion-specific enzymatic analysis using Endonuclease III (Nth) and Formamidopyrimidine DNA Glycosylase (Fpg). The radiosensitizing effect of CCE was also evaluated in Escherichia coli by determining D10 values following irradiation.

Results: CCE significantly reduced radiation- and cisplatin-induced genomic damage. Double-strand breaks decreased by 55%, heat-labile lesions by 69.23%, Nth-sensitive clustered lesions by 70.97%, Fpg-sensitive lesions by 66.95%, and combined clustered oxidative lesions by 64.67%. In bacterial assays, CCE enhanced radiation sensitivity, reducing the D10 value from 2.0 kGy to 0.625 kGy, demonstrating a dual radiomodulatory effect.

Conclusions: These findings identify *Opuntia ficus-indica* cladode extract as a promising natural radiomodulator capable of protecting DNA from oxidative damage while selectively

enhancing microbial radiosensitivity. Such dual functionality may have important implications for reducing adverse effects associated with radiation exposure, improving biomedical applications involving nucleic acids, and supporting the development of safer therapeutic and vaccine-related technologies. Further validation in mammalian and in vivo models is warranted.

Biography

Saloua Kouass Sahbani is an Assistant Professor at the College of Applied Medical Sciences, Taibah University, Saudi Arabia. Sahbani holds PhDs in Radiation Sciences and Biomedical Imaging from the University of Sherbrooke and in Biochemistry and Molecular Biology from Carthage University, with research focusing on radiation-induced DNA damage, radiosensitization, and radioprotection, with particular interest in natural compounds.

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Addressing AMR: A scoping review of wastewater treatment measures

Background: Antimicrobial resistance (AMR) is a One Health issue involving humans, animals, and the environment. Without effective treatment, management, and monitoring, wastewater can serve as reservoirs for antimicrobial-resistant bacteria (ARBs), antibiotic resistance genes (ARGs), mobile genetic elements (MGEs), and antimicrobial residues. However, evidence on treatment effectiveness across technologies, targets, and settings remains fragmented. This scoping review synthesized international evidence on the effectiveness of wastewater treatments in reducing AMR-related contamination.

Methods: A scoping review was conducted using the Population–Concept–Context framework. The review covered hospital and community wastewater systems and sludge/faecal sludge management. Searches of PubMed, ScienceDirect, TCI, WHO, UNEP, World Bank, and Thai government sources identified 29 eligible studies published between 2016 and 2025. Data were extracted on treatment systems, AMR-related indicators, reported performance, reduction mechanisms, and implementation considerations. Treatment approaches were grouped into conventional and engineered biological systems, nature-based systems, membrane-based technologies, additional treatments including disinfection and advanced oxidation, and hybrid systems.

Results: Most studies assessed ARGs or MGEs (96.6%; n = 28/29), followed by culture-based ARBs (62.1%; n = 18/29), while antimicrobial residues were less frequently assessed (24.1%; n = 7/29). Escherichia coli was the most commonly evaluated bacterial indicator (48.3%; n = 14/29). Treatment effectiveness varied across technologies and target indicators. Conventional and engineered biological systems achieved approximately 1–4 log reduction in ARBs and 0.1–3 log reduction in ARGs, while nature-based systems achieved 0.9–4.8 log and 0.3–4.5

log reduction, respectively. Membrane-based systems showed the strongest physical removal, achieving 2.3–7.5 log reduction in ARBs and up to 7.7 log reduction in selected ARGs. Additional treatments achieved 1.3–4.3 log reduction in ARBs, although ARG reduction was more variable. Hybrid or multiple-barrier systems provided the broadest overall control, with >99.9% ARB reduction or non-detection and 0.55–5.2 log reduction in selected ARGs. A 1-log and 5-log reduction correspond to approximately 90% and 99.999% decreases, respectively, in the measured level of the target indicator.

Conclusion: Wastewater and sludge management are important entry points for AMR prevention and control. High coverage of effective and affordable treatment measures, integrated One Health monitoring, and multiple-barrier approaches are needed to limit environmental release of AMR-related indicators and strengthen surveillance.

Biography

Saowalak Rungruang is a Research Assistant at the International Health Policy Program (IHPP) Foundation, Thailand. Rungruang holds a Master's degree in Physiology and a Bachelor's degree in Medical Sciences from Naresuan University, Thailand, with research interests spanning medical and health sciences, antimicrobial resistance (AMR), One Health, public health emergencies (PHE), and disease and environmental health surveillance, and experience in research coordination, evidence synthesis, and scientific communication, with a growing focus on research and policy development addressing AMR, public health preparedness, and sustainable One Health approaches.

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The promise of nanotechnology in personalized & precision medicine: Nano-driven precision vaccinomics of the future

Biodesigners, biotechnologists and biomanufacturers are beginning to realize the promise of personalized and precision medicine (PPM), translating to direct benefit to patients or persons-at-risk.

Both PPM, personalized vaccinomics and nanobiotechnologies are being integrated into a panel of precision tools to manage an array of medical conditions. The next 'golden age' in vaccinomics will be ushered in by the new science of vaccinomics, which will inform and allow the development of personalized vaccines, based on our increasing understanding of immune response phenotype: genotype information.

The ideal vaccine would induce a robust immune reaction without serious adverse effects. In this sense, personalized vaccines promise to fulfill those criteria, aided by in-depth genetic studies of variation in immune responses – vaccinomics, which jointly with nanotechnology have revolutionized global attempts to prevent, treat, and eradicate infectious diseases and cancer in the foreseen future. Nanotechnology is used in vaccinomics in conjunction with advanced tools such as OMICS technologies to achieve more personalized therapeutic strategies. For instance, nanoparticles and nanocarriers have been developed to overcome the limitations of design-driven engineered vaccines and navigate biological barriers - systemic, microenvironmental and cellular - that are heterogeneous across patient populations and diseases. Assuming such barriers can be overcome or minimized, the new systems and synthetic biology, in combination with increasing genotype, phenotype information and low cost, high output genetic screening will inevitably lead toward a more personalized approach to vaccines, just as it has with pharmaceuticals.

Meanwhile, nanovaccines are made up of nanoparticles that are associated with or prepared with components that can stimulate the host's immune system and have the potential to promote rapid as well as long-lasting humoral and cellular immunity. The nanovaccines have several possible benefits, including site-specific antigen delivery, increased antigen bioavailability, and a diminished adverse effect profile. For instance, peptide based vaccines (proteomics-driven vaccines) have shown significant promise in certain types of cancer treatment (preventive and prophylactic pre-cancer vaccines), but have had limited success in combating several viral infectious diseases. Vaccines based on peptides appear to hold the possibility of a quick response against sudden outbreaks of viral epidemics and pandemics, both for communities and individuals. But, recent advances in treatment with multiple peptides, new knowledge of their interaction with the immune system and understanding of characteristics of peptides in vivo environment led us to believe that the prospects of peptide vaccinomics are more promising clinical successes.

