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9TH EDITION OF WORLD CONGRESS ON

INFECTIOUS DISEASES &

5TH EDITION OF

INTERNATIONAL VACCINES CONGRESS

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OCTOBER, 2025

ORLANDO, FLORIDA, USA

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BOOK OF ABSTRACTS

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9th Edition of

World Congress on Infectious Diseases &

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BOOK OF

ABSTRACTS

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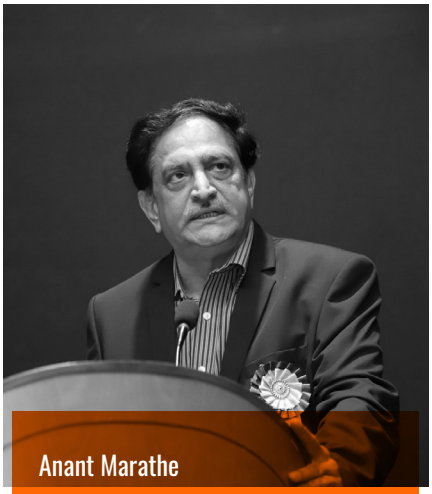

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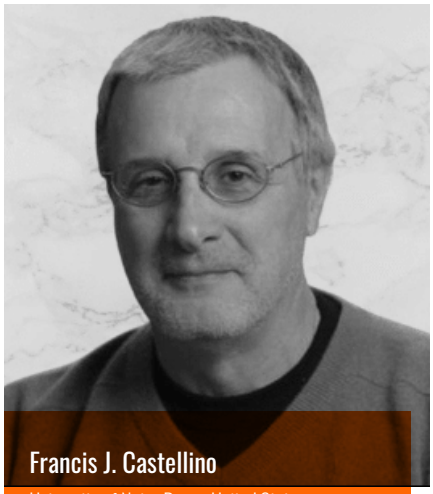

Francis J. Castellino
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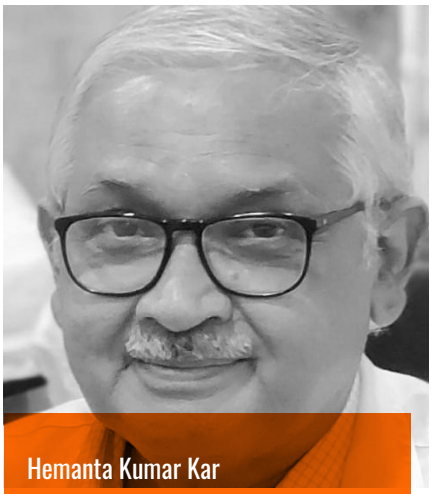

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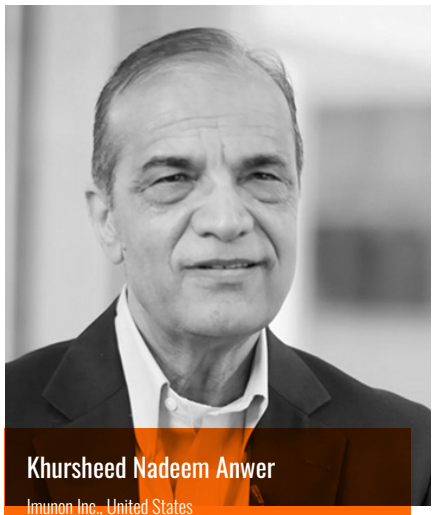
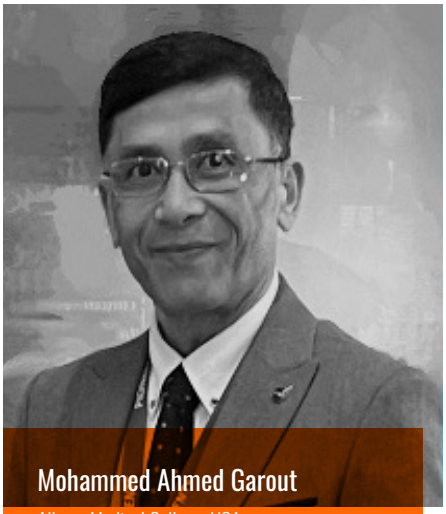


Khursheed Nadeem Anwer
Imunon Inc., United States

Madhu Khanna
Vallabhbhai Patel Chest Institute



Mohammed Ahmed Garout
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ID-FISH Technology, USA

Regina Au
BioMarketing Insight, United States

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Michigan State University, United States

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Shyam Sundar
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Stephen Hsu
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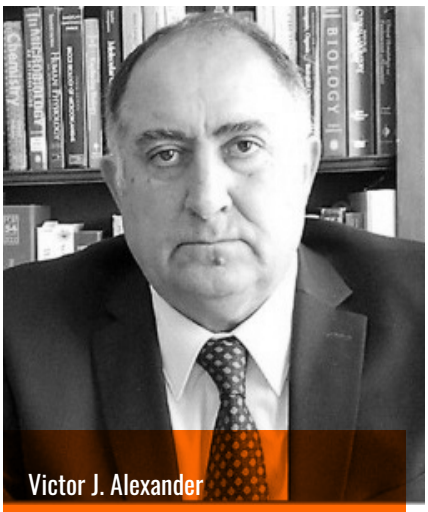
Sunita Girish
Dr. D. Y. Patil School of Allied Health Sciences, Pimpri, Pune, Maharashtra, India



Victor J. Alexander
Capital Stem Cell Research Corporation, United States

Thank You All...

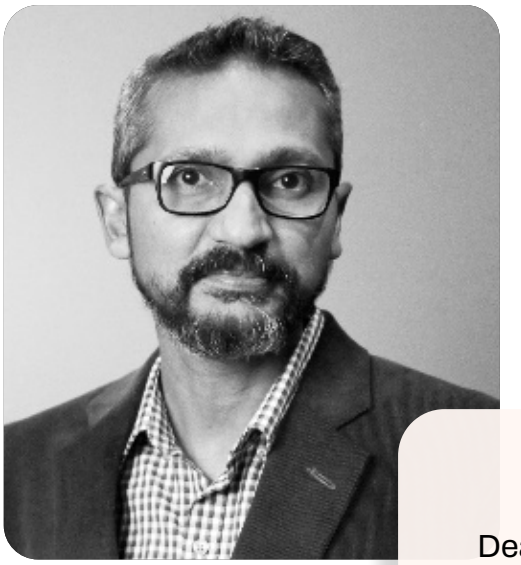
Welcome Message

Dear Colleagues,

It is my great honor to invite you to the 9th World Congress on Infectious Diseases, to be held October 23–25, 2025 in Orlando, United States (hybrid: in-person & virtual). This conference will be a dynamic platform to exchange ideas and drive innovation in disease prevention, detection, and treatment. Under the theme “Global Strategies Against Infectious Diseases: Prevention, Detection, and Treatment,” we will share discoveries and achievements aimed at improving global health. Your participation will meaningfully contribute to the worldwide effort against infectious diseases.

Stephen Hsu PhD

Professor of Augusta University, GA, USA



Welcome Message

Dear Conference Attendees,

It is our great pleasure to welcome you to WCID-2025. Infectious diseases continue to pose serious and evolving threats to human and animal health across the globe. From long-standing challenges to emerging pathogens like SARS-CoV-2, the impact of these diseases is profound and far-reaching. Now, more than ever, collaborative research and global engagement are essential to address these complex issues and develop innovative strategies for prevention, diagnosis, and treatment. WCID-2025 brings together a vibrant community of scientists, clinicians, and public health professionals to share cutting-edge discoveries and foster new collaborations. This year's conference will feature diverse sessions highlighting the latest advances in virology, bacteriology, host-pathogen interactions, immunology, and antimicrobial resistance, among other key areas.

We are honored by your participation and look forward to an exciting exchange of ideas, rigorous discussions, and the opportunity to build lasting connections that will drive the field forward. Welcome, and thank you for being part of this important gathering.

Saurabh Chattopadhyay

University of Kentucky (USA)

Welcome Message

Greeting!

Infectious Diseases (IDs) are the leading cause of morbidity and mortality worldwide. Globalization and increased travel have accelerated the spread if IDs, making them global concern that requires international cooperation and collaboration for effective prevention and control. The theme of WCID 2025 is Global Strategies Against Infectious Diseases Prevention, Detections, and Treatment. IDs continue to play a pivotal role in global health, acting as major contributors, particularly in developing countries. IDs pose substantial challenges not only to the practice of medicine particularly antibiotic resistance, but also tremendous impact to public health systems and economic development which disproportionately affect vulnerable populations. Thus, addressing the global burden of IDs necessitates a multifaceted approach, including strengthening disease surveillance, prevention and evidenced-based management strategies, therefore, improving access to healthcare, and most importantly, addressing the social determinants of health. I welcome you to the WCID 2025. The aim of this event is not only to address some of the most pressing global aspects of IDs via collaborative effects, but also, to share knowledge making meaningful progress in filed of IDs.

Prof. Dr. Nassiri

Michigan State University, United States

Welcome Message

Dear Congress Attendees,

It is my great pleasure and honor to welcome you to the 2025 5th Edition of International Vaccine Congress. This year speakers will cover topics "From Discovery to Distribution: The Path of Vaccines". We all know that bringing a vaccine or drug to market is very complex, time consuming and expensive. The basic research alone in understanding the biology of a disease can take up to 25 years. The drug development process from discovery; finding a lead candidate or active molecule to launching the product can take anywhere from 10 – 15 years with an average of 12.5 years and cost on average for the industry $1.3 - $1.5 billion dollars.

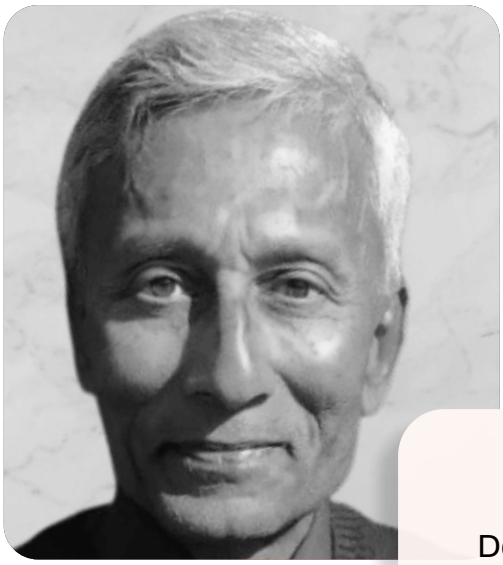
The risks are high in finding a lead candidate in understanding the mechanism of action and getting it through the regulatory approval process can be a huge challenge. Gaining physician and patient acceptance (product adoption) in wanting to use the vaccine/ drug is also a challenge. To be successful, both the R&D and business units must do everything possible to derisk all processes starting with the product development process, then the product launch and finally the product life cycle process.

I would like to invite you to join me for my presentation titled "The importance of post-marketing surveillance and real-world data: For a product to be successful". Post marketing surveillance is mandatory and part of the regulatory process. But planning and incorporating Real World Data into the post marketing surveillance will help to anticipate and ensure that the data reflects the efficacy and safety of the drug/vaccine itself and not be masked by other factors.

I know you will find all the presentations informative. I look forward to seeing you in October.

Regina Au

CEO, BioMarketing Insight, United States



Welcome Message

Dear Conference Participants,

I am honoured to welcome you to the 9th World Congress on Infectious Diseases in Orlando, Florida. USA (WCID 2025) with the theme: Global Strategies Against Infectious Diseases: Prevention, Detection and Treatment. The meeting addresses an area of high priority to health during a time of pandemics and rapidly increasing resistance to antimicrobials. Participants will be highlighting original research findings that will interest early career and established scientists, academics and clinicians. The presentations will enhance knowledge, generate new approaches to research and suggest new solutions for controlling infectious diseases. The Congress will further provide an opportunity for participants to develop networks to advance their research, teaching and clinical practice.

Professor Ranjan Ramasamy Ph.D.

IDFISH Technology, United States

Welcome Message

Dear IVC Participants,

It is my distinct honor and pleasure to welcome you to the International Vaccine Conference 2025, a global forum dedicated to advancing vaccine research, development, and their transformative impact on human health.

I am deeply inspired by the collective expertise and commitment represented at this conference. We are privileged to bring together leading researchers, clinicians, industry experts, and regulators from around the world to share insights, foster collaboration, and shape the future of vaccinology.

Vaccines remain among the most powerful tools in our fight against infectious diseases and cancer. Recent years have further highlighted their critical role in global health security. The conference program reflects the breadth and depth of this field—from cutting-edge innovations in vaccine development and delivery technologies to vital discussions on equity, access, and implementation strategies.

I encourage all participants to engage fully with diverse sessions, challenge conventional thinking, and build meaningful connections that will drive innovation and progress. Whether you are presenting your latest findings, participating in workshops, or networking with peers, your contributions are essential to the success of this conference and to the advancement of vaccine science.

Thank you for joining us and for your unwavering dedication to improving health outcomes worldwide. I look forward to stimulating discussions and transformative ideas that will emerge from our time together.

Khursheed Anwer Ph.D., MBA

Imunon Inc., United States

Welcome Message

With a great honor and immense pleasure I welcome all the attendees of WCID 2025. The microbial sciences have undergone renaissance in last two decades. It has helped millions of people across the world especially during the devastating epidemic of COVID 19, by developing faster, sensitive and specific molecular methods for detection and by developing vaccine. The advances in microbial sciences has also has strengthen the confidence to face any such eventuality. The newer techniques like mRNA and recombinant vaccine will help in the development of better world for the human kind a to live in. I trust all the attendees will gather some intellectual benefit during the event.

Prof. Dr. Anant Marathe

Parul University, India

ABOUT
MAGNUS GROUP

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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Zeynep Burcin Yilmaz, Inonu University, Turkey

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KEYNOTE PRESENTATIONS

Dr. Anant Marathe[1*], Asmabanu Shaikh[2], Bhavita Prajapati[2], Ms. Shital Sangani[3]

[1]Professor & PhD Guide, Department of Microbiology, Parul Institute of Medical Sciences & Research, Vadodara, Gujarat, India

[2]Assistant Professor, Department of Microbiology, Parul Institute of Medical Sciences & Research, Vadodara, Gujarat, India

[3]PhD scholar, Department of Microbiology, Parul Institute of Medical Sciences & Research,Vadodara, Gujarat, India

Genomic study of various virulence factors of *Acinetobacter baumannii* isolated from clinical specimens in patients with VAP and bloodstream infection

Acinetobacter baumannii has evolved over years as a predominant nosocomial pathogen in ICUs especially associated with VAPs and subsequent blood stream Infections. In the present work we have tried to observe genetic make-up of A. Baumannii isolates for virulence factors and their association with patient comorbidities, treatment outcomes. A total 44 isolates of A. Baumannii isolated from Blood and respiratory specimens of patients on mechanical ventilator are included in a study. All isolates are confirmed by Vitek2 and MALDI TOF and WGS analysis carried out for identification of virulence genes. The most common virulence genes found in 44 isolates of A. Baumannii were ompA (95%) and LPS O antigen (73 %) related to adherence, adeF (98%), adeG (100%) and adeH (98%) (AdeFGH efflux pump related VF genes) and pgaA, B, C and D (98%) related to biofilm formation, plc (100%), plcD (98%) related to enzyme and immune invasion related capsular gene (100%) and lpsB, lpsA, lpxB, lpxD and lpxM found in all isolates respectively. This study is among the few to investigate various Virulence Factors (VF) using Whole-Genome Sequencing (WGS) in India. These findings have improved our understanding of the various pathogenic mechanisms underlying *A. baumannii* antimicrobial resistance.