While vaccinomics concerns the effectiveness of vaccines, adversomics concerns their side effects. This area has great potential to address public concerns about vaccine safety and to promote increased public confidence, higher vaccination rates, and fewer serious adverse events in genetically predisposed individuals. Moreover, this knowledge gives us the opportunity in the event of viral epidemics to tailor making vaccines for different communities for maximum efficiency and for immunocompromised individuals. The latter means that advancements in nanobiomedicine have played a crucial role in driving the PPM-guided revolution and precision and personalized vaccinomics, in particular. With the ability to engineer and manipulate materials at the nanoscale, biodesigners have been able to develop innovative solutions for diagnostics, drug delivery, and imaging.

So, the Grand Change and Challenge to secure our Health and Wellness are rooted not in Medicine, and not even in Science! Just imagine WHERE?! In the upgraded Hi-Tech Culture!

Keywords: Personalized & Precision Medicine, Biomarkers, Targets, Nanoparticles, Nanocarriers, Vaccinomics, Nanovaccines, Nanobiomedicine, Nanotechnologies

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.
At present, Dr Sergey Suchkov, MD, PhD, is:

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Carbapenem resistance and carbapenemases in bloodstream Enterobacterales, Busan, South Korea, 2018-2024

Carbapenem-resistant Enterobacterales (CRE) have emerged as a major global public health threat due to limited therapeutic options and high mortality rates, particularly in bloodstream infections. Regional epidemiological data are essential for understanding the dissemination of resistance mechanisms and for guiding infection-control strategies and antimicrobial stewardship.

This study aimed to investigate the distribution of species, antimicrobial resistance patterns, and carbapenemase genotypes among CRE isolates recovered from bloodstream infections in Busan, South Korea, from 2018 to 2024. A total of 609 non-duplicate CRE isolates collected from 51 healthcare institutions were analyzed. Species identification was performed using the Vitek 2 Compact system (bioMérieux, France). Antimicrobial susceptibility testing for four carbapenems (ertapenem, imipenem, meropenem, and doripenem) was conducted using broth microdilution. Carbapenemase genes were detected using multiplex PCR targeting ten major carbapenemase types.

Klebsiella pneumoniae was the predominant species (81.8%), followed by Escherichia coli (11.7%) and Enterobacter spp. (4.6%). Ertapenem resistance (MIC ≥ 2 μg/mL) was observed in 99.3% of isolates, and high-level resistance (MIC ≥ 8 μg/mL) was frequently identified across all carbapenems. Carbapenemase-producing Enterobacterales (CPE) accounted for 98.2% of isolates. Among these, KPC-type carbapenemases were the most prevalent (88.2%), with KPC-2 being the dominant subtype (84.9%). In contrast, NDM- and OXA-type carbapenemases were detected sporadically.

These findings indicate that KPC-2-producing *K. pneumoniae* remains the principal driver of CRE bloodstream infections in Busan. The presence of multiple carbapenemase genotypes across healthcare institutions suggests ongoing regional dissemination of resistance determinants. Furthermore, the sustained dominance of KPC-2 suggests possible clonal dissemination within regional healthcare settings, highlighting the need for targeted infection-control interventions. These findings provide valuable regional evidence to inform antimicrobial stewardship policies and strengthen preparedness against emerging multidrug-resistant pathogens.

Biography

Sohyun Park, PhD, is a public health researcher at the Busan Metropolitan City Institute of Health and Environment, Republic of Korea. Park plays a leading role in regional surveillance of infectious diseases, antimicrobial resistance, and foodborne pathogens, contributing to national public health monitoring systems, and integrates laboratory-based diagnostics with epidemiological analysis to support rapid and evidence-based responses. Park has conducted key surveillance programs, including norovirus monitoring and antimicrobial resistance studies, and research on carbapenem-resistant Enterobacterales (CRE) has provided important insights into regional resistance trends and supports strengthening infectious disease response capacity.

Som Dipielte Estelle Mireille[1*], N'goran Sodji Emilie Karen[1,2], Bahan Armel[1,2], Yapi Alexia[1,2], Edi Ivann Marie[1], Coulibaly-Diallo Yeperi Marina[1], Kacou-N'douba Adele[1,2]

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Detection of the *rpoB* gene of rifampicin-resistant *Mycobacterium tuberculosis* at the Angre University Hospital in 2024, Ivory Coast

Background: The emergence of multidrug-resistant strains of Mycobacterium tuberculosis (MTB) represents a global public health challenge. The challenge in managing tuberculosis lies in the rapid diagnosis of these resistances. The objective of this study was to determine the proportion of MTB resistant to rifampicin.

Methods: This was a retrospective cross-sectional study conducted from January to December 2024. The study population consisted of outpatients and inpatients at Angré University Hospital suspected of having tuberculosis who were tested for rifampicin-resistant *Mycobacterium tuberculosis* using GeneXpert MTB/RIF (Cepheid). Data were collected from laboratory records and analyzed using Epi Info software.

Results: The study population consisted of 615 patients and included 305 (49.59%) men and 310 (50.41%) women, with a sex ratio (M/F) of 0.9. The 30-40 age group was the largest (131; 21.30%), with an average age of 44.9 ± 26.6. Gastric fluid was the most commonly collected sample (339; 55.12%), followed by sputum (182; 29.59%). 527 (85.69%) of patients were newly screened and 58 (9.43%) were being monitored. 45 (8.02%) were positive for Mycobacterium tuberculosis, with 11 (24.44%) sensitive to the rpoB gene and 9 (20%) with indeterminate results.

Conclusion: MTB RIF resistance was found in 24.44%. A strategy for monitoring these patients should be put in place to reduce the spread of this resistance.

Biography

Dr. Som Dipielte Estelle Mireille is a Medical Biologist, Quality Auditor, and epidemiologist, a graduate and mentor of the FETP, currently working at the Angre University Hospital Center (CHU), where Som participated in laboratory accreditation according to ISO 15189:2022. Som participated in the 7th International Conference on Prevention & Infection Control in Switzerland in 2023, presenting a poster entitled Seroprevalence of SARS-CoV-2 in blood transfusion centers in Côte d'Ivoire, and last year presented Analyzing the database of Acute Flaccid Paralysis in Côte d'Ivoire from 2021 to 2023 at the 9th edition of the World Congress on Infectious Diseases.