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 postdoctoral 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.

David Craig Wright[1*] M.D., Emily Wright, Michael Bowe, Jacob Hoadley, Peter Pushko[2] PhD., Vitor Serrao[3] PhD.

[1]D4 Labs, LLC Pacific Grove, California, USA

[2]Medigen, Inc. (Frederick, Md. USA)

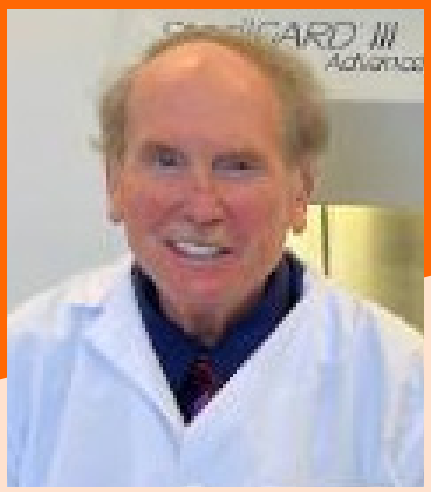
[3]Department of Chemistry and Biochemistry, UCSC, California, USA

Nanoscopic SubATVax™ adjuvanted vaccines against Influenza A types H3N2, H1N1 and influenza type B for subcutaneous administration

Nanoscopic structures are small vehicles for delivery of vaccines or drugs that are measured in nanometers and best visualized by electron microscopy. An example of the first approved human nanoscopic vaccine was Dr. Jonas Salk's formalin inactivated polio vaccine. The inactivated polio vaccine is approved currently for Intramuscular and subcutaneous administration. It is used in several countries like India as a three dose intradermal priming vaccination before administration of multiple doses of the attenuated oral polio vaccine (Sabin vaccine).

Two examples of nanoscopic vaccines using our SubATVax™ technology are our SARS-COV-2 vaccine (USPTO# 11,911,461 B1 "Adjuvanted vaccines containing modified S1 spike protein of SARS-COV-2 variant C.1.2 for subcutaneous administration and methods of use") and an interesting nanoscopic Influenza vaccine, using an FDA approved antigen preparation from another vaccine company, mixed with preformed SubATVax™ nonphospholipid liposomes. How these adjuvanted vaccines are prepared and electron micrographic studies of nanoscopic vaccines will be reviewed.

Biography



Dr. Wright completed an undergraduate degree in Biology from the University of Virginia in 1972, his M.D. degree from the University of Virginia in 1976, an internship in internal medicine at Columbia P&S Harlem Hospital in New York City in 1977. He then spent 3 years in the Army in Germany seeing patients before returning to the United States to complete a two residency in Internal Medicine, a 3 year research fellowship in Infectious Disease both at Walter Reed Army Medical Center in Washington D.C and tropical medicine training at Walter Reed Army Institute of Research. During his fellowship he set-up the first HIV-1 clinic in the military which he continued to run until 1988. He then left to cofound Univax Biologics, the third biotechnology company in Maryland. In 1993 he cofounded Novavax. Dr. Wight left Novavax in 2006. He has set-up 3 additional companies LPJP, Inc., David Craig Wright, M.D. Inc. (both California S corporations) and D4 Labs, LLC (California LLC). Dr. Wright has authored or co-authored over 20 issued US patents since 1989.

Sheiny Tjia-Fleck, Bradley Readnour, Yetude Ayinuola, Francis J. Castellino*

Department of Chemistry and Biochemistry, University of Notre Dame, Notre Dame, Indiana 46556

Binding and activation of fibrinolytic components to Streptococcus pyogenes enhances microbial pathogenicity

Binding and activation of components of the human fibrinolytic system enhances the pathogenicity of *Streptococcus pyogenes* (GAS) by allowing a potent serine protease, Human Plasmin (hPm) to be present on the surface of these cells. The major receptors of hPg and hPm on these cells are Streptococcal M-Protein (PAM) of Pattern D strains of GAS, as well as Streptococcal Enolase (SEn). We have studied the binding of intact hPg to these proteins at high resolution using Cryogenic Electron Microscopy (cryoEM) and have obtained resolutions <3.6Å, thus allowing the mechanisms of binding to be determined. These studies were combined with activation analyses of hPg by GAS-secreted Streptokinase (SK) to correlate plasminogen binding, activation and pathogenicity. We find that only Pattern D strains of GAS directly bind hPg and hPm via a short region of the hPg, termed kringle 2, and the a-domain of PAM. Binding to SEn is more complex with several hPg kringles interaction with an internal lysine isostere of SEn.

However, the complex of Sen and hPg does not result in its enhanced activation by SK, but this binding does promote slightly enhanced activation of hPg by host tissue-type plasminogen activator. We conclude that the pathogenicity of Pattern D GAS is primarily accomplished by hPg binding to PAM.

Biography

Dr. Castellino studied Chemistry as an undergraduate at the University of Scranton (PA) and graduated with a BS in 1964. He then was a graduate student in Biochemistry at the University of Iowa with Robert Barker, where he graduated with a M.S. and PhD. In 1968. Following this, he was a 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 remained to this day. He is currently the Kleiderer-Pezold Professor of Biochemistry.

Hemanta Kumar Kar

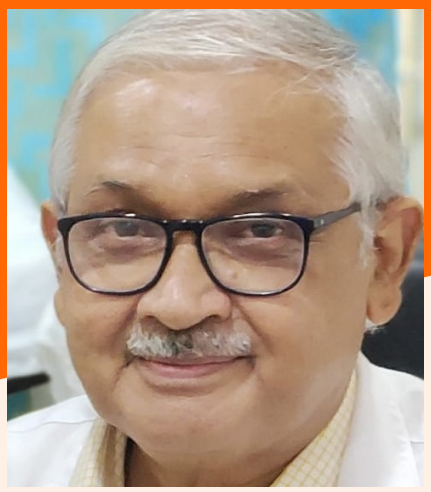
Emeritus Professor, Dermatology and Leprosy. KIMS, KIIT University, Bhubaneswar, Odisha, India

Innovative bactericidal drugs pulse regimens for treatment of leprosy – Advancing towards zero leprosy

WHO recommended Multi-Drug Therapy (MDT) in leprosy has proven effective; BUT challenges like treatment adherence, drug resistance, dapsone/ clofazimine bacteriostatic actions/side effects persist. Grosset et al suggested that PMM regimen consisting of Rifapentine, Minocycline and Moxifloxacin would be the most superior supervised pulse drug regimen. In the past researchers using Rifampicin, Ofloxacin and Minocycline (ROM) as an alternative to WHO MDT with good success, have demonstrated comparable efficacy to standard MDT, with the added benefit of reduced adverse effects. WHO expert committee of Leprosy, seventh report also suggested ROM 24 months' regimen for those who do not accept clofazimine pigmentation. RMM (Rifampicin, Minocycline and Moxifloxacin), have demonstrated greater efficacy and lesser side effects than conventional treatments. RCM (Rifampicin, Clarithromycin and Minocycline) ongoing trial regimen in our centre shows positive outcome both clinically as well as bacteriologically. However, higher incidence of type 2 leprosy reaction has been observed as compared to WHO MDT regimen.

Brodiquiline is another potential bactericidal found very effective, made all viable bacilli dead in four weeks monotherapy regimen, this drug needs to be explored in monthly pulse regimen. RMM trial done in USA showed successful treatment and remission of Hansen in 10 treated patients. All will be discussed in this talk.

Biography



Prof. Hemanta Kumar Kar, Emeritus Professor at KIMS, KIIT University, Odisha, India earned his MBBS in 1975 and MD (DVL) in 1982. He served at CLTRI (1982–85), Dr. RML Hospital as Professor and Consultant (1993–2013), and as Dean and Director until 2015. He later worked at North DMC Medical College (2016–19) and KIMS (till 2023). Active in leprosy research since 1982, he contributed to chemotherapy and vaccine (MIP) development, authored 32 leprosy chapters including in Harrison's Principles of Internal Medicine, editor of IAL Textbook of Leprosy, and published 145 research papers. Presently involved in international PEP++ research project and Bedaquilin trial in leprosy.

Jesse L Kuiper PhD

Merck & Co., Inc., Rahway, NJ, USA

Evaluating the immunogenic impact of process impurities in mRNA vaccine production: Establishing integrated control strategies and specifications

The advent of mRNA vaccines has revolutionized the landscape of immunization, particularly highlighted during the COVID-19 pandemic. It is well known that the production process for these vaccines can introduce various impurities, such as endotoxins, double-stranded RNA (dsRNA), and residual proteins, which may influence the overall immunogenicity and efficacy of the final product and its LNP carriers. This talk aims to illuminate the immunogenic responses elicited by these process impurities as well as the LNP delivery systems with an eye towards effective integrated control strategy and phase appropriate specification setting. Thereby enabling the delivery of safe and effective vaccines for the global population.

Biography

Dr. Jesse L. Kuiper, PhD is a Principal Scientist in the Vaccines Analytical Research and Development group in Merck Research Laboratories at the West Point, PA campus. He holds a BSc degree in Chemistry and Biochemistry from the University of Michigan, Ann Arbor and a PhD in Chemistry from the University of Illinois at Urbana Champaign. Jesse has been with Merck for over 18 years, with experience in analytical development for small molecule drug products, biopharmaceutics, and vaccines. Jesse has extensive experience interacting with regulatory-CMC organizations across modalities and has recently served as the analytical lead for Dengue and mRNA programs. Through his time at Merck, he has several patents and publications to his credit as well as three successfully marketed products. He is currently a Development and Commercialization Lead for Merck mRNA vaccines.

Khursheed Anwer*, Douglas V. Faller, Stacy Lindborg

Imunon Inc., Lawrenceville, NJ, USA

A promising novel approach to DNA vaccines

Nucleic acid-based vaccines (mRNA or DNA) present a promising alternative to traditional vaccines due to their ability to induce both humoral and cellular immune responses. While mRNA vaccines have been recognized for their ability to provide efficient protection, concerns remain regarding their safety, durability, and poor thermal stability, reinforcing the need for continued research into alternative nucleic acid vaccine strategies. DNA-based vaccines are well-positioned to address the limitations of current vaccines. However, due to low delivery efficiency, physical delivery devices—such as electroporators or needle-free jet injectors—have been employed for DNA delivery, posing challenges related to user compliance, additional costs, and global accessibility.

Here, we introduce a novel DNA vaccine platform, PlaCCine, designed to overcome the limitations of current vaccines. Its flexible design allows for encoding one or more antigens within a single gene expression plasmid, and its synthetic delivery system eliminates the need for a virus or specialized device. Additionally, it demonstrates thermal stability at practical temperatures, along with a rapid, scalable, and cost-effective manufacturing process. This presentation will highlight the advancements in PlaCCine technology, demonstrating efficacy against various pathogens across multiple species. In a recently completed human clinical trial, a proof-of-concept PlaCCine vaccine targeting a SARS-CoV-2 spike variant was found to be safe and immunogenic following intramuscular administration in healthy participants. Mild to moderate reactogenicity events —primarily tenderness, induration, pain, redness, swelling, and itching at the injection site — were observed

Biography

Khursheed Nadeem Anwer, Ph.D., M.B.A., is Executive Vice President & Chief Science Officer at IMUNON Inc. since June 2014. Dr. Anwer has served as President and Chief Science Officer of EGEN, Inc. from 2009 until June 2014 when he successfully led the merger of EGEN, Inc. with IMUNON Inc. Dr. Anwer has over 25 years of experience in the discovery and development of gene-based therapeutics. He is the inventor on over one hundred U.S. and international patents, recipient of NIH and FDA funding, and has authored about fifty peer reviewed scientific publications in his active career in research and development.

but were not dose-dependent and resolved spontaneously. Vaccination with PlaCCine resulted in a dose-dependent increase in neutralizing antibody titers against the variant of concern and subsequent variants. The robust immunogenicity observed in healthy human volunteers, even those previously vaccinated or infected multiple times with the pathogen, underscores the PlaCCine technology platform's potential to facilitate the development of safe and effective vaccines.

Madhu Khanna*, Prashant Kumar, Binod Kumar & Roopali Rajput

Virology Unit, Department of Microbiology, Vallabhbhai Patel Chest Institute, University of Delhi, Delhi-110007, India

Effectiveness of influenza vaccine in elderly populations

Influenza viruses continue to cause severe emerging and remerging outbreaks worldwide. Recent viral pandemics of the 2009 [pandemic influenza A (H1N1)] and 2019 (SARS-CoV-2), have enhanced the need of vigilance for combating such emerging and re-emerging viral outbreaks and mitigate the global socio-economic losses. Flu vaccination has been considered effective for older population (individuals aged 65 years or more). The growing age imposes a higher risk to older population and makes them vulnerable for developing serious complications. In one of our studies, we evaluated the effectiveness of inactivated trivalent split influenza vaccine, VAXIGRIP in elderly population. The vaccine was administered to individuals who had no history of flu or flu vaccination at least a year prior of the date of vaccination. Antibody titres against influenza strains A/H1N1, A/H3N2 and B were assessed by HAI and MN assays, pre- and post-vaccination (after 21 days, 3 months, 6 months and 9 months of vaccine administration) to determine existing and vaccine influenced antibody titres in old individuals. We found that the VAXIGRIP conferred protection to the elderly for about 6-9 months, with a requirement of a booster dose within 9 months of the vaccination. The need towards better preparedness against unprecedented viral outbreaks led us to investigate gene silencing mediated inhibition of viral replication in mammalian cells and BALB/c mice. The synergistic effect of siRNAs and ribozymes by constructing siRNA-chimeric-Rz molecules specific to M1 gene transcripts was analyzed. The chimeric

Biography

Prof. Madhu Khanna obtained her Ph.D. degree from King George's Medical University, Lucknow, India. She has done postdoc fellowship at WHO influenza center, Melbourne and Royal Children hospital. She has been holding the position of Professor of the Department of Virology Unit at Vallabhbhai Patel Chest Institute, University of Delhi, since 2008. She has over 30 years of experience in virology research and diagnostics. Prof. Khanna has received several prestigious national and international awards, including the Global Health Travel award from Bill and Melinda Gate Foundation to attend the Keystone Symposium on HIV and (Re)Emerging Viruses: Aligning Lessons Across Pandemics, Shakuntala Amir Chand Award, BOYSCAST Fellowship, Bronze Award (AVG Award), and IVS Fellow Award. She has published more than several research articles in high-impact national and international journals.

constructs consisted of small hairpin siRNA joined by a short intracellular cleavable linker to a known, hammerhead Ribozyme (Rz). Wild type and mutated versions containing alterations either in siRNA or Rz were tested. The entire wt construct showed 67% reduction of RNA levels in cells. The mt-siRNA-wt-Rz construct showed 33% gene silencing effect, while the wt-siRNS-mt-Rz exhibited 20% reduction M1 RNA levels. This wt chimeric construct showed an impressive >80% protection against influenza virus in BALB/c mice and was much more effective than the selectively disabled mutant constructs. The virus titre in mice lung tissues was done by plaque assay, real time RT-PCR, and western blotting. The reduced viral plaque forming units in the mice lungs indicated potency of the chimeric constructs. Additionally, the animal survival assay demonstrated a dose-dependent efficacy. Our results validate the siRNA-chimeric-ribozyme constructs as potent protective agents against lethal influenza A virus challenge. Two important strategies to circumvent emerging and re-emerging influenza virus infections in human population were investigated: Vaccination for better preparedness and disease outcomes & proof-of-concept of an effective antiviral approach against one of the major viral diseases of epidemic or pandemic potential.