Subhas Chandra Datta, PhD

Department of Zoology, Visva-Bharati, and Kanchannagar D.N. Das High School (HS), West Bengal, India

Innovation to implementation of owl-natural-biomedicine-vaccination: Emerge as global perspectives on advancing vaccine science, technology, and global-health impact

Background: Many highly pathogenic pathogens—such as influenza, avian influenza (bird flu) A (H5N1), Ebola, Monkeypox, Nipah, and coronaviruses—originate in animal reservoirs. The world still faces many infectious diseases that affect public health, epidemiology, microbiology, and vaccine and drug development. These diseases lead to illness and death, and are also connected to poverty, sanitation, and climate issues, posing health challenges from vector-borne illnesses to malnutrition. It also affects the 'PM POSHAN-Midday Meal' program, hampering human civilization, global health and education, research, science, and well-being, biodiversity conservation, ecological balance, food-producing systems, climate regulation, enrolment, classroom hunger and malnutrition, socialization, attendance, dropouts and retention rates. Recently, it has been suggested that there is about a 50 per cent chance of another pandemic similar to COVID-19 occurring in the next 25 years.

Objectives: The main objective is to confirm the implementation of owl-natural-biomedicine-vaccine (ONBMV) against global pathogens and assess its impact.

Materials and Methods: Here, the naturally growing barn owl (Tyto alba L.) populations on the campus of Kanchannagar D.N. Das High School (HS) in Burdwan-713102, West Bengal, India, are used as a natural aerial biomedicine vaccine against naturally occurring pathogens.

Results: ONBMV achieves naturally significant positive impacts; it influences the control of coronaviruses responsible for COVID-19 and avian influenza (bird flu) A (H5N1), which spreads among birds and poultry and can be transmitted to mammals, including humans, through contact with infected animals.

Conclusion: This work focuses on the barn owl as an aerial natural-booster-biomedicine vaccine, with implications for school and public health, the environment, biodiversity, migration, and food security. By focusing on nature-based clinical studies, scientists and policymakers recognise the dual benefits for the environment and human well-being. Biodiversity, ecology, and nature-based solutions promote a sustainable approach to coexistence in the long term. Integrating 'Owl-Natural-Biomedicine' into vaccination strategies represents an emerging frontier in eco-friendly, preventive healthcare, merging ecological conservation with natural immunology, acting as a community booster and expanding the scope of modern vaccine science to positively impact global health and environmental sustainability. Advancing vaccine science combines modern biomedical innovation with effective implementation, and integrating nanocarriers, mRNA platforms, and edible plant-based vaccines can vastly improve global health outcomes. Zoonotic vaccines play a dual role in protecting both human and animal populations, reducing the risk of spillover events, and collaborative efforts between veterinary and human health sectors are driving the development of vaccines targeting livestock, wildlife, and vectors. This integrated One Health approach is critical for pandemic preparedness, especially as human-animal interactions increase due to urbanization and environmental change.

Keywords: Innovation, Implementation, Owl-Natural-Biomedicine-Vaccination, Global Perspectives, Vaccine Science, Technology, Global Health Impact.

Biography

Dr Subhas Chandra Datta, M.Sc., PhD, President Awardee, as an Innovative Researcher in various fields from 1993, Assistant Teacher, and Headmaster of Kanchannagar at D.N. Das High School (HS) from 1996 to 2007 to date. Dr Datta has expertise in evaluation and a passion for improving health and wellbeing. His research interests are in healthcare, biomedicine, Physiology, Education, Environment, Plant Protection, Agriculture, Pathology, Allelopathy, and homoeopathy. His open and contextual evaluation model based on responsive constructivism creates new pathways for improving healthcare. His 1st-plant-based biomedicines in homoeopathic forms 'Cina' achieve the 'World's Top Most Articles' in the 'Public Medical Health of WHO'. His valuable work received a Patent under the Central Silk Board (CSB) in 2005. He is the honorary Member of different prestigious organizations. He has published more than 147 papers in reputed journals and has been serving as an editorial board member of repute.

Amaya L. Bustinduy[1], Andrew Edielu[1,2], Gloria K. Ayebazibwe[2], Racheal Nakyesige[3], Victor Anguajibi[3], Simon Mpooya[3], Jacent Nassuna[2], Moses Adriko[3], Alison Elliott[1,2], Govert van Dam[4], Paul Corstjens[5], Sophie Pach[1], Hannah W. Wu[6,7], Susannah Colt[6,7*], Patrice A. Mawa[2,8], Edridah Muheki[3], Narcis B. Kabatereine[3], Emily L. Webb[9], Jennifer F. Friedman[6,7]

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Praziquantel for the treatment of preschool-aged children with schistosomiasis: Results of an RCT

Background: Optimal dosing of praziquantel for schistosomiasis for children younger than 5 years is not established and some studies suggest this age group might need a higher dosing per kilogram. Our aim was to assess the safety and efficacy of 80 mg/kg of praziquantel tablets given in a single day to preschool children versus the recommended single dose of 40 mg/kg for treatment of *Schistosoma mansoni.*

Methods: We conducted a 2 × 2 factorial design, placebo-controlled, phase 2 randomized trial in Uganda (ClinicalTrials.gov NCT03640377). Children aged 12–47 months infected with *S. mansoni* were randomly assigned in a 1:1:1:1 ratio to receive crushed praziquantel tablets at 40 mg/kg versus 80 mg/kg at baseline and either the same dose or placebo after 6 months.

Results: Among 354 children included for analysis, cure rate at 4 weeks was 67% in the 40 mg/kg group and 90% in the 80 mg/kg group (absolute difference 23% [95% CI 14–31]; p<0.001), and the egg reduction rate difference was 2% (95% CI 1–3; p<0.001) based on geometric mean and 22% (95% CI 5–59; p<0.001) based on arithmetic mean. No severe adverse events related to the study drug were reported. At 12 months, biannual versus annual treatment reduced prevalence of fecal occult blood and 80 mg/kg dose reduced prevalence of elevated fecal calprotectin.

Conclusions: The 80 mg/kg dose is safe, well tolerated, and more effective in achieving parasitic cure than the current proposed 40 mg/kg dose. Until a pediatric formulation of praziquantel is widely available in endemic areas, the use of crushed tablets with this dosing strategy can be recommended for young children living in *S. mansoni* endemic areas.

Biography

Dr. Colt received a doctoral degree from Cornell University, studying international nutrition, immunology, and epidemiology, with areas of study including neglected tropical diseases and maternal and child nutrition. Prior to studying schistosomiasis, Colt led clinical research studies relating to human leptospirosis in the Federated States of Micronesia and dengue virus infection in Ecuador, and in recent years received awards from the Thrasher Foundation (2022) and the National Institutes of Health (2023) to investigate relationships between vitamin A deficiency and schistosomiasis immunopathology.

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Cloning, expression and characterisation of *Wuchereria bancrofti* L1-recombinant filarial protein

Lymphatic filariasis (LF) is a neglected tropical vector-borne disease that infects an estimated 657 million people in 39 countries. It results in irreversible morbidity and disability in infected cases. Though efforts toward global elimination via mass drug administration are in progress, there is a pressing need for efficient diagnostic tests for surveillance purposes in endemic areas. A diagnostic method needs to be developed to diagnose early-stage LF, which demonstrates the limitations of the current methodology. Using the NCBI database, the Wuchereria bancrofti L1 (WbL1) gene sequence was identified and cloned into a PET-30a(+) plasmid vector, following transformation into competent Escherichia coli BL21 (DE3) cells for IPTG induction. The produced protein was isolated through sonication and purified by immobilised Ni-NTA metal affinity chromatography (IMAC). The purified recombinant filarial protein was characterised and examined through SDS-PAGE, followed by silver staining, western blotting, and LC-MS to confirm its identity, sequence integrity, and intact molecular mass. The purified WbL1 recombinant filarial protein (WbL1 rFP) has a molecular weight of 17.1 kDa; western blot verified the rFP using a histidine tag antibody. Intact mass analysis and peptide mass fingerprinting show 18037 Da molecular mass and 97% sequence coverage.

Keywords: *Wuchereria bancrofti,* Diagnostic Antigen, IPTG Induction.

Biography

Prof. Dr. Vijay Jagdish Upadhye is Associate Director of the Research & Development Cell and Professor at Parul Institute of Applied Sciences, Parul University, Vadodara. With over 19 years of expertise in immunodiagnostics, biomarkers, enzyme kinetics, and infectious disease research, Upadhye has made significant contributions to diagnostic kit development and

translational research, having published over 196 research papers, authored seven books and 18 book chapters, and holding 40 intellectual property rights. Upadhye's research has attracted national and international funding, earning numerous scientific awards and recognition.

Wanwisa Kaewkhankhaeng*, Naroeporn Nopwinyoowong, Saowapa Khotchalai, Angkana Lekagul, Viroj Tangcharoensathien
International Health Policy Program Foundation, Thailand

Strengthening one health monitoring and evaluation systems for evidence-informed antimicrobial resistance policies in Thailand

Background: Antimicrobial resistance (AMR) is a critical threat to infectious disease control, undermining the treatment of common pathogens at the human-animal-environmental interface. Monitoring the transmission and prevalence of resistant infections requires an integrated One Health approach. In Thailand, establishing multi-sectoral surveillance systems is vital for tracking pathogen dynamics, which serves as a cornerstone for evaluating the progress of the National Strategic Plan on AMR (NSP-AMR).

Objectives: This study sought to strengthen national surveillance and control of drug-resistant infections by generating comprehensive evidence on antimicrobial consumption (AMC) and AMR patterns across human and animal sectors, alongside public knowledge on AMR and awareness.

Methods: Data were synthesized from the national surveillance systems covering the human and animal health sectors and population-based surveys. This longitudinal dataset, anchored to a comprehensive 2017 baseline, provides the empirical foundation for monitoring progress from Phase I (2017–2022) through Phase II (2023–2027) of the NSP-AMR. The principal output of this study is the synthesis intended to render nearly a decade of multi-sectoral data legible as a single, coherent story of progress and remaining gaps.

Results: In 2023, human antimicrobial consumption was 55.1 Defined Daily Doses (DDD) per 1,000 inhabitants per day (DID), representing a 3.1% increase from the 2017 baseline (53.4 DID). In contrast, veterinary antimicrobial consumption declined substantially to 219

.8 mg/PCUThailand in 2023, reflecting a 66.6% reduction from the 2017 baseline (658.7 mg/PCUThailand) and exceeding national reduction targets. With respect to resistance patterns, the prevalence of third-generation cephalosporin-resistant Escherichia coli declined in human clinical isolates (41.0% in 2023 versus 44.0% in 2017) and in chicken caeca (1.2% in 2023 versus 1.7% in 2017), whereas resistance increased in pig caeca (11.6% in 2023 versus 9.6% in 2017). Public knowledge on AMR improved by 7.5 percentage points; however, certain misconceptions regarding antibiotic use persisted.

Conclusion: The findings demonstrate the value of an integrated One Health M&E system in tracking national progress, identifying implementation gaps, and supporting evidence - informed policy decisions. Crucially, the collaborative HPSR-AMR Network, established in 2017 has proven that trust-based, multi-sectoral partnerships are essential for generating scientific evidence to mitigate infectious threats. This approach enhances Thailand's capacity to contain AMR and strengthens health security against emerging infectious disease risks at the regional and global levels.

Biography

Miss Wanwisa Kaewkhankhaeng is a Senior Research Assistant at the International Health Policy Program (IHPP) Foundation, Thailand. Wanwisa work focuses on antimicrobial consumption and use, antimicrobial resistance (AMR), and public knowledge and awareness on AMR. Wanwisa applies a One Health approach to support evidence-informed AMR policy development. Wanwisa is a member of the Health Policy and Systems Research on Antimicrobial Resistance (HPSR-AMR) Network and contributes to the Thailand One Health Report on Antimicrobial Consumption and Antimicrobial Resistance. This annual report, compiled using data since 2017, is used to monitor progress in implementing Thailand's National Strategic Plan on AMR.

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Context-dependent arbuscular mycorrhizal symbiosis: An integrative review of plant–rhizosphere interactions and microbiome dynamics

Arbuscular mycorrhizal fungi (AMF) form symbiotic associations with plant roots and contribute to plant nutrition, stress tolerance, soil health, and rhizosphere microbial regulation. Recent transcriptomic, metabolomic, and rhizosphere microbiome analyses have expanded our understanding of microbially induced plant responses. Emerging evidence suggests that AMF may influence plant health not only through nutrient acquisition but also by restructuring microbial communities and enhancing plant defense. However, these effects vary across biological and environmental conditions. This integrative review aimed to synthesize recent evidence on AMF-mediated plant–rhizosphere interactions, focusing on microbiome remodeling, plant defense, soil processes, and the ecological and biological factors determining symbiotic outcomes. Recent literature published from 2024 through 2026 was searched using Google Scholar. Search terms included combinations of arbuscular mycorrhizal fungi, plant–microbe interactions, rhizosphere microbiome, plant defense, soil carbon, metabolomics, transcriptomics, and metabarcoding. Studies were selected based on their relevance to AMF-mediated plant responses, rhizosphere microbial dynamics, and symbiotic outcomes. The selected literature was reviewed and synthesized across four domains: plant nutrition and stress responses, rhizosphere microbial composition and potential pathogen suppression, carbon allocation and soil processes, and ecological or genetic factors affecting symbiotic efficiency. Evidence derived from transcriptomic, metabolomic, microbiome, and metabarcoding approaches was also considered to provide an integrated perspective on AMF-mediated interactions. The reviewed evidence indicates that AMF act as multidimensional regulators of the plant–soil–microbiome interface. AMF enhance nutrient acquisition and environmental stress tolerance while contributing to soil aggregation, glomalin production, and beneficial

microbial activity. Microbiome analyses further indicate that combined microbial inoculation can restructure root and rhizosphere communities, enrich beneficial bacterial taxa, and reduce the prevalence of potential pathogens. AMF-associated interactions may also enhance plant defense through improved nutrient status, increased phytoalexin production, and microbiome shifts favoring beneficial microorganisms. Moreover, AMF increase photosynthate allocation to roots and rhizosphere soils, supporting microbial biomass, soil aggregation, and soil organic carbon dynamics. Nevertheless, these benefits are not universal. Fungal associations and symbiotic efficiency vary according to ecological proximity, host genetic differentiation, propagule type, soil conditions, microbial partners, and nutrient availability. Collectively, these findings suggest that the functions of AMF extend beyond nutrient acquisition to include active regulation of rhizosphere microbial communities, plant defense, and soil processes. Their context-dependent effects highlight the need to identify the ecological and biological conditions that optimize beneficial symbiosis and support the development of microbiome-based strategies for sustainable plant health and disease management.