Mohammed Ahmed Garout

Department of Community Medicine and Health Care for Pilgrims, Faculty of Medicine, Umm Al-Qura University, Makkah 24538, Saudi Arabia

Leading through crisis: Saudi Arabia's experience in managing COVID-19 and influencing global health strategies

Saudi Arabia effectively managed infectious diseases and pandemics, including MERS-CoV (2014) and COVID-19 (2020), by implementing an integrated, evidence-based approach. Its strategy emphasized strategic planning, international collaboration, and rapid adaptability to evolving health threats. Below are different key strategies and actions which had been successfully implemented:

1. **Rapid and Integrated Response:** Saudi Arabia acted swiftly during outbreaks, forming crisis management committees composed of epidemiologists, physicians, and government officials. Decision-making prioritized minimizing infections and mortality through scientific data and statistical models. Early interventions, such as lockdowns and curfews during COVID-19, effectively slowed virus transmission.

2. **International and Local Collaboration:** The Kingdom partnered with international organizations, including the WHO, for technical support and access to updated information. It also collaborated with pharmaceutical companies and took part in vaccine trials to inform decisions about vaccine procurement and distribution, ensuring rapid and evidence-based implementation of preventive measures.

3. **Healthcare Infrastructure Expansion:** The government quickly expanded healthcare facilities, building field hospitals and increasing ICU capacity to handle rising

Biography

Dr. Mohammed, a Professor of Public Health at Umm Al-Qura University, Makkah, is a clinical epidemiologist and infection control consultant. Since 2008, he has served as the IPC specialty team leader with CBAHI, The Saudi Arabian national accreditation organization. With over 20 years of experience, he has held executive roles in infection control and healthcare management. Dr. Mohammed contributed significantly during the 2014 MERS-CoV outbreak and the 2020 COVID-19 pandemic, advising the Ministry of Health and collaborating with WHO and CDC. He has provided extensive consultations on infection control, patient safety, and quality improvement strategies across healthcare organizations in Saudi Arabia. He has published more than 80 research articles in different national and international journals.

cases. It also implemented digital health solutions, such as the “Tawakkalna” and “Sehhaty” apps, to monitor cases, provide remote healthcare, and ease the burden on hospitals while enabling data-driven decision-making.

4. **Public Awareness and Communication:** Saudi Arabia prioritized public education through extensive media campaigns to promote hygiene, social distancing, and mask-wearing. Continuous engagement fostered compliance with health guidelines and raised awareness about vaccination. These initiatives ensured transparency and built trust in the government’s health measures.

5. **Vaccination and Immunization Campaigns:** Saudi Arabia launched one of the largest vaccination campaigns globally, prioritizing healthcare workers, the elderly, and high-risk populations. The rollout was guided by scientific research and collaboration with international organizations. Efficient organization and rapid decision-making ensured high vaccination rates, contributing to virus containment and community protection.

Conclusion: Saudi Arabia’s experience managing MERS-CoV and COVID-19 highlights a proactive and systematic approach to infection prevention and control. Through rapid responses, international collaboration, infrastructure development, and public engagement, the Kingdom created a model for effective pandemic management. Its emphasis on evidence-based decision-making, digital health technologies, and vaccination programs demonstrates resilience and preparedness for future health crises.

Ping Xie

Department of Cell Biology and Neuroscience, Rutgers University, Piscataway, New Jersey 08854, USA

Commensal bacteria drive B-cell lymphomagenesis in the setting of innate immunodeficiency

Myeloid cells are central players in innate immunity and inflammation. Their function is regulated by the adaptor protein TRAF3. We previously reported that aging myeloid cell-specific TRAF3-deficient (M-Traf3$^{-/-}$) mice spontaneously develop chronic inflammation and B-cell lymphoma. Here we aimed to identify the internal trigger of this disease phenotype in these mice. We first detected gut microbiota dysbiosis and transmigration of commensal bacteria to the liver in aging M-Traf3$^{-/-}$ mice. Interestingly, depletion of commensal bacteria using antibiotics effectively prevented B-cell lymphoma development in these mice. Systemic IgG responses against commensal bacteria were induced and the IgH CDR3 sequences of malignant B-cell clones of M-Traf3 $^{/-}$ mice showed high homology to prevalent bacteria-reactive Ig clonotypes. Furthermore, M-Traf3$^{-/-}$ mice with B-cell lymphomas exhibited high serum titers of antibodies against commensal bacteria. Together, our findings offer insights into the mechanisms underlying increased risks of B-cell lymphomagenesis observed in patients with compromised innate immunity.

Biography

Dr. Ping Xie is an Associate Professor in the Department of Cell Biology and Neuroscience at Rutgers University. Dr. Xie received the PhD from the Hong Kong University of Science & Technology, followed by postdoctoral work at the University of Illinois at Chicago and the University of Iowa. She joined the faculty of Department of Cell Biology and Neuroscience at Rutgers University in 2008. She was a Special Fellow of the Leukemia & Lymphoma Society. Her laboratory's research has been supported by the USA NIH, DoD, New Jersey Commission on Cancer Research, and the Cancer Institute of New Jersey.

Ranjan Ramasamy

ID-FISH, 556 Gibraltar Drive, Milpitas, CA 95035, USA

Mosquito vectors adapting to salinity from coastal environmental changes heighten disease transmission risk

Changes in temperature, rainfall and humidity due to climate change affect mosquito-borne disease transmission. However, coastal areas worldwide are also influenced by the expansion of brackish water mosquito habitats as a result of global warming leading to higher sea levels and the accumulation of man-made waste containers collecting brackish water. Typical fresh water mosquito vectors such as the arbovirus vectors *Aedes aegypti* and *Aedes albopictus* as well as the malaria vectors *Anopheles stephensi* and *Anopheles culicifacies* have recently been documented to develop in coastal brackish water habitats in the 1025 km^2 Jaffna peninsula in northern Sri Lanka. Salinity-tolerant *Ae. aegypti* has also since been reported in Florida, USA. Adaptation of *Ae. aegypti* to oviposit and undergo preimaginal development in brackish water is accompanied by thickening of larval and adult cuticles and concomitantly greater resistance to common larvicides and adulticides respectively. Brackish water habitats of Aedes vectors are not presently targeted in vector control programmes. Because brackish water *Ae. aegypti* and *Ae. albopictus* are infectible with dengue virus, they can constitute a neglected reservoir of dengue virus that initiate epidemics with the onset of seasonal rains. This may also apply to brackish water-adapted malaria vectors and malaria. These findings highlight the importance of extending mosquito vector control programmes to coastal brackish water habitats for the better control of mosquito-borne diseases.

Biography

Ranjan Ramasamy graduated in 1971 and then a PhD in 1974 from the University of Cambridge, UK. He was the Chairman of the National Science Foundation of Sri Lanka, Professor of Life Sciences at the Institute of Fundamental Studies in Kandy in Sri Lanka, Professor of Biochemistry in the University of Jaffna in Jaffna SriLanka, Professor of Immunology in the University Brunei Darussalam Medical School and held institute appointments at the Babraham Institute, Cambridge, UK and Scripps Clinic and Research Foundation, La Jolla, USA. He has more than 280 publications.

Regina Au CEO

New Product Planning at Bio Marketing Insight, Boston, MA, USA

The importance of post-marketing surveillance and real-world data for a product to be successful

Why is post-marketing surveillance and real-world data important for the success of your product? Post-marketing surveillance or phase IV is required by the FDA after the product is approved and launched. Phase IV is mainly focused on pharmacovigilance, drug safety and reporting adverse events to the FDA. Unfortunately, once the product is approved, physicians are generally not required to report adverse events to a national registry, except for specific cases like adverse events to vaccines and serious injuries or deaths related to medical devices. This is a problem in collecting real-world data that can provide critical insights into long-term safety, effectiveness, and population-level impact to name a few. This session will cover why post-marketing surveillance and real-world data is needed and how it can validate your product. I will cover the top five (5) reasons you need post-marketing surveillance plus gather, monitor and analyse real-world data and the tools to capture this data to enhance your product marketing strategies for commercial success.

1. Clinical Trials (controlled environment) vs. Real World (Wild Type)
2. Clinical Trials (Homogenous) vs. Real World (extremely Heterogeneous)
3. Clinical Trials (adverse report) vs. Real World (under reporting, lack of information)
4. Need for long-term data
5. Serendipitous or repurposing

Biography

Regina Au is CEO, New Product Planning at Bio Marketing Insight with 20+ years of experience in the life science industry. She helps companies define their target product profile (TPP) to be able to compete in the market and be better in meeting the company's goals. Ms. Au was a member of the Advisory Board for Regis College Master of Regulatory and Clinical Research Management Program, an Adjunct Professor at Northeastern University in the Biotechnology Program and currently on the Editorial Board for the International Journal of Clinical Pharmacology & Pharmacotherapy. She has published over 22 articles in scientific and business journals and given over 30 presentations at international conferences. Regina has a BS in microbiology from the University of Michigan, an MBA in Marketing from the University of Connecticut and a Masters in International Management from Thunderbird, Global School of Management.

In capturing real-world data, electronic health records, wearable technologies, and mobile health apps have revolutionized how real-world data are collected and analyzed. AI can also aid in gathering and analyzing this data.

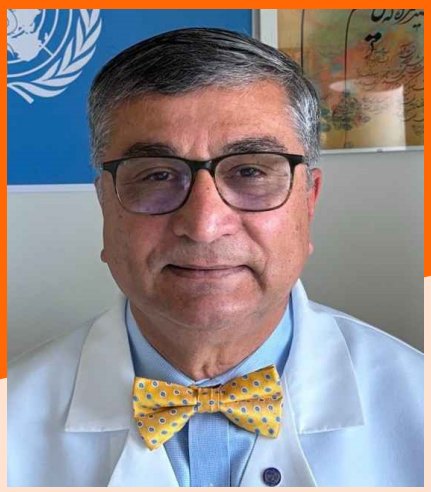
Prof. Dr. Reza Nassiri

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

Global clinical impact of the burden of antibiotic resistance

Antibiotics are the foundation of modern medicine. Antibiotic Resistance (ABR) leads to unintended consequences including suboptimal therapeutic outcomes, increased morbidity and mortality, longer hospital stays, and higher healthcare costs. ABR is a global public health challenge that can also make treatment of infections more challenging, or in some cases, impossible to treat. ABR is a major issue that can potentially compromise the success of medical procedures such as chemotherapy, organ transplants, and surgeries. Although ABR affects countries across all income levels, its impact is disproportionality severe in low- and middle-income countries where public health infrastructure are weaker. In the US, nearly 3 million antimicrobial-resistant infections occur each year, resulting in more than 35,000 mortalities. Physicians have very few other options available to treat MDR and XDR infections. The World Health Organization (WHO) acknowledges ABR is one of the top global public health and development threats. Numerous bacterial pathogens and 18 antibiotic regimens (targeted and empirical) currently contribute to the global ABR. There are countries that face nosocomial MDR *K. pneumoniae* isolates. ESBL-producing *K. pneumoniae* is a threat to S.E. Asia and certain regions of Africa and the Middle East. *A. baumannii* has a higher carbapenem resistance rate than *P. aeruginosa* and *Enterobacter* spp. with a proportion of more than 50% among Chinese isolates. Although an uptick of new broad-spectrum antibiotics approved by the FDA within the last ten years geared toward MDR pathogens such as

Biography



Prof. Dr. Nassiri is a former dean of global health at MSU, East Lansing, Michigan, USA. He is also a former Director of the Institute of International Health at MSU. He is a French-trained hematologist with training in clinical pharmacology and has expertise in Global Health/ One Health, Infectious Diseases, and Antibiotic Resistance. He is currently a professor of clinical pharmacology at MSU. He is on the editorial board of 4 medical journals and has written extensively (viewpoint) about antibiotic resistance and COVID-19.

Ceftolozane/Tazobactam, Ceftazidime/Avibactam, Meropenem/Vaborbactam, Delafloxacin, Omadacycline, Eravacycline, Imipenem/Relebactam and Cefiderocol, these new agents, too, may acquire resistance if the principle of antibiotic stewardship is not rationally practiced. Given the rapid worldwide dissemination of resistant bacteria, a global perspective is essential in addressing this issue.

Addressing this urgency will require innovative models for antibiotic research and development, improved global coordination and collaboration (One Health), and equitable access to new treatments across all regions. Additionally, efforts must be focused on educating healthcare professionals for making appropriate therapeutic decisions, improving surveillance, leadership, action plan, tracking and reporting. Particularly, laboratory infrastructure including molecular epidemiological methods and genetic analysis of resistant pathogens take urgent priority to contain the escalation of AR.

Saurabh Chattopadhyay*, Pracheta Sengupta, Manoj Veleeparambil, Santanu Das, Izabella McNamara, Ritu Chakravarti

Department of Microbiology, Immunology and Molecular Genetics, University of Kentucky, Lexington, KY, USA

Novel functions of the interferon system against virus infection

The Interferon (IFN) system is a central component of the innate immune response to viral infection. Viral invasion triggers both antiviral and inflammatory pathways that establish host protection. While early inflammation is beneficial, excessive inflammatory responses—such as cytokine storms—can drive viral pathogenesis. Our research focuses on understanding how components of the IFN system coordinate the balance between antiviral defense and inflammation. Using both cell-based and mouse models, we have identified novel mechanisms by which the host curbs excessive inflammation to prevent cytokine-mediated damage. These findings have important translational implications for combating respiratory viral infections.

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 in Lexington, Kentucky. His research focuses on viral infections and their interplay with host immune responses. His laboratory has been supported 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 degree in Biotechnology from the Indian Institute of Technology Delhi and completed his postdoctoral training in Virology at the Cleveland Clinic. Prior to joining the University of Kentucky, he served as an Associate Professor at the University of Toledo College of Medicine in Ohio.

Shyam Sundar

Banaras Hindu University, India

Elimination of visceral leishmaniasis from India – The story

The current epidemic of Visceral Leishmaniasis (VL, kala-azar) in India started in early 1970s and in the late 1990s, it became apparent that there is widespread SbV resistance with its cure rate nose-diving to 35%. There was an urgent need for alternative treatments. In 2002, miltefosine the first oral antileishmanial drug was approved in India and became available for the treatment of VL. This drug along with early and rapid diagnosis with rk39 antigen-based rapid diagnosis strip test, became the backbone of the Kala-Azar Elimination Programme (KAEP) jointly launched in 2005 in India, Nepal and Bangladesh. In 2010 a landmark paper was published which demonstrated 95.6% efficacy of single-dose Liposomal Amphotericin B (LAmB)with a dose of 10 mg/kg without any safety concerns. This proved to be a true game changer in the management of VL in India, the American manufacturer of this highly expensive LAmB announced a free donation of the drug to India, Nepal and Bangladesh. In 2014 miltefosine was replaced by the single dose LAmB treatment. There was a dramatic fall in the incidence of kala-azar in all three countries, and in 2023 India achieved the target of KAEP in all affected 633 blocks. The elimination target has been maintained in the year 2024, and the country need to hold this in 2025 also to obtain the World Health Organization certification.

Biography

Dr. Shyam Sundar is presently working as a Professor of Medicine Head, Department of Medicine at Institute of Medical Sciences Banaras Hindu University (BHU), Varanasi, India. Dr. Shyam Sundar first to successfully conduct multidrug therapy of VL, and these regimens are also approved by WHO as the second most preferred regimen. Combination of paromomycin and miltefosine is also being used at primary health centers by the National Control Programme. He has also done excellent work on lipid associated amphotericin B. His work with single dose liposomal amphotericin B is considered as a major breakthrough and has earned worldwide acclaim. This single dose regimen is now the most preferred according to WHO recommendations, and it is being used in the control programme in India. He led the pivotal paromomycin trial, based on which the drug was approval by the Government of India.

Stephen Hsu[1,2*], Douglas Dickinson[2], Nicolette Frank[2]

[1]Department of Oral Biology & Diagnostic Sciences, Dental College of Georgia, Augusta University, Augusta, Georgia

[2]Camellix Research Laboratory, Camellix, LLC, Augusta, Georgia, USA

FAST nanotechnology and its practical applications

FAST (Facilitated Self-Assembling Technology) is a powerful nanotechnology that enhances the effectiveness of hydrophobic molecules in aqueous formulations. Unlike traditional nanotechnology, FAST requires only one or two water-miscible organic solvents to form stable nanoparticles from lipid-soluble compounds without engineering procedures or additives. Numerous drugs and drug candidates with poor solubility and bioavailability can self-assemble into highly hydrophilic and stable nanoparticles using FAST. This presentation highlights practical applications of EC16 (Epigallocatechin-3-Gallate-Palmitate, or EGCG-palmitate) nanoparticles in disease control and prevention, demonstrated by prototypes of nasal sprays, oral rinses, skin disinfectants, and a norovirus drug candidate. Results indicate that FAST significantly amplifies the antimicrobial activity of EC16, showcasing its potential to revolutionize drug development, enhance the efficacy of existing drugs, and dramatically reduce manufacturing costs.

Biography

Dr. Stephen Hsu earned a Ph.D. degree from University Cincinnati College of Medicine. He joined Memorial Sloan-Kettering Cancer Center as a Research Fellow and served as a lecturer in the National University of Singapore. He is currently a tenured professor at Dental College of Georgia, Augusta University. Dr. Hsu invented several technologies and products to treat various diseases and conditions such as xerostomia and viral infections based on results from phase II clinical trials. Dr. Hsu's NIH support is on novel virucidal disinfectants against bacterial spores, and nasal nano-drug intervention on Long COVID associated neurologic symptoms.

Sunita Girish

Dr. D. Y. Patil School of Allied Health Sciences, Pimpri, Pune, Maharashtra, India

A modulation of DNA methylation of vitamin D genes: A connecting link between vitamin D levels and grade of SARS-CoV-2 infection

The mechanistic relationship between the methylation process of the vitamin D gene and its impact on the vitamin D levels and COVID-19 infection severity remains a subject of ongoing investigation. However, lack of vaccine and targeted treatment in initial phase of pandemic has stimulated considerations regarding the potential use of vitamin D as a strategy for managing the disease. Vitamin D genes regulate the vitamin D synthesis through epigenetic changes such as methylation, which affect the various gene expressions. However, it is yet to discover how methylation controls the deficiency status and severity of COVID-19 infection. Therefore, we have investigated the relationship between low levels of vitamin D and the percentage of vitamin D gene methylation in COVID-19 patients. Our study concludes that the percent methylation of the vitamin D genes is associated with vitamin D levels and COVID severity.

Keywords: COVID-19, Vitamin D deficiency, Methylation, Vitamin D genes.

Biography

Dr. Sunita Girish studied Medical Biochemistry at the Pune University, India in 1994. She then joined the B. J. Government Medical College, Pune as a medical teacher in 1999 and worked till 2023. She received her PhD degree, Medical Biochemistry in 2004 at the same institution. She has completed Fogarty fellowship in 2013. She received her PhD degree, Genetics in 2025 at Dr. D. Y. Patil Medical College, Hospital and Research Center, Pune India. She has published more than 20 research articles various national and international journals.)

Victor J. Alexander

Capital Stem Cell Research Corporation, United States

Transforming immune therapy: A reverse pathway in B-lymphocytes for super-antibody technology to cure infectious diseases and cancer

Until today, the contemporary Adaptive Immunology is using Clonal Selection Theory (CST) as a main Theory of Adaptive Immunology for explanation of how Adaptive Immune system is working in mammals.

But after 5 years (2010-2015) of my theoretical research results did show that CST is totally wrong!

I have theoretically discovered 2 novel main mechanisms which will change whole MAI Conception and Theories and will bring very powerful novel Super-Antibody Technology for curing of all of Infectious Diseases and Cancer! My novel Discoveries are:

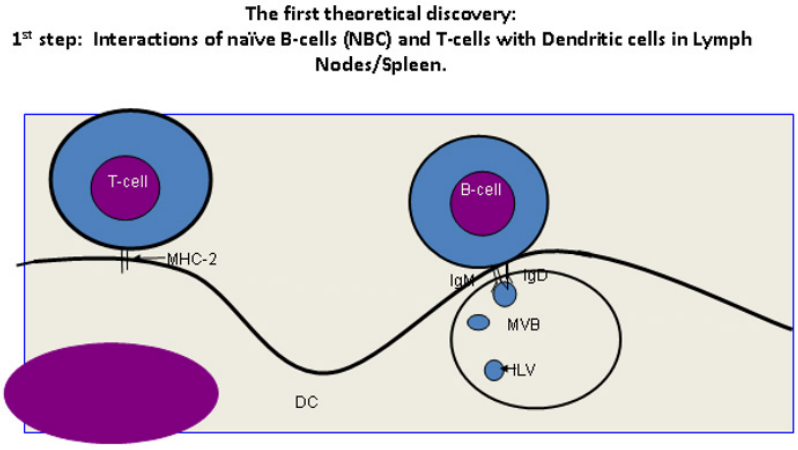
1. (First Discovery) All of NBCs which are synthesizing in bone marrow are the same structure! There is not random rearrangements as CST is alleging! All of the NBC's have on membrane surfaces the same IgM and IgD, which are not affine to any AE! They are using as a receptors for interaction with Dendritic Cells (DC) for getting one of the Intraluminal Vesicles (ILV) with Antigen Epitopes (AE) on MHC-2 from Multivesicular Body (MVB) of DC!

The cells do not have this mechanism! Th cell activation and production of massive Th-cell Cytokines depends quantities (at least 50-to 100) of AE's on MHC-2) which

Biography

Victor Alexander was born in 1952 in the Genge Region of the Azerbaijan Republic, located in the Southern Caucasus. He graduated from high school with a Gold Medal and went on to complete his medical education at the State Medical University, earning his MD diploma in 1976. He worked as a medical doctor at State Hospital #1 for three years. Have got PhD in Medicine degree and Diploma in 1984 and worked as an assistant of Professor in the Pharmacology Department and continued my Research project in embryonic, pre- and post-natal development area! Two times he was the winner of All-Union Competition of young Pharmacologists of USSR in Moscow, in 1973 and 1975. After eruption of long war between Azerbaijan and Armenia, he immigrated to USA, CA and became CA, USA citizen (2001) as an advanced PhD degree Research Scientist. From 2006 to 2008, he trained in stem cell research at UC Davis. Since 2009, he has been actively engaged in research as the President and Principal Investigator of his private stem cell research company based in Sacramento, California. Victor Alexander has

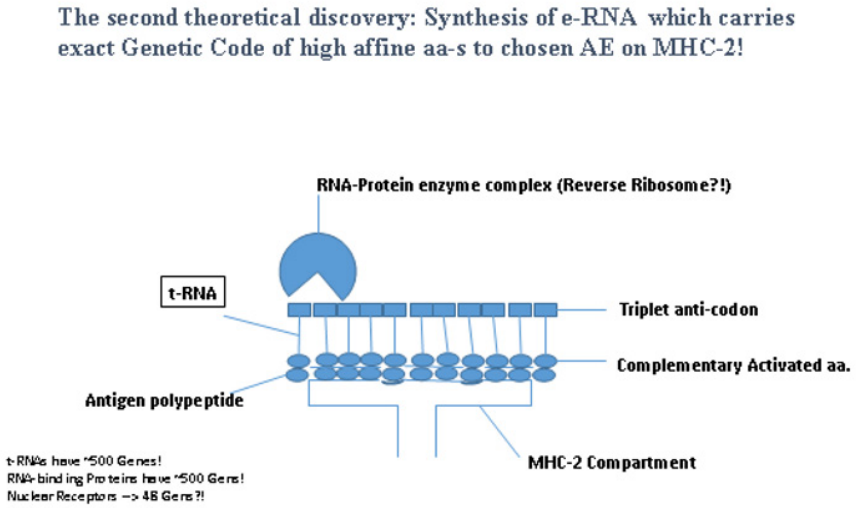
made significant contributions to theoretical adaptive immunology and is the author and originator of the novel Reverse Pathway Theory and Super-Antibody (SAb) Technology. His groundbreaking work has been recognized with Certificates of Recognition from two international congresses: The World Congress on Molecular Immunology and Immunogenetics in London (2018) and the World Congress on Biotechnology in Philadelphia (2019).



NBC has got from DC! Th cell connected with small amount of AE's on DC can't be activated by DC! Th cells just docking on the DC, but not being activated!

2. (Second Discovery) After interaction and activation Th cell by NBC, Th cell is producing massive amount of Cytokines, which are bringing activation of NBC. Under Th Cytokines, NBC produces unknown yet enzyme which connects triplets of t-RNA with activated amino-acids which are noncovalently connected with affine aa of AE and creates short endosomal RNA (e-RNA) in the endosome of NBC! Then with the help of Nuclear Receptor(s) this nascent e-RNA relocates to VDJ section of Heavy Chain (HC) and replace Replicable Module (p-N-D-N-p) of HC DNA and only after that V part of HC is coding affine aa-s to giving AE! I have call this mechanism Reverse Pathway mechanism, which explain why IgG is the first and abundant (75% of all Ig-s in the blood) and affine Ig-s in the body!

My novel conception and reverse pathway theory scientifically explain all of real processes



which are happening in molecular adaptive immunology! Contemporary CST is wrong and have to be replaced with my novel conception and reverse pathway theory, which will bring a novel and very powerful super-antibody technology for curing of all of infectious diseases and cancer!

9th Edition of

World Congress on Infectious Diseases &

5th Edition of

International Vaccines Congress

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ORAL PRESENTATIONS

Adhaar Kohli*, Rachana R

Department of Biotechnology, Jaypee Institute of Information Technology, Noida, Sec-62, Uttar Pradesh, India, 201309

Integrating next-generation vaccine technologies, immunoinformatic, and public health policy for rapid disease control: Insights from India

The rapid rise of emerging pathogens highlights the critical need for accelerated vaccine design approaches that integrate computational vaccinology, advanced immunoinformatic and scalable production platforms. Drawing from India's successful COVID-19 response and polio eradication programs, we propose an integrated framework that leverages reverse vaccinology, AI-driven epitope prediction, and in silico immunogenicity modeling to streamline the preclinical development process. In a case study using a hypothetical zoonotic virus, the complete proteome was analyzed using the IEDB and NetMHCpan pipelines, yielding candidate B- and T-cell epitopes with 87% predicted HLA population coverage. Epitope selection was narrowed down from over 150 peptides to 12 high-confidence epitopes, each demonstrating antigenicity scores above 0.8 in the VaxiJen analysis. Machine learning–based clustering and immune escape prediction eliminated redundant sequences, reducing the wet-lab validation requirements by 60%. These epitopes were subsequently mapped onto mRNA and nanoparticle vaccine platforms, with in silico simulations forecasting a 2.5-fold increase in IFN-□ responses compared to the baseline viral antigens. Simulated bioprocessing models further projected scalable yields of 5×10^{13} particles per 200-L fermenter run, with predicted thermostability exceeding 18 months at 2–8°C. Policy integration scenarios, modeled on India's polio campaign, emphasize cold-chain logistics and equitable distribution in resource-limited settings. Together, this AI-enhanced immunoinformatic framework demonstrates the potential to compress vaccine development timelines, maximize population coverage, and ensure scalable and equitable deployment, contributing to global pandemic preparedness and Neglected Tropical Disease (NTD) vaccine innovation.

Keywords: Next-Generation Vaccines, Reverse Vaccinology, Immunoinformatic, AI/ML in Vaccinology, Scalable Bioprocessing, Population Coverage, Pandemic Preparedness.

Biography

Adhaar Kohli is a final-year Integrated BTech – MTech Biotechnology student at Jaypee Institute of Information Technology (JIIT), Noida, and the first in his family to pursue higher education. Complementing his major, he is completing a Computer Science minor from IIT Mandi, driven by a deep interest in bioinformatics and biosensor development. His interdisciplinary journey has been shaped by a Molecular Imaging Fellowship at Stanford University and participation in the AI Winter School at Brown University—experiences that have honed his

approach to data-driven biological research. Under the mentorship of Prof. Rachna, Adhaar Kohli's current research integrates next-generation vaccine technologies, immunoinformatics, and public health policy to accelerate disease detection and response.

Aghapy Yermans Yakoup
Zewail City of Science and Technology, Egypt

Characterization, antibacterial, and cytotoxic activities of silver nanoparticles using the whole biofilm layer as a macromolecule in biosynthesis

Recently, Multi-Drug Resistant (MDR) bacteria are responsible for a large number of infectious diseases that can be life-threatening. Globally, new approaches are targeted to solve this essential issue. This study aims to discover novel antibiotic alternatives by using the whole components of the biofilm layer as a macromolecule to synthesize silver nanoparticles (AgNPs) as a promising agent against MDR. In particular, the biosynthesized biofilm-AgNPs were characterized using UV-Vis spectroscopy, electron microscopes, Energy Dispersive X-ray (EDX), zeta sizer, and potential while their effect on bacterial strains, and normal cell lines was identified. Accordingly, biofilm-AgNPs have a lavender-colored solution, spherical shape, with a size range of 20–60 nm. Notably, they have inhibitory effects when used on various bacterial strains with concentrations ranging between 12.5 and 25 µg/mL. In addition, they have an effective synergistic effect when combined with phage ZCSE9 to inhibit and kill *Salmonella enterica* with a concentration of 3.1 µg/mL. In conclusion, this work presents a novel biosynthesis preparation of AgNPs using biofilm for antibacterial purposes to reduce the possible toxicity by reducing the MICs using phage ZCSE9.

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 have 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. She is working currently 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, she 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.