Biography

Lin Yucheng studied fungal infection and plant–microbe interactions, focusing on how arbuscular mycorrhizal fungi influence plant health and host responses. His research investigates the dual roles of Funneliformis mosseae in *Vigna angularis, Vigna radiata, Ipomoea batatas, and Allium tuberosum.* In June 2026, he presented this research at Infection 2026, the 10th Edition of the World Congress on Infectious Diseases in Barcelona, highlighting host-dependent fungal colonization and the balance between beneficial symbiosis and adverse plant responses. His related work was also presented at the 2025 International Union of Immunological Societies (IUIS) Congress.

Zeynep Burcin Yılmaz
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Is functional cure possible in chronic hepatitis B? HBsAg loss in chronic hepatitis B in a real-life cohort: A single-center retrospective study

Background and Aims: Hepatitis B surface antigen (HBsAg) loss is the strongest indicator of functional cure in patients with chronic hepatitis B (CHB) infection; however, its annual incidence remains low in real-life cohorts. In this study, we aimed to determine the frequency of HBsAg loss and its associated clinical characteristics in a single-center, real-life cohort of patients with CHB.

Methods: Patients with HBsAg-positive CHB followed at the Infectious Diseases outpatient clinic of a Faculty of Medicine were retrospectively evaluated. Patients were classified into four disease-stage groups: HBeAg-negative chronic infection (inactive carrier), HBeAg-negative chronic hepatitis, HBeAg-positive chronic infection (immune-tolerant), and HBeAg-positive chronic hepatitis. Demographic data, concomitant viral serology, antiviral treatment status, history of cirrhosis/liver transplantation, and the development of HBsAg loss during follow-up were recorded. In patients who achieved HBsAg loss, the follow-up duration (in years) until loss was also noted.

Results: A total of 474 patients (280 male [59.2%], mean age 49.6 ± 13.8 years) were included in the study. Distribution by disease stage was as follows: 246 (51.9%) inactive carriers, 158 (33.3%) HBeAg-negative chronic hepatitis, 49 (10.3%) HBeAg-positive chronic hepatitis, and 20 (4.2%) immune-tolerant patients. Of the patients, 162 (34.2%) were receiving antiviral treatment; 30 patients (6.4%) had cirrhosis and 13 (2.8%) had a history of liver transplantation.

During follow-up, HBsAg loss was observed in a total of 9 patients (1.9%); the median time to loss was 10 years (range, 1–15 years). Of the patients who achieved HBsAg loss, 8 (88.9%) were inactive carriers at diagnosis, none of whom were receiving treatment; the remaining patient (11.1%) had HBeAg-positive chronic hepatitis and was on treatment. Loss rates by disease stage were 3.3% (8/246) among inactive carriers and 2.0% (1/49) among those with HBeAg-positive chronic hepatitis; no HBsAg loss was observed in the HBeAg-negative chronic hepatitis or immune-tolerant groups during follow-up.

Conclusion: In this single-center, real-life cohort, the rate of HBsAg loss was low (9/474, 1.9%) and occurred predominantly (88.9%) in untreated inactive carriers; among treated patients, HBsAg loss was observed in only a single case (0.6% of the 162 treated patients). This low rate suggests that continuous suppressive nucleos(t)ide analogue therapy itself does not accelerate HBsAg loss, and may instead limit the immunological stimulus required for the immune system to clear HBsAg by suppressing viral replication. The current paradigm in the literature is shifting toward the view that planned discontinuation of treatment in patients meeting appropriate stopping criteria may trigger HBsAg seroconversion through reactivation of the host immune response. Our cohort findings support the hypothesis that planned treatment discontinuation in eligible treated patients may increase functional cure rates, and prospective evaluation of this strategy in this population stands out as a recommended area for future research.

Biography

Zeynep Burcin Yilmaz graduated from medical department of Hacettepe University, Ankara, Turkiye in 2012. Then she joined the infectious disease and clinical microbiology residency program at Inonu University, Malatya, in 2018. She has been working as an assist. prof. at Inonu University for one year. She has a deep interest in CMV infections in transplant patients and she is currently pursuing her medical career with a focus on this specialty.

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Development of VSV-vector based vaccine against H5N1 avian influenza by targeting both H5N1 hemagglutinin and matrix protein 2

Human (avian) influenza A viruses, especially highly pathogenic avian influenza (HPAI) viruses, pose a significant public health threat, and a multivalent vaccine is the primary prophylactic measure to control these viruses. To this goal, we generated two vesicular stomatitis virus (VSV)-based vaccine candidates simultaneously targeting H5N1 hemagglutinin (HA) and matrix protein 2 (M2) (V-EtM2e/H505 and V-EtM2e/H522) and characterized their ability to induce protective immune responses. Our results revealed that vaccine immunization induced high humoral immune responses against both the HPAI HA protein and the ectodomain of M2 protein in mice. Intriguingly, vaccine-immunized mice sera exhibited highly efficient neutralizing activity against the corresponding H5 pseudovirus and mediated potent and broad antibody-dependent cellular cytotoxicity (ADCC) activity against M2e derived from human and avian influenza H5, H1, H3, and H7 viruses. Furthermore, both intranasal (IN) and intramuscular (IM) immunization provided efficient protection against HPAI H5N1 virus challenge in mice, with a 100% survival rate and a nondetectable viral load in several tissues. Notably, noninvasive mucosal delivery of V-EtM2e/H522 achieved protection equal to that of IM delivery at a 100-fold lower immunizing dose. These findings provide convincing evidence for the high efficiency of a multivalent VSV-based vaccine against human (avian) influenza A viruses.

Biography

Dr. Zhujun Ao obtained M.D. and PhD degrees at Zunyi Medical University and at the University of Montreal, respectively. Since 2007, Ao has worked as Postdoctoral Fellow and Research Associate at the Laboratory of Molecular Human Retrovirology in the Department of Medical Microbiology, University of Manitoba. Ao's research projects have been in fundamental research to explore HIV and host protein interactions and their functional roles during HIV-1 replication, and to develop new approaches against HIV-1. In recent years, Ao has been the Lead Research Associate working on the development of vaccines, particularly with respect to HIV, SARS-CoV-2 and influenza viral infections, has published more than 60 peer-reviewed scientific papers, and was the recipient of a New Investigator Award (2005) and a Mark Wainberg Fund Grant (2023) of the Annual Canadian Conference on HIV/AIDS Research/Canadian Institutes of Health Research.