Ahmed
BHRUT Trust, United Kingdom

The role of immunity in the pathogenesis of SARS-COV-2 and in the protection generated by COVID-19 in different age groups

This study aims to review the available data regarding the central role of immunity in combating SARS-CoV-2 infection and in the generation of protection by vaccination against COVID-19 in different age groups. Physiologically, the immune response and the components involved in it are variable, both functionally and quantitatively, in neonates, infants, children, adolescents, and adults. These immunological differences are mirrored during COVID-19 infection and in the post-vaccination period. The outcome of SARS-CoV-2 infection is greatly dependent on the reaction orchestrated by the immune system. This is clearly obvious in relation to the clinical status of COVID-19 infection, which can be symptomless, mild, moderate, or severe. Even the complications of the disease show a proportional pattern in relation to the immune response. On the contrary, the commonly used anti-COVID-19 vaccines generate protective humoral and cellular immunity. The magnitude of this immunity and the components involved in it are discussed in detail. Furthermore, many of the adverse effects of these vaccines can be explained on the basis of immune reactions against the different components of the vaccines. Regarding the appropriate choice of vaccine for different age groups, many factors have to be considered. This is a cornerstone, particularly in the following age groups: 1 day to 5 years, 6 to 11 years, and 12 to 17 years. Many factors are involved in deciding the route, doses, and schedule of vaccination for children. Another important issue in this dilemma is the hesitancy of families in making the decision about whether to vaccinate their children. Added to these difficulties is the choice by health authorities and governments concerning whether to make children's vaccination compulsory. In this respect, although rare and limited, adverse effects of vaccines in children have been detected, some of which, unfortunately, have been serious or even fatal. However, to achieve comprehensive control over COVID-19 in communities, both children and adults have to be vaccinated, as the former group represents a reservoir for viral transmission. The understanding of the various immunological mechanisms involved in SARS-CoV-2 infection and in the preparation and application of its vaccines has given the sciences a great opportunity to further deepen and expand immunological knowledge. This will hopefully be reflected positively on other diseases through gaining an immunological background that may aid in diagnosis and therapy. Humanity is still in continuous conflict with SARS-CoV-2 infection and will be for a while, but the future is expected to be in favor of the prevention and control of this disease.

Keywords: COVID-19; SARS-CoV-2; Children Vaccination; Immune Response; Multisystem Inflammatory Syndrome in Children (Mis-C); Vaccines.

Biography

Ahmed Abdulazeez graduated from the Faculty of Medicine at Yarmouk University in Jordan, ranking among the top of his class. He successfully passed the UK medical licensing exams and currently practice medicine in the United Kingdom. During his studies, he conducted research in Jordan under the supervision of Professor Zainulabdeen Abdullah, focusing on topics related to vaccines. His academic excellence and research experience have contributed to my strong interest in advancing healthcare through evidence-based practices and innovation.

Aini Syahida Mat Yassim[1*], Anis Atifah Mohd Hisham[1], Nik Nur Atiqah Nik Daud[1], Nur Diana Anuar[2], Ti-Myen Tan[2], Rapeah Suppian[1], Mat Jusoh Siti Asmaa[1,3], Amiratul Aifa Mohamad Asri[1], Maryam Azlan[1], Nur Suhaila Idris[3], Rosediani Muhamad[3], Mohd Nor Norazmi[1,4]

[1]School of Health Sciences, Universiti Sains Malaysia, 16150 Kubang Kerian, Kelantan, Malaysia
[2]Sengenics Corporation, Level M, Plaza Zurich, Damansara Heights, 50490 Kuala Lumpur, Malaysia
[3]School of Medical Sciences, Universiti Sains Malaysia, 16150 Kubang Kerian, Kelantan, Malaysia
[4]Malaysia Genome and Vaccine Institute, National Institutes of Biotechnology Malaysia, Jalan Bangi, 43000 Kajang, Selangor, Malaysia

Differential neutralizing, IgG-S and IgG-N antibody levels against circulating SARS-CoV-2 VoCs following homologous and heterologous boosting with BNT162b2: A 22-month prospective study

This 22-month cohort study investigated the durability and dynamics of humoral immune responses in 327 Malaysians vaccinated with either CoronaVac or BNT162b2 in early 2021, monitored up to 52 weeks following a BNT162b2 booster. Using the ImmuSAFE™ COVID+ microarray, we evaluated IgG-S and NAb against Wuhan-Hu and VoCs (Alpha, Beta, Delta, Omicron), as well as IgG-N responses to Wuhan-Hu.

BNT162b2 induced higher IgG-S levels and seropositivity than CoronaVac after primary immunization. While a heterologous CoronaVac-BNT162b2 temporarily increased IgG-S levels, long-term IgG-S levels and seropositivity remained comparable between the two groups across all variants. NAb levels were higher in BNT162b2 recipients than in CoronaVac recipients, with homologous BNT162b2 boosters sustaining higher NAb levels for Wuhan-Hu compared to heterologous BNT162b2-CoronaVac. However, responses to other variants varied. Expectedly, CoronaVac uniquely induced IgG-N responses, resulting in elevated IgG-N levels in heterologous BNT162b2-CoronaVac recipients compared to homologous BNT162b2 recipients. Overall, BNT162b2 boosters conferred robust and durable antibody responses regardless of the primary vaccine used. Higher IgG-N levels prior to immunization, compared to pre-pandemic levels, suggest that prior exposure to circulating SARS-CoV-2 VoCs (other than Wuhan-Hu) in Malaysia shaped immune imprinting, influencing responses before immunization with the Wuhan-Hu-based vaccine. Consequently, this study reports higher IgG-S and NAb levels against VoCs—except Omicron—compared to Wuhan-Hu after COVID-19 vaccination.

Biography

Dr. Aini Syahida Mat Yassim is a Postdoctoral Research Fellow at Universiti Sains Malaysia, supervised by Prof. Dr. Norazmi Mohd Nor. She earned her Ph.D. in Synthetic Biology (2019) and B.Sc. in Biotechnology (2012) from the University of Queensland. Her research focuses on vaccine development and immunology, particularly COVID-19 and meningococcal disease, in collaboration with Assoc. Prof. Dr. Frank Camacho Casanova. She has recently published in Vaccine and Scientific Reports, and is currently working on the development of a meningococcal vaccine targeting serogroups A, C, W, X, and Y.

PhD. cand Anila Cake*, Prof. Asc. Ergys Ramosaco
University of Medicine, Faculty of Technical Medical Sciences, Tirana

The importance of assessing the mental health of nurses and midwives from COVID 19

The mental health welfare of nurses and midwives is an urgent need that requires institutional support for professionals. Recent studies show the connection between SN and COVID 19 damages. This is the project of my PhD topic and the first study, on the impact of the mental health of nurses and midwives in Albania.

Objective: The impact of COVID 19 on the mental health of nurses and midwives in Albania.

Research methods: Descriptive research. The research question, has the outbreak of COVID 19 affected the mental health of nurses, midwives and how much do they need psychological support?

Instrument: Anonymous questionnaire with language translation and cultural adaptation, approved by its drafting team, published in Archives of Psychiatric Nursing, Psychological effects of nurses and midwives due to COVID-19, The case of Turkey Yasemin Erkal Aksoy and Vesile Koçak, there are 15 University, Municipal and Regional hospitals, which have approved the survey of nurses and midwives.

Methodology: Personal information form, state-trait anxiety inventory and intolerance of uncertainty scale, the measurement unit of the degree of damage.

Conclusion: This project will have direct benefits, the recognition of the psychological state of nurses - midwives, indirect benefits, for health policy makers in Albania and the world, to support and improve the mental health of professionals.

Keywords: Importance, Assessment, Mental Health, Nurse, Midwife, COVID 19.

Biography

Dr. Anila Cake is currently working in Department of Medical Technical Sciences, University of Medicine, Tirana, Albania. She has published numerous research papers and articles in reputed journals and has various other achievements in the related studies. She has extended his valuable service towards the scientific community with her extensive research work. She has been recognized with prestigious honors including, ‘‘2nd Global Nursing Congress’’ held during June 21-22, 2021, Berlin, Germany, “6th Edition of Nursing World Conference” held on October 27-29, 2022 in Orlando, Florida, USA, Harvard Medical School and appreciation from prestigious magazines ELSEVIER.

Asmabanu Shaikh*, Dr. Anant Marathe

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

Species identification of lactose non-fermenting isolates from ventilator-associated pneumonia using VITEK 2 and MALDI TOF MS: A comparative study with next-generation sequencing

Bacterial identification is essential for effective patient care, particularly in critical care settings with common severe infections. In most Indian laboratory settings, the VITEK 2 system is widely utilized for identifying clinical isolates and antimicrobial susceptibility testing. To assess the accuracy of bacterial identification, a comparative study was undertaken to evaluate the concordance and correlation between the VITEK 2 system and MALDI-TOF MS-based biomarker identification, with Next-Generation Sequencing (NGS) serving as a confirmatory reference method. A total of 97 isolates were recovered from blood and respiratory specimens. Subsequent identification of these isolates was performed using three distinct methods: VITEK 2, MALDI-TOF, and Next-Generation Sequencing (NGS).Our study revealed a high degree of concordance between the identification methods, with a 97% agreement rate between VITEK2 and Next-Generation Sequencing (NGS), and a 90% agreement rate between VITEK2 and MALDI-TOF MS.The VITEK 2 system is a viable and sufficient option for bacterial identification and susceptibility testing in resource-limited settings.

Biography

Asmabanu Shaikh holds an M.Sc. degree in Medical Microbiology from Baroda Medical College and is currently pursuing her Ph.D. at Parul University under the esteemed guidance of Dr. Anant Marathe. Presently, she serves as a Tutor in the Department of Microbiology. Her research endeavours have yielded four published papers in reputable scientific journals.

Bhavita Prajapati[1*], Dr. Anant Marathe[2], Asmabanu Shaikh[1], Ms. Shital Sangani[1]

[1]PhD scholar, Department of Microbiology, Parul Institute of Medical Sciences & Research, Parul University, Vadodara, Gujarat, India
[2]Professor & PhD Guide, Department of Microbiology, Parul Institute of Medical Sciences & Research, Parul University, Vadodara, Gujarat, India

Whole genome sequencing for genetic analysis of virulence factors of nosocomial extensively resistant *Klebsiella pneumoniae* isolated from different clinical specimens from ICUs

Klebsiella pneumoniae is the most common pathogen causing nosocomial infections owing to their potent virulence factors Viz. capsule, Fimbriae, siderophores, Efflux pump, regulatory secretions & secretory system. Since most of the nosocomial *K. pneumoniae* infections are MDR/XDR the treatment choice has narrowed down over time and very few options are left. It is imperative to search for other modalities of tackling this potent pathogen basically hindering the virulence factors pathways. With that view the present study comprised of study of various virulence factors by whole genome sequencing. A total of 188 *K. pneumoniae* isolates from various nosocomial infections were collected, identified by VITEK 2 as well as MALDI-TOF-MS. The present study includes 42 isolates that were subjected to WGS for study of different virulence factors.

The genes for type I fimbriae were found in all clinical specimens. Variation is seen in type III fimbriae found in isolated from Blood Stream Infections. Besides the virulence factors seen in other Enterobacterals, the *K. pneumoniae* also possessed virulence factors like enterobactin siderophore, aerobactin, salmochelin & yersiniabactin siderophores. Additional secretory system type 1 and 3 was detected in our strains and variation was observed in type 2.

Biography

Bhavita Prajapati is a Medical Microbiologist who holds a Master of Science degree in Medical Microbiology from Baroda Medical College and is pursuing a PhD at Parul University under the guidance of Dr. Anant Marathe. She presently serves as a Tutor in the Department of Microbiology and has made research contributions, including the completion of an intramural project.

Dr. Palak Badhwar[1], Dr. Bhupender Singh Khanuja[2*], Dr. Kapil Singh[3], Dr. Ashwani Verma[1]

[1]Health Systems Strengthening Unit, United Nations Development Programme, New Delhi, Delhi, India

[2]Immunization Technical Support Unit, John Snow India Private Limited, New Delhi, Delhi, India

[3]Health Section, United Nations Children's Fund, New Delhi, Delhi, India

The last mile: Addressing India's immunization gap with zero-dose insights from WUENIC estimates

This poster aims to understand the various plausible factors contributing towards shaping the burden of zero-dose children in India across the recent years i.e. 2023 and 2024 and review the efforts made by the Government of India in this direction. Multiple indicators such as immunization coverage, zero-dose children burden, antigen-wise coverage such as DPT, Measles- and Rubella-containing vaccine, BCG etc, Breath of Protection (BOP) have been assessed for India vis-à-vis Global coverage through data synthesis from WUENIC and NFHS coverage. Recent WUENIC 2024 estimates reported an immunization coverage recovery of 43% reduction in the number of zero-dose children in India from 2023 WUENIC estimates which offers vital insights about India’s resilient health care system as well as efforts made by India to address this challenge. However, there was a 2% increase in Zero dose children in India in the year 2023 WUENIC estimates even after making post pandemic recovery in immunization coverage. An attempt has been made to explore the possible reason for the rise of zero dose children by 2% as well along with factors contributing to a fall by 43% in number of zero dose children.

India has adapted a “Guidance Document on Strategic Approach for Reaching Zero-dose children in India” with an aim to vaccinate all children and leaving no one behind. The guidance document aims to define a Zero Dose Implementation plan (ZIP) through a health system strengthening approach. The poster briefly discusses the 11 interventions which have directly impacted this steep recovery of immunization coverage. Factors like pollical instability, health care worker strikes, climate change are often overlooked for their transient impact as well as poor documentation of their impact on program interventions.

The poster concludes that developing risk models that reconcile health sector information, such as immunization coverage, presence of zero dose, climate data for extreme weather impact could help predict and intervene appropriately on programmatic challenges.

Biography

Dr. Bhupender Singh Khanuja completed his graduation in Dental Surgery in 2005 and a Master's in Business Administration in 2011 from Indore, Madhya Pradesh, India. He is a seasoned Public Health Leader with over 17 years of experience in health systems strengthening, immunization, maternal and child health, and policy influence across India. For the past five years, he has been providing techno- managerial support to the Ministry of Health and Family Welfare, Government of India, in the National COVID-19 Vaccination Programme and the Universal Immunization Programme.

Carson Bridgers[1*] DO, Kathryn Kimes[2] DO, Sandra Till[2] DO, Paul Gilbert[1] MD, Brittney Adams[1] DO

[1]Honor Health Thompson Peak Medical Center, 7400 E. Thompson Peak Pkwy, Scottsdale, AZ 85255, United States

[2]Honor Health Scottsdale Shae Medical Center, 10200 N. 92nd St, Scottsdale, AZ 85258, United States

Mycobacterium abscessus complex causing rapidly progressive necrotizing pneumonia

Introduction: *Mycobacterium abscessus* complex is a group of fast growing, multidrug resistant mycobacteria that are clinically challenging to treat given rapid progression and antibiotic resistance patterns of this group. Treatment for this group requires a multidrug regimen for long durations with relatively poor overall resolution and high risk of side effects. We present a case of rapidly progressive *mycobacterium* abscessus causing necrotizing pneumonia complicated by a bronchopulmonary fistula and subcutaneous emphysema.

Case Description: Our patient is a 71-year-old female with a medical history significant for *mycobacterium abscessus* causing severe bronchiectasis previously treated with azithromycin, and hypothyroidism that initially presented with hemoptysis and shortness of breath. Initial imaging showed likely right lower lobe pulmonary artery hemorrhage, large right upper lobe cavitary lesion, and extensive right lower lobe cavitation. She underwent IR embolization for the pulmonary artery hemorrhage. Empiric antimicrobials consisting of piperacillin-tazobactam, linezolid, and voriconazole were started. She was admitted to the ICU for septic shock and acute hypoxic respiratory failure requiring intubation. On serial imaging she developed a loculated pneumothorax, the consolidative findings on the right rapidly progressed, and she developed new consolidations on the left. She also developed substantial subcutaneous emphysema that was present on imaging and physical exam. Given rapid progression and continued clinical deterioration with overall poor prognosis, the family opted to transition the patient to comfort care, and she passed shortly thereafter.

Discussion: *Mycobacterium abscessus* complex most commonly causes skin/soft tissue infections and pulmonary infections but has been associated with infections in virtually all organ systems. Treatment is due to high rates of resistance to macrolides, which comes from an inducible erm41 gene that is present in approximately 20% of isolates in the United States. Treatment to macrolide susceptible strains requires at least three medications, while treatment of macrolide resistant strains requires at least four medications. Antimicrobials commonly used include amikacin, imipenem/cefoxitin, tigecycline, azithromycin/clarithromycin, clofazimine, and linezolid. Ideal treatment duration is unclear due to a lack of robust data, but recommendations are typically to treat for at least 12 months, with at least 4 months of those being with parenteral therapy.

Conclusion: *Mycobacterium abscessus* complex infection confers significant mortality/morbidity, with up to 15% of patients experiencing impaired quality of life or death, given its rapid clinical progression and rising prevalence of resistance to antimicrobials, especially due to the erm41 gene. Treatment should ideally be started after acquiring susceptibility results and should be done in conjunction with infectious disease specialists given the need for close monitoring of progression and medication side effects. Furthermore, nontuberculous mycobacterium infections overall have several shortcomings in current treatment strategies-development of additional antimicrobial therapeutics and further delineation of optimal treatment strategies are needed. This case highlights the need for having efficacious treatment options without significant toxicity as this would likely have led to the patient pursuing more aggressive early treatment and avoiding progression of the infection to this extent.

Biography

Dr. Bridgers studied biomedical engineering at ASU in Tempe, Arizona and graduated with a BS in 2016. They went to medical school at Midwestern University in Glendale, Arizona and graduated with a DO in 2024. They are currently a resident of the Internal Medicine program at Honor Health in Scottsdale, Arizona.

Charles Ugochukwu Ibeneme[1]*, Sheillah Nsasiirwe[2], Alemeyehu Duga[1], Glory Onyeugo[1], Reena Doshi[3], Imran Mirza[3], Nebiyu Dereje[1], Marta Urrutxi[4], Neil Saad Duque[4], Chioma Ejekam[2], Alba Vilajeliu[2], Ann Ottosen[3], Chinara Israilova[3], Ajiri Okpure Atagbaza[2], Nora Sylvana Efire Emagha[1], Senga Sembuche[1], Raissa Beyande Litete[1], Ngoy Polydor Mutombo[1], Marie-Claire Therese Fwelo[1], Alexandra Hill[2], Malika Bouhenia[2], Yap Boum II[1], Fiona Braka[2], Jean Marie Yameogo[2], Abou Beckr Gaye[2], Shanelle Hall[1], Ngashi Ngongo[1]

[1]Africa Centres for Disease Control and Prevention (Africa CDC), Addis Ababa, Ethiopia

[2]World Health Organization Regional Office for Africa, Brazzaville, Republic of Congo and HQ/Geneva

[3]United Nations Children's Fund (UNICEF), New York, USA/Copenhagen, Denmark

[4]Gavi, the Vaccine Alliance, Geneva, Switzerland

Mpox vaccination in Africa: One year on – lessons and milestones from the continental response

Introduction: Mpox, long endemic in Central and West Africa, re-emerged as a continental threat during 2022–2024, with over 45,000 cases and nearly 1,500 deaths across 12 countries. The surge in Clade Ib cases in DRC and beyond led Africa CDC to declare a Public Health Emergency of Continental Security (PHECS), swiftly followed by WHO's PHEIC. Vaccination became the cornerstone of the joint continental response. To help ensure a fair, equitable and efficient distribution of mpox vaccines, the Technical Review Committee (TRC) was established by the Access and allocation mechanism to review country plans and offer recommendations for quality operational plans and advise on the allocation of doses between countries to the continental mpox Incident Management Support Team (IMST). This paper aims to explore the lessons learnt and milestones during one year of equitable distribution of mpox vaccines on the continent.

Methods: A continental Incident Management Support Team (IMST), co-led by Africa CDC and WHO with UNICEF and Gavi, coordinated vaccine access, allocation, and deployment. Data were collected from national vaccination plans, regulatory processes, and country dashboards between August 2024-August 2025.

Results: By July 2025, over 2.1 million doses were allocated over five rounds by the Technical Review Committee of the Access and Allocation Mechanism based on country requests and vaccination plans, and above 1.5 million doses of MVA-BN shipped to 12 countries, including DRC, Nigeria, Rwanda, Uganda, and Liberia. By Mid-August 2025, 9 countries had rolled out Mpox vaccination on the continent prioritizing high-risk populations which included health workers, case contacts, and vulnerable groups. Targeted rollouts and dose-sparing strategies were adopted to maximize scarce supply. Regulatory alignment through AVAREF accelerated

emergency approvals, while innovative community engagement helped counter hesitancy. Despite progress, challenges included global vaccine shortages, funding delays, and logistical bottlenecks.

Conclusion: One year on, Africa's mpox vaccination campaign demonstrates both progress and fragility. Regional solidarity, dose-sparing innovation, and integration with existing health systems strengthened the response. However, supply insecurity and funding gaps remain critical barriers. Lessons from this effort which centered on community trust, agile logistics, and strong regional coordination remain pivotal not only for mpox control but also for building Africa's preparedness against future epidemics.

Biography

Charles Ugochukwu Ibeneme is a seasoned field epidemiologist and public health expert, currently serving as a Senior Country Representative at Africa CDC and Vaccination Pillar Co-Lead for the Continental Mpox Incident Management System Team (IMST). He holds dual master's degrees in public health (MPH) - Field Epidemiology from ABU, Zaria; and Epidemiology/Disease Control from FUTO, Owerri; and PhD fellow of Texila American University. He is a GOARN Fellow, WHO Scholar, GBD Collaborator, and Technical Consultant on epidemiology and public health issues. A published author on outbreak investigations who has played a pivotal role in shaping Strategic Health Development and Preparedness Plans across Africa.

Deen Mark G. Toroy MD

Armed Forces of the Philippines Medical Center – Victoriano Luna General Hospital
Victoriano Luna Avenue, Quezon City, Philippines

Clinical profile and selected viral genome sequence analysis of SARS-CoV-2 infected pediatric patients in a tertiary military hospital in Quezon City from January 2021–July 2023: A cross sectional study

Background: SARS-CoV-2 displays distinct characteristics in terms of virulence and disease severity in pediatric population. Hence, patient's clinical profile and viral genome may contribute to patient's symptoms and disease severity.

Objectives: To determine the clinical profile and to analyze the selected viral genome sequence of pediatric patients infected with SARS-CoV-2 in a tertiary military hospital in Quezon City from January 2021–July 2023.

Methods: This is a single center cross sectional study determining the SARS-CoV-2 infected pediatric patients clinical profile consisting of age, sex, residence, comorbidities, presenting symptoms, hospitalization and disease severity. Selected samples were subjected to next generation sequencing to analyze the SARS-CoV-2 genome sequence. All data were recorded with utmost confidentiality.

Results & Conclusion: From January 2021 to July 2023, a total of 630 pediatric patients who got tested for SARS-CoV-2 RT-PCR were confirmed to have SARS-CoV-2. Two hundred thirty-nine (239) were included in this study. Among the study population, 61.51% were male, more than 60% were less than 4 years old and residing in Quezon City. In terms of clinical presentation, 78% had mild symptoms, 20% had radiologic findings of pneumonia, 40% presented with fever, 12% with diarrhea, and 8% with dyspnea. Ten percent (10%) of patients had concomitant seizure disorder. More than 70% were admitted to the hospital and all of the study subjects recovered from the illness. Only ten samples were subjected to next generation sequencing and all were Omicron variants. Majority of the SARS-CoV-2 virus belong to Clade 22B and 23E; and identified pangolin lineages were BA.5.2, BA.2.3.20, XBB.1.5, GJ.1.2 and FL.23.2.

Keywords: Sars-Cov-2, Next Generation Sequencing, Viral Variants, Clinical Outcomes.

Biography

Dr. Deen Mark G Toroy is a graduate of Biology and Doctor of Medicine from West Visayas State University. He had his Post Graduate Internship Training at the Philippine General Hospital – University of the Philippines. He is an active military officer of the Armed Forces of the Philippines. He completed his Pediatric Residency Training and currently an active Pediatric Consultant at the Armed Forces of the Philippines Medical Center. His current research was created in collaboration with the US Army Medical Component of the Armed Forces Research Institute of the Medical Sciences (USAMC-AFRIMS PH).

Deepak Jacob[1]*, Michael L J Pais[2]

[1]Department of General Medicine, Senior Resident, St John's Medical College, Bengaluru, Karnataka, India

[2]Department of General Medicine, Post Graduate student, St John's Medical College, Bengaluru, Karnataka, India

A rare encounter: Disseminated nocardiosis following myasthenia gravis treatment

Nocardiosis is an uncommon opportunistic infection caused by filamentous gram-positive bacteria of the genus Nocardia, predominantly affecting immunocompromised hosts. Immunosuppressive therapy, such as rituximab, significantly increases susceptibility to such infections. Myasthenia gravis poses a unique challenge in such cases as the aminoglycosides and fluoroquinolones are restricted to prevent exacerbations.

Here we report the case of a 45-year-old male with myasthenia gravis, diagnosed 8 months' prior, presenting with diminished vision in his right eye 20 days after receiving Rituximab. Initially diagnosed with endophthalmitis, he subsequently developed fever, productive cough, and pustular skin lesions on his chest and left forearm. A CT chest revealed cavitary consolidation in the left lingula with perifocal consolidation. Wound swabs grew filamentous gram-positive bacteria, while blood cultures grew Nocardiaspp later identified as *Nocardia farcinica*. MRI brain revealed multiple fronto-temporo-occipital abscesses, consistent with CNS dissemination.

The patient was treated with intravenous imipenem-cilastatin, cotrimoxazole, and linezolid for six weeks. By the end of this regimen, there was marked improvement in respiratory symptoms and resolution of skin lesions. Repeat MRI brain showed significant reduction in abscess size. Due to resource constraints, antibiotic sensitivity testing was not performed. The patient was discharged on oral Cotrimoxazole, planned for a 12-month course with monthly follow-up.

This case highlights the critical need for vigilance in immunocompromised patients, particularly those on biologic therapies like rituximab. Early diagnosis and prolonged combination antibiotic therapy are key to successful outcomes in disseminated nocardiosis.

Biography

Dr. Deepak did his MBBS (Bachelor of Medicine and Bachelor of Surgery) at Jubilee Mission Medical College and Research Institute, Thrissur India and completed his MD Internal Medicine at PSG Institute of Medical Sciences and Research. He currently works at St John's Medical College Bengaluru India as a Senior Resident.

Dr. Dhrubajyoti J. Debnath

Additional Professor, Department of Community and Family Medicine, All India Institute of Medical Sciences, Mangalagiri, Andhra Pradesh, India

The inherent value of human life: Navigating health economics and ethics in services for prevention of mother to child transmission of HIV

The Prevention of Mother-To-Child Transmission (PMTCT) of HIV is one of the most needed public health interventions. Effective implementation of PMTCT services will reduce paediatric HIV infections and improve maternal and child health outcomes. This presentation examines the intersection of health economics and ethics, exploring how financial constraints, policy decisions, and moral responsibilities shape the implementation and sustainability of PMTCT programs.

Health Economics Perspective:

Considering that the lifetime cost of treating an HIV-positive child is significantly higher than the cost of prevention, implementation of PMTCT guidelines becomes imperative. Without intervention, the risk of mother to child transmission of HIV ranges from 15–45%. This can be reduced to less than 2% by implementing PMTCT strategies. Countries such as the United Kingdom, Botswana, Iran, Cuba, Belarus, and Thailand have demonstrated success in PMTCT programs.

Economic aspects:

- The lifetime cost of treating a HIV-positive child can range from $200,000 to over $500,000 influenced by cost of treatment depends on the healthcare system, provision, and access to uninterrupted supply of anti-retroviral drug, drug pricing, Early Infant Diagnosis (EID), quality of care, socio-economic conditions, transport cost, social support system, government, and donor funding.
- The cost of PMTCT services per mother-child pair is estimated between $100 and $1,000. Thus, prevention of HIV infection is far more cost-effective than treatment.

Beyond individual healthcare costs, providing PMTCT services reduces long-term healthcare expenditures for the child. A child born who is HIV negative can do his/her schooling and higher studies effectively, can join an occupation of his choice making him/her economic independent thus strengthening national economies. However, despite its cost-effectiveness, funding constraints in Low- and Middle-Income Countries (LMICs) may hinder widespread implementation. Many healthcare systems in LMICs may rely on donor funding, raising concerns about financial sustainability. Integrating PMTCT into routine maternal and child health services is a part of strategy to optimize resources and ensure long-term affordability.

Ethical Considerations:

While economic factors influence healthcare decisions, PMTCT is fundamentally a human rights issue—ensuring access to life-saving interventions for both mother and child. Key ethical concerns include:

- **The Inherent Value of Human Life** – Attaching a monetary value to human life raises moral questions. Every child has the right to be born HIV-free, and financial constraints should not come in the way to access essential PMTCT services.
- **Equitable Access** – In many resource-limited settings, socioeconomic and geographical barriers prevent pregnant women from accessing PMTCT services. Addressing these disparities remains a moral obligation and a global health priority.

Conclusion: Navigating through health economics and ethics in providing PMTCT services requires a comprehensive approach. Policymakers need to ensure sustainable funding, equitable access, and the integration of PMTCT into routine healthcare services. Investing in PMTCT is not just a financially responsible decision—it is a moral imperative that safeguards future generations from the burden of HIV. Every child has the right to be born HIV-free, and financial constraints should never be a barrier to that.

Biography

Dr. Dhrubajyoti J. Debnath studied M.B.B.S. at the B. J. Government Medical College, Pune, India and graduated in 2000. He received M.D. in Preventive and Social Medicine from the same Institute in year 2006. He received his Ph.D. degree in Faculty of Medicine for research on 'HIV' from the Maharashtra University of Health Sciences, India in 2018. He did WHO Fellowship Training in Epidemiology in year 2011. He has over 19 years of teaching and research experience. He has completed several Funded and Institute supported research projects, written chapters for books and many publications in National and International journals.

Diomande Jean Louty

Alassane Ouattara university, Bouaké, Côte d'Ivoire

I. Tiembre National Institute of Public Hygiene Abidjan, Côte d'Ivoire

B Y.G. Zamina National Institute of Public Hygiene Abidjan, Côte d'Ivoire

M. Soro National Institute of Public Hygiene Abidjan, Côte d'Ivoire

W. Pierre African Field Epidemiology Network Abidjan, Côte d'Ivoire

J. B. Otshudiandjeka African Field Epidemiology Network Abidjan, Côte d'Ivoire

Analysis of measles surveillance data from the regional health center of excellence in man, Ivory Coast, January 2014 to June 2024

Introduction: Measles is a contagious viral disease that causes numerous deaths among young children worldwide, particularly in low-income countries, including Côte d'Ivoire, despite the availability of a safe and effective vaccine. The lack of surveillance data analysis led us to analyze measles surveillance data from the Man Regional Health Center of Excellence, with the aim of assessing data quality.