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OCTOBER 2026

POSTER PRESENTATIONS

Camila Ferro[1]*
Fundacao Oswaldo Cruz (Fiocruz), Brazil

The largest histamine poisoning outbreak in Brazil: An experience report from a One Health perspective in Fernando de Noronha

Background: Histamine poisoning is a foodborne illness associated with the consumption of improperly preserved fish and represents a major public health concern, particularly in island territories that rely heavily on artisanal fisheries and tourism. The One Health approach provides an integrated framework to understand this condition by addressing the interactions among human health, food safety, environmental factors, and fish production practices. Objective: To report the investigation and response to the largest documented histamine poisoning outbreak in Brazil, which occurred in Fernando de Noronha (Pernambuco State), highlighting the integrated surveillance and health education actions developed under a One Health perspective. Case Report: Between 2015 and 2016, 37 confirmed cases of histamine poisoning were identified across eight epidemiological clusters. Laboratory analyses detected histamine concentrations far exceeding the limits established by Brazilian legislation. Sanitary inspections revealed critical failures throughout the fish production chain, including inadequate refrigeration, insufficient use of ice during fishing and transportation, and poor food handling practices. An integrated intervention involving Health Surveillance, Epidemiological Surveillance, laboratory monitoring and health education targeted fishermen, food handlers, restaurant owners and the local community, enabling identification of outbreak determinants and implementation of preventive measures. Conclusion: Coordinated actions integrating surveillance, food safety, health education and community engagement were essential to interrupt the outbreak and prevent new cases. This experience reinforces the value of the One Health approach for preventing and responding to foodborne diseases in vulnerable island territories.

Keywords: One Health; Histamine Poisoning; Food Safety; Public Health Surveillance; Health Education

Biography

Camila Ferro is a veterinarian at Fundação Oswaldo Cruz (Fiocruz), working in the One Health sector. Camila research focuses on food safety, zoonoses, epidemiological surveillance and integrated One Health strategies, with emphasis on foodborne diseases and public health.

Camila Ferro[1*], Expedito Jose de Albuquerque Luna[2]
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Socioenvironmental determinants of zoonotic sporotrichosis in vulnerable urban territories: Evaluation of surveillance and veterinary underreporting from a one health perspective

Background: Zoonotic sporotrichosis is an emerging infectious disease and an important public health concern in Brazil, particularly in vulnerable urban territories where socioenvironmental conditions may contribute to disease persistence and transmission. In Rio de Janeiro State, one of the areas most affected by zoonotic sporotrichosis worldwide, challenges remain regarding the integration of human, animal, and environmental health surveillance, as well as the underreporting of animal cases in veterinary practice.

Objective: This study aims to analyze the socioenvironmental determinants associated with the persistence of zoonotic sporotrichosis in vulnerable urban territories of the Metropolitan Region of Rio de Janeiro, evaluate the effectiveness of surveillance and control actions, and investigate veterinarians' knowledge, practices, and barriers regarding mandatory disease notification.

Methodology: A mixed-methods study will be conducted in selected municipalities based on epidemiological, socioeconomic, operational, and territorial criteria. Secondary data on human and animal cases will be integrated with socioeconomic and environmental indicators and analyzed using Geographic Information Systems to identify spatial patterns and priority areas. Surveillance and control actions will be evaluated according to Donabedian's framework, considering structure, processes, and outcomes. A cross-sectional survey will assess veterinarians' knowledge and practices regarding mandatory notification, while semi-structured interviews with health managers, surveillance professionals, and community representatives will explore barriers and perceptions related

to disease surveillance. Quantitative and qualitative findings will be integrated through methodological triangulation within a One Health framework.

Conclusion: The study is expected to identify socioenvironmental determinants associated with disease persistence, characterize weaknesses in integrated surveillance, and identify barriers to veterinary notification, generating evidence to strengthen prevention and control strategies and support public health policies for zoonotic sporotrichosis in vulnerable urban settings.

Keywords: Zoonotic sporotrichosis; One Health; Epidemiological surveillance; Socioenvironmental vulnerability; Veterinary notification.

Biography

Camila Ferro is a veterinarian at Fundacao Oswaldo Cruz (Fiocruz), working in the One Health sector. Her research focuses on food safety, zoonoses, epidemiological surveillance and integrated One Health strategies, with emphasis on foodborne diseases and public health.

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Molecular characterization of nucleoporins–influenza A virus interactions: Potential host-directed therapeutic target

Influenza A virus (IAV), a negative-sense single-stranded RNA virus, primarily relies on the host nucleocytoplasmic transport machinery for trafficking of viral ribonucleoprotein (vRNP) complexes. The nuclear pore complex (NPC), composed of nucleoporins (NUPs), serves as a crucial interface exploited by viruses for molecular exchange between the nucleus and cytoplasm. In the present study, we investigated interactions between human nucleoporins and influenza A virus, integrating in *silico* and experimental approaches. We performed molecular docking to predict binding affinities at the protein–protein interface, and molecular dynamics simulations were carried out to evaluate the conformation and structural stability of the protein complexes under physiological conditions. Computational analyses revealed significant interactions between nucleoporins, namely NUP54 and NUP62, with the IAV vRNP protein throughout the 100 ns simulation period. Our results indicated that the NUPs interact with the influenza virus nucleoprotein via diverse mechanisms, with the NUP54-NP complex exhibiting dynamic rearrangements, whereas NUP62-NP remains stable. Subsequently, *in vitro* studies were performed to validate the functional relevance of these interactions. Increased NUP54 expression was observed with viral NP accumulation at the early stages of infection, suggesting an active role for NUP54 during viral replication. Notably, siRNA-mediated silencing of NUP shows approximately 60-70% reduction in viral infection, indicating that NUP54 contributes substantially to vRNP trafficking. This study provides novel insights into the role of NPC-associated proteins during influenza A virus replication. The identification of conserved host factors involved in virus infection highlights their potential for antiviral therapeutics to overcome rapid antigenic drift and antiviral resistance. Our findings provide a framework for functional characterization of host-virus mechanisms that may contribute to the development of effective host-directed vaccine strategies.

Biography

Kajal Sharma is a Ph.D. scholar under Prof. Madhu Khanna at the Department of Virology, V.P. Chest Institute, Delhi University, India. Sharma's thesis is titled 'Role of host cellular proteins in influenza virus genome delivery and innate immune responses' and Sharma has expertise in molecular biology, in vitro infection models, proteomics, virus–host interactions, and siRNA-mediated gene silencing for functional validation of host factors during viral replication, and also utilizes *in silico* approaches to analyze virus–host protein interactions. Sharma is additionally working on the Viral Research and Diagnostic Laboratory (VRDL) project, investigating viral co-infections in clinical specimens to understand disease outbreaks and diagnostic challenges.