Method: We conducted a descriptive cross-sectional study from January 1, 2014, to June 31, 2024. Data were extracted from the MAGPI database. Measles cases recorded in the database with correct or corrected data were used for the study. Data were analyzed by person, time, and location using Excel, Epi-Info 7, and QGIS 3.36 software.

Results: 122 data were deleted as irreparable out of the total of 4800 with 11.52% missing data. The confirmation rate was 13% (635/4678) which remains underestimated because 62% of cases had no results reported. The age group of 0 to 5 years represented 63% with a median age of 2 (1 to 77) years. The sex ratio was 1.15. Vaccination status was unknown for 47.26% of cases with 22.13% of vaccinated cases. The majority of cases resided in rural areas, i.e. 85%. The highest incidences were observed in 2022 (24.69 per 100,000 inhabitants) and 2023 (20.62 per 100,000 inhabitants).

Conclusion: Missing data complicate the evaluation of vaccination efforts and the identification of at-risk populations. The high incidences noted in 2022 and 2023 indicate a worrying resurgence of the disease, especially among children under 5 years of age, requiring immediate action to strengthen public health interventions. This study demonstrates the importance of improving data quality to better understand measles dynamics and better guide health policies to reduce the morbidity and mortality associated with this disease.

Keywords: Analysis, Surveillance, Measles, PRES Man, Ivory Coast

Biography

Dr. Diomandé Jean Louty received his doctorate in medicine in 2010 from the University of Cocody, Abidjan. He held the position of chief physician at Zeo (western Ivory Coast) for eight years from 2014 to 2020. Since 2020, he has been deputy to the Regional Director of Health in Gbeke. In addition, he has a master's degree in health economics obtained in 2021 from the Allassan Ouattara University in Bouaké, advanced FETP resident.

GR Wu[1], Rui Li[1], XX Wang1, WW Zhao[1], L Cheng[2], DS Li[1*]

[1]Hubei Yuchenda Biotech Co., Ltd, Wuhan Biotech Institute

[2]Frontier Science Center for Immunology and Metabolism, Medical Research Institute, Wuhan University, Wuhan, Hubei, China

The humanized mice transplanted with edited CCR5Δ32 hematopoietic stem cells are resistant to HIV infection

The Acquired Immune Deficiency Syndrome (AIDS) remains to be an incurable fatal infectious disease, while several documented cases demonstrated that the patients with AIDS achieved clinically defined viral clearance following transplantation of hematopoietic stem cells with homozygous CCR5Δ32 from either bone marrow or umbilical cord blood. Unfortunately, the homozygous CCR5Δ32 genotype is found only 1% among European populations. Asian and other populations predominantly carry the wild-type CCR5 alleles. This genetic landscape underscores the urgent need for generating allogeneic homozygous CCR5Δ32 hematopoietic stem cells via gene editing. In this study, the authors engineered a CRISPR/Cas9 RNP complex incorporating in vitro-synthesized Chimera guide RNA and single-stranded Homology-Directed Repair (HDR) templates. This complex was electroporated into human Cord Blood Hematopoietic Stem Cells (CB-HSCs) using anionic polymer Poly-F-Glutamic Acid (PGA) as a Nano-carrier. The edited CB-HSCs exhibited up to 85% efficiency of CCR5Δ32 and the loss of protein level of CCR5 is up to 92%. Upon transplantation into the immunodeficient mice, these edited CB-HSCs successfully reconstituted the hematopoietic system in mice, yielding 85%~90% CCR5Δ32 genotype in immune cells and a 94% reduction in CCR5 protein expression. Critically, the mice transplanted with edited cells are resistant to HIV infection, comparing with its wild-type CCR5 parental mice. These results raise the potential of using CRISPR/Cas9 to produce a broader resource of CCR5△32/△32 hematopoietic stem cells, which are probably curative for the patients with AIDS.

Biography

Dr. Dong S. Li graduated from Xiang-Yale Medical College at Changsha and practiced as a neurosurgeon for 13 years before he went to UK, Canada and United States to do his post-doc, including 3 years of working at WiCell in Madison Wisconsin with Dr. James Thomson. Dr. Li has participated several national research projects such as “973” Plan and Major Project of Science and Technology Bureau, and published several his works in the prestigious journals such as Nature Biotechnology, Nature Method, Nature Protocols, etc. Presently, he is mainly focused on the cell-based gene therapy for AIDS.

Eric Tsao
Synermore Biologics, China

SYN023 mAb cocktail for rabies prophylaxis

SYN023 is a mixture of two anti-rabies humanized monoclonal IgG1κ antibodies which bind to distinct and non-overlapping antigenic sites on the rabies virus glycoprotein. A Phase 2b and a Phase 3 randomized double-blinded trials were conducted to demonstrate the safety and efficacy of SYN023 in 1448 Category III rabies patients. The analysis of the safety profile of SYN023 based on the integrated data from all 6 clinical trials demonstrated that SYN023 was generally well tolerated when administered alone or with rabies vaccine in subjects with rabies exposure as well as healthy subjects and has a favorable safety profile. The safety profile was similar to that of the currently approved HRIG in the US. Overall, the incidence of serious TEAEs throughout the studies was low (<5.0%) and similar between the SYN023 and HRIG groups. No TEAE led to study withdrawal in subjects treated with SYN023. The most common solicited TEAEs with SYN023 and HRIG were injection site swelling, injection site pain, headache, and injection site erythema. A higher incidence of these TEAEs was noted in subjects treated with HRIG than in subjects treated with SYN023. Across 6 clinical trials, RVNA appeared to be adequate at the 0.3 mg/kg dose level to rapidly establish RVNA of ≥0.5 IU/mL in the rabies-exposed person. The primary endpoint for the ISE was the GMC of the RVNA on Study Day 8 in the FAS (SYN023, N=978; HRIG, N=469). The GMC ratio of RVNA (SYN023 vs HRIG) on Study Day 8 was 13.977 (97.5% CI: 11.887, infinity; P<0.0001); SYN023 was considered superior to HRIG with respect to GMC of RVNA on Study Day 8, as the lower bound of the 97.5% CI was above the prespecified margin 1.2. The immune response (RVNA ≥0.5 IU/mL) rate ratio (SYN023 vs HRIG) was 0.99 (95% CI: 0.96, 1.01; P<0.0001); SYN023 was considered noninferior to HRIG with respect to immune response rates on Study Day 99, as the lower bound of the 95% CI was above the prespecified margin 0.9. There were no deaths, serious adverse events, or AEs leading to study discontinuation up to 365 days after dosing.

Biography

Dr. Eric Tsao has served as the Chief Executive Officer of Synermore Biologics since the founding of the company in 2013. He has over 25 years of direct experience with more than 20 products in clinical development, four US and EU approved products on the market, and eight biotech manufacturing facilities. His areas of expertise include biological product development, process design, facility engineering, and operations. Under his leadership, SYN023, an innovative anti-rabies monoclonal antibody cocktail, has been expertly developed and commercialized for rabies post-exposure prophylaxis. Since 2008, Dr. Tsao has worked with Morningside Group on biotech investments. He was instrumental in enhancing portfolio companies' CMC capabilities. Dr. Tsao was the Vice President of Technical Operations at Aeras, a Gates Foundation sponsored vaccine development

organization. At MedImmune, Dr. Tsao rose to the position of Vice President of Process and Manufacturing Sciences responsible for process development as well as manufacturing of monoclonal antibodies and recombinant vaccines. The development and manufacturing efforts led to the successful licensing of Synagis, FluMist, and Cervarix. He was a process development scientist at Johnson & Johnson, where he focused on the development of cell culture processes and start-up of the commercial manufacturing facility for erythropoietin. Dr. Tsao received his Ph.D. in Chemical Engineering from the University of Michigan.

Erika Nnodi[1*] BS, Jide Sowemimo[1], Nauri A. Roa[1], Steven A. Garzon[2] MD, Rena J. P. Linderer[1] DO, Silvana Carr[1] MD

[1]University of Illinois at Chicago, Department of Pediatrics

[2]Department of Pathology, Chicago, IL, United States

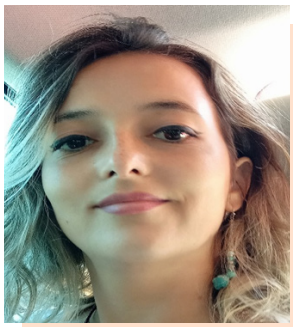
Congenital HHV-6 infection and the clinical significance of HHV6 positivity on the film array meningitis/encephalitis panel

Introduction: HHV6 is a herpesvirus ubiquitous in children known to cause Roseola Infantum. Congenital HHV6 infection is possible through germline passage of the chromosomally integrated HHV-6 DNA from a parent (ciHHV6). Less commonly, it occurs through transplacental transmission during acute infection or viral re-activation during the pregnancy. In this case study, we examine an infant found to have a positive HHV-6 (variant B) CSF PCR at birth while evaluating for neonatal sepsis. The infant's blood and placenta HHV6 PCRs were also positive and undetectable in the mother. The presence of HHV-6 in the infant's blood, CSF, and placenta raises the question the etiology of the viral congenital transmission: transplacental or a ciHHV6.

Case Report: The patient is a newborn female born at 32 weeks and 5 days GA from a 33-year-old mother via urgent C-section due to complete breech presentation with difficult extraction resulting in right head contusion with depressed skull fracture and underlying subdural hematoma at birth head CT. Pregnancy was complicated by maternal grade III heart failure and T2DM; mother tested negative for HIV with no h/o STI's or infections during pregnancy. The patient was admitted to the NICU for respiratory failure and to rule out sepsis. She was positive for HHV-6 on CSF and blood PCRs. CBC showed no cytopenia and LFTs remained WNL; CSF study revealed a bloody tap: total nucleated cells: 12, RBC: 575, glucose: 59 (40-70 mg/dl), TP: 244 mg/dl (15-45 mg/dl). IV ampicillin and gentamicin were discontinued at 36 hours due to negative sepsis on work up and resolved respiratory distress. No HHV-6-specific anti-viral therapy was given. Patient and maternal serum IgG were positive, and IgM was negative; infant's blood HHV-6 PCR was 2,600,000 DNA copies/ml and undetectable in maternal blood. A CUS at DOL #23 showed grade I IVH resolved on follow-up CUS at DOL #65. Patient was asymptomatic with adequate growth and development at 6-month follow-up.

Biography

Erika Nnodi graduated from the University of Illinois at Chicago in 2021 with a bachelor's degree in biological sciences. She spent a year working as a behavioral technician before matriculating at the University of Illinois College of Medicine in 2023. She is currently interested in pediatrics as a specialty.



Esra Çakmak Taşkın

Department of Pediatric Infectious Diseases, Kocaeli City Hospital, Kocaeli, Turkey

A case of visceral leishmaniasis in a non-endemic region

Leishmaniasis is a tropical parasitic infection transmitted by sand flies. It is sporadically seen in the Aegean, Mediterranean and Central Anatolia regions of Turkey. Here, we wanted to present a non-endemic case of visceral leishmaniasis. A 5-year-old girl was admitted to the hospital with abdominal distension and fever for 1 month. She had membranous tonsillitis on physical examination. The liver was 3 cm and the spleen was 7 cm. Laboratory tests showed pancytopenia. There were no blasts or atypical cells in the peripheral smear, and lymphocytes predominated. Ultrasonography showed hepatomegaly, massive splenomegaly and splenic vein dilatation. She had no fever during follow-up, but her neutropenia deepened. Parvovirus IgM was negative, EBV VCA IgM and IgG were positive. However, since the patient's cytopenia did not improve and splenomegaly remained the same, bone marrow aspiration was performed. Hemophagocytosis and leishmania amastigotes were seen in bone marrow smear. Leishmania PCR and serology were positive. There was no history of travel to endemic areas. The patient, whose general condition was good, was given ambizome 3 mg/kg/dose for 7 days. Splenomegaly regressed by 3 cm on the 4th day of treatment. Hemogram improved on the last day of treatment. Regression was observed in splenic vein and splenomegaly. The patient did not have hepatosplenomegaly at the 1st month follow-up. Although Kocaeli is not endemic for visceral leishmaniasis, it has been observed sporadically in recent years, with a few cases per year. Global warming and the increase in reservoirs may also be factors in this. In this case, EBV serology positivity could have caused the case to go unnoticed. However, the persistent pancytopenia and the presence of massive splenomegaly directed us to bone marrow aspiration. In conclusion, visceral leishmaniasis should be kept in mind in the presence of persistent pancytopenia and massive splenomegaly even in non-endemic areas.

Biography

Dr. Çakmak Taşkın studied Medicine at the Istanbul University, Cerrahpasa Medical Faculty, Türkiye and graduated in 2011 with a seventh place. She became a pediatric specialist in 2016. She completed her pediatric infection specialist training at Ankara University Faculty of Medicine in 2020. She currently works at Kocaeli City Hospital as a pediatric infection specialist. She has published more than 10 research articles in SCI (E) journals.

Hua Luo*, Yingxin Lin
MICU, Peking University Shenzhen Hospital, Shenzhen, China

Key thoughts and strategies based on PBL for rapid managing of suspected gram-positive bacterial infection in ICU

According to the spirit of international sepsis guidelines and clinical practice in China, we explored the rapid diagnosis and treatment ideas and strategies of different pathogenic infections in ICU to shorten the diagnosis time and improve the rescue efficiency. Taking gram-positive bacterial infection as an example, we propose ten key questions in the diagnosis process step by step by using Problem-Based Learning (PBL) method.

Question 1: According to the medical history, is the patient infected in the community or in the hospital?

Question 2: Where is the patient infected? It needs to be analyzed from multiple angles, such as intra-and extra-pulmonary, lobar and lobular distribution, alveolar lesions and interstitial lesions.

Question 3: What are the possible pathogens? Differential diagnosis between different pathogens such as bacteria, fungi, viruses, mycoplasma and tuberculosis is required.

Question 4: Is it G+ or G-bacterial infection? Based on imaging, PCT level and pathogenic cultures.

How to interpret the differences of PCT variation curve in different pathogen infection?

Question 5: Is it a pyogenic or non-pyogenic infection? In general, the presence of necrosis is often indicative of pyogenic infection.

Question 6: Is there a drug-resistant infection? Clinical manifestations, imaging, drug sensitivity and NGS results were used to judge the results.

Question 7: How virulent are bacteria? Leukocidin and decreased white blood cells may indicate bacterial virulence.

Question 8: Is there any structural lung disease? From common etiologies and imaging to aid analysis.

Question 9: What is the tissue permeability of antibiotics? The tissue permeability was analyzed from the pharmacological point of view.

Question 10: How sensitive are antibiotics? What is the effect of this medicine on bacteria and virulence?

Biography

Dr. Hua Luo, MD, Chief Physician, Director of Medical Intensive Care Unit, Peking University Shenzhen Hospital, SCIE Journal editor, and PVRI Fellow. He had specialized in Critical Care Medicine and Pulmonary Vascular Diseases. He is proficient in treating sepsis related to hematological and autoimmune disease, severe pulmonary vascular diseases, coagulation and bleeding disorders. He set up special infection cases database and Chinese largest PCT database which were recognized as one of national CCM Advances in 2015. He proposed international template of COVID-19's treatment protocol in 2020 and built Rapid Response Team (RRT) for severe infections caused by unknown pathogens.