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Evaluation of biomedical waste management practices and compliance in a tertiary care oncology centre

Introduction: Biomedical waste generated in hospitals poses significant risks to healthcare workers, patients, caregivers, the community, and the environment. Therefore, adequate knowledge, training, and strict implementation of Biomedical Waste Management (BMWM) practices are essential. Continuous monitoring of BMWM processes, from waste generation to final disposal, is necessary to ensure compliance and safety.

Objective: To review the existing Biomedical Waste Management practices and assess compliance with the Biomedical Waste Management Rules, 2016 among healthcare workers in our hospital.

Methods: This observational study was conducted across 18 hospital facilities, including Wards, Daycare units, ICUs, Recovery wards, Operation Theatres, and Laboratories. Key parameters assessed included the availability of BMWM prerequisites, onsite waste segregation, transportation, storage, labelling, staff training, immunization status, documentation, and overall compliance practices. Descriptive statistics were used to present frequencies and percentages.

Results: The assessment covered 500 nursing staff and 223 housekeeping staff involved in handling and transporting biomedical waste. Most BMWM processes were adequately followed by all respondent groups, demonstrating a high level of compliance with the Biomedical Waste Management Rules, 2016. Major non-compliances identified included transportation of infectious and non-infectious waste in a common transport bin and disposal of transfused blood bags in yellow bags without prior autoclaving. These issues were rectified immediately in accordance with BMWM Rules, 2016 and the latest National Accreditation Board for Hospitals & Healthcare Providers (NABH) standards.

Minor deficiencies observed included a shortage of small yellow bags in 3 wards (16.66%) and improper fitting of colour-coded bags in 1.85% of bins. Overall, waste segregation practices were satisfactory; however, the condition of waste receptacles was found to be unsatisfactory in 45 out of 632 bins (7.12%). Unfavourable biomedical waste management practices were identified in 11 bins (1.74%). The majority of staff members were vaccinated against Hepatitis B, while a few newly recruited staff members were undergoing vaccination. Waste transportation and documentation practices were compliant with regulatory requirements. However, newly recruited staff demonstrated comparatively lower awareness regarding biomedical waste handling and spillage management than experienced staff.

Conclusion: Effective biomedical waste management requires interdisciplinary coordination, continuous training and education, commitment from healthcare workers, and regular monitoring. The study highlights both strengths and areas requiring improvement to ensure sustained compliance, safety, and adherence to biomedical waste management regulations.

Biography

Dr. Minal Poojary is a dedicated hospital administrator with over three years of experience at a tertiary care oncology centre, actively involved in overseeing hospital administrative operations, patient service management, equipment procurement, staff coordination, regulatory compliance, and NABH accreditation activities. Responsibilities include managing appointment systems, addressing patient concerns, reviewing administrative processes, and ensuring adherence to statutory regulations such as FDA, AERB, CDSCO, and PCPNDT guidelines. Poojary also serves as a mentor and demonstrator for students undertaking projects, internships, and training programs, and is committed to strengthening patient-centric services, operational excellence, quality compliance, human resource development, innovation integration, and holistic institutional growth.

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Standardization of lipid identification and quantification in mRNA Vaccines: A Universal Approach via AQbD

mRNA platform vaccines utilize lipid nanoparticle (LNP) technology to deliver mRNA into the body. LNPs are composed of four distinct lipid components, and the identification and content analysis of these lipids are critical quality attributes designated as essential requirements for national lot release. However, due to the absence of standardized methods in official pharmacopeias, manufacturers currently rely on their own proprietary methods. To ensure consistent and efficient quality control for the increasing number of mRNA vaccines, the standardization of these analytical methods is imperative.

In this study, we aimed to establish a standardized lipid identification and content analysis method applicable across different manufacturers using the Analytical Quality by Design (AQbD) approach and to verify whether proprietary methods from two major manufacturers could be integrated into a single universal method. Initially, a cross-applicability study was conducted using the methods from Pfizer and Moderna; both methods satisfied the suitability criteria for samples from both manufacturers. Nevertheless, to enhance versatility, an optimized universal method was developed via AQbD. Based on literature reviews indicating that mobile phase composition and column temperature are critical factors affecting chromatographic resolution in HPLC-CAD, we established the Method Operable Design Region (MODR) through risk assessment and Design of Experiments (DoE), ultimately deriving optimal analysis conditions with improved desirability.

The developed method is currently undergoing validation in accordance with ICH Q2(R2) guidelines. To date, the results demonstrate excellent specificity (no interference), precision (%RSD ≤ 5.0%), accuracy (recovery ± 10%), and linearity (R 2≥ 0.990) across all lipid components. Tests for intermediate precision and robustness are currently in progress.

Following validation, a Standard Operating Procedure (SOP) will be established, and a quality control manual for biological products will be developed. Furthermore, we plan to evaluate the applicability of this method to national lot release and disseminate the results through technical workshops. This research is expected to enhance the efficiency, consistency, and reliability of quality evaluations for mRNA platform vaccines, thereby contributing to the improvement of public health.

Biography

Park Jongshik is a Scientific Officer at the Vaccine Division, Biopharmaceutical & Herbal Medicine Evaluation Department of National Institute of Food and Drug Safety Evaluation, Ministry of Food and Drug Safety (MFDS). Jongshik's expertise lies in national lot release and the regulatory review of test methods. Jongshik currently focused on standardizing lipid analysis for mRNA vaccines, applying Analytical Quality by Design (AQbD) to optimize and validate testing procedures.

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Artificial intelligence–driven clinical decision support for differentiating viral and bacterial infections to reduce antibiotic misuse

Artificial intelligence (AI) has emerged as a powerful tool in modern healthcare, particularly in improving diagnostic accuracy and clinical decision-making. One of the major challenges in infectious disease management is the differentiation between viral and bacterial infections. Misdiagnosis often leads to unnecessary antibiotic prescriptions, contributing to the global crisis of antimicrobial resistance.

This study explores the potential of AI-driven clinical decision support systems (CDSS) to assist healthcare professionals in distinguishing viral from bacterial infections using patient clinical data, laboratory parameters, and predictive algorithms. Machine learning models can analyse large datasets to identify patterns and biomarkers associated with specific types of infections, enabling more precise and timely diagnosis.

The implementation of AI-based diagnostic tools in clinical settings can significantly reduce inappropriate antibiotic use, improve treatment outcomes, and support antimicrobial stewardship initiatives. Additionally, such systems can aid physicians in resource-limited settings by providing evidence-based recommendations and reducing diagnostic uncertainty.

The integration of artificial intelligence with clinical diagnostics represents a promising approach to addressing the growing burden of antimicrobial resistance worldwide. By improving diagnostic accuracy and guiding appropriate treatment strategies, AI-driven decision support systems have the potential to transform infectious disease management and enhance global public health outcomes.

Biography

Dr. Pooja Bagdi is the Principal at Trinity Educational Institute, Ramgarh, Jharkhand, India, actively involved in academic research and educational development, particularly focusing on healthcare awareness and scientific education in tribal and rural regions of India. Bagdi's research interests include artificial intelligence in healthcare, infectious diseases, and metabolic disorders such as diabetes, and Bagdi has contributed to research exploring the application of AI in medical diagnostics and clinical decision support systems. Dr. Bagdi is committed to promoting innovative, technology-driven healthcare solutions and advancing interdisciplinary research to address emerging public health challenges.

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Burkholderia cepacia infection outbreak in an oncology set-up: Investigation and infection control response

Background: *Burkholderia cepacia* complex (BCC) is a non-fermenting Gram-negative bacillus known for its ability to survive in aqueous environments, disinfectants, and medical solutions. It is an opportunistic pathogen that poses significant risk to immunocompromised patients, particularly those in oncology and bone marrow transplant (BMT) units. Bloodstream infections caused by BCC are associated with contaminated medical products and invasive devices. In March 2026, a cluster of BCC bloodstream infections was detected in patients admitted to the Hematolymphoid (HL) ward and BMT unit of our hospital, prompting an urgent outbreak investigation.

Problem: Within one week, three patients developed bloodstream infections due to Burkholderia cepacia. The first case, identified on 14 March 2026 in the BMT ward, yielded BCC from both Hickman catheter lumens and peripheral blood. On 16 March, a second patient grew the same organism from central venous catheter (CVC) and peripheral samples. A third patient, reported on 19 March, also tested positive for BCC. All patients had undergone recent invasive procedures involving ultrasound (USG) guidance, during which USG gel had been used. The temporal clustering and microbiological similarity suggested a common source outbreak, necessitating immediate epidemiological and microbiological investigation.

Work-up and Action Taken: An outbreak investigation was promptly initiated. Environmental surveillance samples were collected from the BMT ward, ICU, and operating theatre. These included water samples; potential fomites; disinfectant solutions; ECG and USG gel bottles (opened and unopened); and USG probe surfaces. All samples were cultured in the in-house microbiology laboratory.

Burkholderia cepacia was isolated from multiple ECG and USG gel bottles across different clinical areas, including unopened containers. Other environmental samples did not yield the organism. This strongly implicated contaminated gel as the outbreak source, possibly due to intrinsic contamination during manufacturing or contamination during bulk storage and handling.

Immediate corrective measures were implemented. All suspected gel products were withdrawn and replaced with sterile, single-use gels. An advisory was circulated hospital-wide, discontinuing the use of non-sterile gel for invasive procedures. Infection control practices were reinforced, emphasizing sterile technique, avoidance of multi-use gel bottles, and strengthened surveillance. Patient management included removal of infected lines and antibiotic therapy, resulting in negative follow-up blood cultures.

Inferences and Take-Home Messages: The outbreak was attributed to contaminated ECG/USG gel serving as the vehicle for BCC transmission. The organism's ability to survive in aqueous products, disinfectants, and moist environments likely facilitated persistence and spread. Contributing factors included use of non-sterile gel for invasive procedures, sharing of gel bottles between patients, possible refilling or reuse of containers, and prolonged storage under warm, moist conditions.

Key take-home messages include:

- Always use sterile, single-use gel for invasive procedures such as central line insertions
- Avoid multi-use gel containers to prevent cross-contamination
- Maintain strict adherence to aseptic techniques
- Ensure vigilant infection control surveillance and rapid outbreak response
- Recognize that intrinsically contaminated commercial products can serve as outbreak sources.

This outbreak underscores the critical importance of infection control vigilance, particularly in high-risk oncology and transplant settings, where even seemingly benign products can result in significant morbidity.

Biography

Dr. Prasanth Chandrasekhar Bhat is the Medical Superintendent at Tata Memorial Centre – ACTREC, a premier oncology tertiary care centre under the Central Government, with more than 22 years of experience as a hospital administrator responsible for the management of the 380-bed oncology centre. Bhat's responsibilities, apart from the smooth conduct of patient services, include quality and safety for patients and staff, and Bhat serves as Chairperson of the Hospital Infection Control Committee and is associated with the National Accreditation Board for Hospitals & Healthcare Providers (India) as Principal Assessor for Hospital Accreditation.

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Development of multivalent anti-urogenital chlamydia vaccine

Over 130 million cases of urogenital chlamydial infection are globally recorded yearly, making it one of the top sexually transmitted diseases among the 15-45-year age group. This infection results in severe conditions like ectopic pregnancy, infertility, and pelvic inflammatory diseases if not treated. Despite antibiotic treatment, reinfections are often recorded. Thus, vaccine development against Chlamydia trachomatis (C. t.) infection is urgently required. Because of the antigenic variation of C. t., the major outer membrane protein (MOMP), a key factor for its pathogenicity, has diverse serovars, making it difficult to develop an efficient vaccine against it. Currently, the FDA has not authorized any C. t. vaccine, and the main challenge is the generation of efficient vaccines that cover urogenital C. t. serovars.

It is known that urogenital C. t., including serovars (D, E, F, G), shares variable domains VD1 and VD4, which are surface-exposed sequences, making them important targets for neutralizing antibodies. In our study, the $VD4^{D-G}$ sequence was fused with the DC-targeting domain of the Ebola glycoprotein to make the Ebo-VD4D-G immunogen, and it was co-expressed with $VD1\text{-}4^{D-G}$ and/or MOMPF immunogens in a recombinant vesicular stomatitis virus (rVSV) vector as anti-urogenital C. t. vaccine candidates. The immunogenicity results have clearly shown that immunization with each of these vaccines has induced significantly high levels of antibodies against C. t. MOMP protein derived from serovar D and L. Furthermore, *in vitro* analyses revealed that the vaccine-induced mouse sera exhibited some levels of ADCC and neutralizing activity. More detailed information will be presented at the conference.

Biography

Dr. Xiaojian Yao, PhD and MD, Professor, is the director of the Laboratory of Molecular Human Retrovirology, in the Department of Medical Microbiology, Faculty of Medicine, University of Manitoba. He obtained his M.D., M.Sc., and Ph.D. degrees, respectively, at Suzhou Medical University, the National Institute for the Control of Pharma & Biol. products in China, and the University of Montreal. Dr. Yao's research projects have been in fundamental research to explore HIV and host protein interactions and their functional roles during HIV-1 replication, and the development of new approaches against HIV-1. In recent years, his lab has also focused on developing multivalent vaccines against different high-risk viral and bacterial pathogens, including HIV-1, SARS-CoV-2, influenza A viruses and urogenital chlamydia.

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