Jeniffer Adungosi[1*], Eba Ajima[1], Seranne Motilal[1], Emmanuel Okurut[2], Clarence Mbanga[3], Lewis Kabuga[4]

[1]Child Health: Global Vaccines Programme, Clinton Health Access Initiative

[2]Vaccines Supply Chain Systems: Country Programs - Clinton Health Access Initiative, Uganda

[3]Vaccines: Country Programs-Clinton Health Access Initiative, Cameroon

[4]Vaccine Supply & Logistics: Country Programs - Clinton Health Access Initiative, Kenya

Transforming vaccines access through cost-efficient last-mile delivery models in lmics

Background: In Low- and Middle-Income Countries (LMICs), persistent vaccine stockouts at the last mile hinder Routine Immunization (RI) coverage and exacerbate zero-dose burdens, particularly in hard-to-reach areas. Traditional 'pull' distribution models often require health workers to leave facilities to collect vaccines, leading to service disruptions, out-of-pocket expenses and inequitable access. Between 2019 to now (2025) Kenya, Uganda and Cameroon piloted cost-efficient Last Mile Delivery (LMD) models that shifted vaccine transport responsibility to sub-national teams, integrated supervision into deliveries and optimized ordering and routing.

Approach: In Kenya, CHAI partnered with the National Vaccines and Immunization Programme to pilot LMD in three counties, pairing scheduled sub-county deliveries with optimized ordering cycles. Uganda tested integrated transport for vaccines and other health commodities in high zero-dose districts. Cameroon's Expanded Program on Immunization piloted LMD in four diverse districts (urban, rural and security-compromised), replacing monthly pull-based collections with direct facility deliveries and on-site formative supervision. Mixed-methods evaluations combined routine logistics data, cost analysis and stakeholder interviews to assess changes in stock availability, timeliness and expenditure. Cost analyses captured pre- and post-pilot expenditures including out-of-pocket costs previously borne by health workers.

Findings/Results: Across countries, LMD substantially reduced stock outs and improved supply chain reliability.

Kenya:

- Facility-reported stockouts dropped by ~50% and prolonged stockouts (>28 days) by ~57%.
- Distribution costs from sub-national stores to facilities fell by 61–79%.
- Pre-pilot, 52% of vaccine collection costs were paid out-of-pocket by health workers under LMD, this burden was eliminated, though some costs shifted to government budgets.

Uganda:

- Integrated delivery reduced ad-hoc trips, improved cold chain utilization, and freed staff time for service delivery.
- Cost modelling suggested savings when commodity integration was maximized, with potential to reallocate resources toward performance monitoring.

Cameroon:

- Adequate stock levels rose from 41% to 58%, stockouts fell from 38% to 23% and delivery timeliness exceeded 99%.
- The average cost per vaccinated child was ~47 FCFA, with an incremental cost of ~242 FCFA per additional child reached highly efficient given geographic and security challenges.
- Integration of other health products such as oxytocin during LMD further optimized delivery rounds.

Common enabling factors included predictable delivery schedules, embedded supervision and improved data use for ordering and allocation. Barriers included limited vehicles, road inaccessibility and perceptions among policymakers that LMD increases costs, largely due to unaccounted pre-pilot out-of-pocket spending.

Recommendations: Evidence from Kenya, Uganda and Cameroon demonstrates that LMD can transform vaccine access by reducing stockouts, lowering distribution costs and protecting health worker time.

For scale-up, countries should:

- Institutionalize LMD within national immunization operational plans, adapting models to local contexts.
- Mobilize and optimize financing, reallocating budgets to cover costs previously borne by health workers and leveraging donor support for start-up infrastructure and training.
- Integrate deliveries across health commodities to maximize cost-efficiency.
- Invest in logistics capacity vehicles, cold chain equipment and digital ordering tools to sustain reliability.
- Strengthen advocacy using cost-benefit evidence to address misconceptions and build political will.

With sustained investment and strategic adaptation, LMD offers a scalable, cost-efficient pathway to close last-mile equity gaps and accelerate progress toward zero-dose reduction in LMICs.

Biography

Jeniffer Namazzi Adungosi is a seasoned public health professional with extensive experience in health supply chains, pharmacovigilance, and immunization programs. She holds qualifications in International Health, Executive Business Administration, Health Systems Management and Pharmacy. Jeniffer currently serves as Associate, Vaccine Cold Chain Logistics at Clinton Health Access Initiative (CHAI)'s Global Vaccines Delivery team, supporting several countries including Kenya, Rwanda, Nigeria, Uganda and Cameroon. She has contributed to several peer-reviewed publications and global health summits. Her work integrates data-driven strategies, digital health solutions and stakeholder collaboration to strengthen vaccine access and health system resilience across LMICs.

Jian Shen
Qilu Medical University, China

Conserved antisense RNAs significantly inhibit pan-coronaviruses

The continuing pandemics of Severe Acute Respiratory Syndrome (SARS), Middle East Respiratory Syndrome (MERS), and novel coronavirus disease 2019 (COVID-19) underscore the urgent need for the development of anti-pan-coronavirus drugs that can target emerging coronaviruses and their variants. Despite this pressing need, there is currently no experimental report effectively targeting pan-coronaviruses. In response to this challenge, we have invented a novel strategy employing conserved antisense RNAs against pan-coronaviruses (CAR-pCoV). The promising results of our study will be presented orally during the conference.

Biography

Dr. Shen studied pharmacy at Nankai University, receiving his bachelor's degree in 2014. He then joined the research group of Professor Xinyi Lu at the State Key Laboratory of Medicinal Chemical Biology at Nankai University, receiving his doctorate in 2022. In 2023, he joined Shandong Jincheng Pharmaceutical Group Co., Ltd. as a senior R&D engineer. In 2024, he joined the faculty at Qilu Medical University, where he was promoted to associate professor. He has published 5 research papers in SCI(E) journals.

Johnson J. H. Wang
Wang Electro-Opto Corporation, Marietta, GA, USA

Scientific traditional Chinese medicine for low-cost and effective prevention, detection, and treatment of infectious diseases

COVID-19 pandemic, sweeping the world from November 2019 to April 2025, is estimated to have caused 18 to 34 million deaths. Confirmed deaths were 7.1 million, of which 1.2 million happened in the United States—the richest country with best vaccines, medical equipment and facilities. Furthermore, confirmed deaths per population in the U.S. were among the highest, at 3493/million, while death rates in Far East Asian countries were among the lowest—between 85/million in China and 1076/million in Malaysia. Consistent with these data, since late 2020, a top expert practicing Traditional Chinese Medicine (TCM) in South Korea has been claiming the curing power of his TCM herb medicine against this coronavirus infection. Recently, he summarized that he had successfully cured sixteen-thousand patients worldwide having respiratory diseases, including infection, allergy and cancer, over the past fifty years, at low cost and achieving whole-body health.

Indeed, since 1990 healthcare systems in advanced nations have been degrading rapidly, with rising costs, rampant chronic diseases, and aging demographics. In response, governments and private sectors have been seeking solutions from untapped fields, such as the 47-century-old TCM. Today, TCM is included in the national health care systems, as integrative and complementary health care, in major countries of East Asia, used by 60-75% of the population. Elsewhere, TCM operations are still in back alleys. TCM's dilemma is rooted in its inability to meet the standards of science and evidence-based modern medicine.

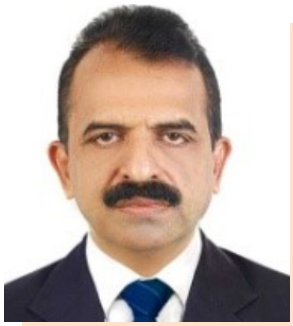
In 2018 this author began to develop a scientific theory of Chee based on modern sciences and seven postulates. ("Chee" was coined to differentiate from the commonly used "qi.") The theory was formulated by following the pioneering footsteps of Albert Einstein in his creation of the theory of relativity and Julius Stratton in his consummating macroscopic Electromagnetic (EM) theory, and by leveraging this author's experience in numerical computations and EM measurements. The first postulate is that Chee is a vector power intensity containing four components: Electromagnetic (EM), Mechanic (ME), Thermal (TH), and Biochemical (BC), denoted by χEM, χME, χTH, χBC, respectively. TCM procedures were distilled and synthesized, one by one, to metamorphose TCM to Scientific TCM (STCM). Theoretical results were presented in four IEEE international symposiums and published in medical journals.

Empirical validation and characterization of the canonical biomarker Chee were successfully conducted using oscilloscopes, with the understanding that its frequency is between 0.1 and 200 Hz, limited by its source—neurons. Modulated by the 60 Hz AC power supply in America, EM component of Chee is a robust periodic function with a stable frequency of 60 Hz. Preliminary results were published in 2025 and will be summarized and updated in this conference. Tests on the ME and TH components of Chee, χME and χTH, were also conducted; but their data lack the accuracy, richness, and significance of the EM components.

Our findings are giving rise to new and fundamental visions for biology, physiology, and medicine, which should have broad impact on diagnosis, treatment, and prevention of infectious diseases, among others. STCM procedures of acupuncture, herb medicine, Tui Na, cupping, etc. should be able to provide effective low-cost measures to prevent, diagnose, and treat infectious diseases.

Biography

Dr. Johnson Wang studied Electrical Engineering at National Taiwan University, Taiwan and graduated as BSEE; received MS from Florida State University, Tallahassee, FL; and PhD from Ohio State University, Columbus, OH in 1968. After serving as Geophysicist at Arctic Research Institute, Ice Field Range Glacier, in 1968, he worked in four companies in defense-aerospace industry. Dr. Wang served in the faculty of Georgia Institute of Technology, Atlanta, GA during 1975-1995. Since 1991 he has been Chief Scientist and President of Wang Electro-Opto Corporation. He has presented and published numerous research papers, including an advanced textbook in electromagnetic theory and numerical computation.



Yacob Mathai Kunnathazhath
Marma Health Centre, Kaloor, Kochi, Kerala, India

Why is the vaccine life-threatening if people get a fever after a COVID-19 vaccination?

If the body becomes inflamed after consuming a substance, our immune system tells us that the substance is against the body. If the substance further increases inflammation, reduces blood flow, and affects organ function, the substance is life-threatening. Vaccination is given to protect against various diseases like flu, polio, measles, mumps, rubella, diphtheria, tetanus and COVID-19. After vaccination, most people experience a fever. It can occur up to two weeks after the shot and can last for two or three days. Also, muscle pain, headache, chills, and joint pain, soreness or swelling at the injection site, restlessness, fatigue, loss of appetite, vomiting, runny nose, cough, and a faint red rash, puffy eyes. These things are the same in many deadly diseases. If these complications occur when the vaccine is not taken, it is considered a symptom of many deadly diseases, from the common cold to cancer.

If fever is a symptom, the question should be what is post-vaccination disease? Can the vaccine cause a disease that was not present in the body before vaccination? Why is the injection site sore after vaccination? After vaccination, is infection at the injection site a disease or a symptom? After vaccination, muscle atrophy and loss of flesh at the injection site is not a fatal disease? What is the treatment for post-vaccination disease? Many such questions need to be answered. Fever is one of the least knowledgeable topics in modern science. The science of fever is unknown to modern science.

After vaccination, the body becomes inflamed because the toxic substances in the vaccine do not adapt to the body. The immune system created a local temperature at the site of the vaccine injection. Initially, blood flow increases at the injection site. As swelling increases and the swelling spreads to nearby organs, blood flow to other parts of the body is reduced. During this time, the immune system produces a fever to reduce inflammation and increase blood flow. Decreased blood flow due to severe inflammation is the sole trigger for fever. Fever occurs within two weeks of vaccination. Some experts mistake fever as evidence that the immune system is responding to the vaccine. No need to wait two weeks for immunity to respond to the vaccine. Fever often occurs after vaccination due to temperature-reducing treatment and reduced blood flow due to inflammation.

If we look closely, we can see that the effects and side effects after vaccination are due to increased inflammation and decreased blood flow. Studies have shown that milk production decreases for a few days in both humans and animals after vaccination. Milk is produced from blood. When blood flow decreases, milk production also decreases. Studies have shown a decrease in milk production and supply during lactation following the COVID-19 vaccination. The number of women affected by decreased milk supply ranged between 5% after a first dose and 23% after a second dose. Post-vaccination swelling and reduced blood flow can be life-threatening. Inducing fever to increase blood flow during this time is a life-saving strategy. The danger is not the fever after vaccination, but the increased inflammation and reduced blood flow. Fever is always a protective shield of the immune system to increase blood flow and prolong the life of an organ or system.

Giving paracetamol to prevent and reduce fever after vaccination is a hundred times more dangerous to life. There is a fundamental contrast between the basic action of fever and the basic action of paracetamol. The essence of today's fever treatment is fever can be cured by using fever-creating substances. In India - Kerala, patients were given paracetamol to prevent fever after COVID-19 vaccination. Paracetamol is given to reduce prostaglandin E2. It is not a fever-causing substance. It has hyperthermic and anti-inflammatory properties. As a result, blood flow is reduced due to inflammation in the body. During this time, the immune system produces fever to increase blood flow and reduce inflammation to protect life and organs. For fever, when the blood flow is reduced due to inflammation, reducing the heat is not compatible with any current science in the world, because reducing the heat will increase the inflammation again, reduce the blood flow again, and even cause death. During this time, immunity does not stop producing fever.

Post-vaccination swelling and reduced blood flow can be life-threatening. Inducing fever to increase blood flow during this time is a life-saving strategy. The danger is not the fever after vaccination, but the increased inflammation and reduced blood flow. Fever is always a protective shield of the immune system to increase blood flow and prolong the life of an organ or system. Giving paracetamol to prevent and reduce fever after vaccination is a hundred times more dangerous to life. There is a fundamental contrast between the basic action of fever and the basic action of paracetamol. The essence of today's fever treatment is fever can be cured by using fever-creating substances. Paracetamol is given to reduce prostaglandin E2. It is not a fever-causing substance. It has hyperthermic and anti-inflammatory properties.

In India - Kerala, patients were given paracetamol to prevent fever after COVID-19 vaccination. Taking paracetamol after COVID vaccination to prevent or reduce fever is twice life-threatening. Kerala has seen the highest number of deaths after the COVID-19 vaccination. So the only solution to fever is to reduce inflammation and increase blood flow. This is an immutable scientific fact. Not knowing what the temperature of the fever is and not knowing the correct mode of action of paracetamol is the cause of giving paracetamol after vaccination and increasing deaths due to it. If people had not been given paracetamol after vaccination, the inflammation would not have worsened and so many people would not have died.

Keywords: Vaccination, Antipyretics, Life-Threatening, Immune System, Infection.

Biography

Yacob Mathai is practicing physician in the field of healthcare in the state of Kerala in India for the last 34 years and very much interested in basic research. His interest is spread across the fever, inflammation and back pain. He is a writer. He already printed and published Ten books on these subjects. He wrote hundreds of articles in various magazines. After scientific studies, we have developed 8000 affirmative cross checking questions. It can explain all queries related to fever.

K. R. Aneja[1,2*], Ashish Aneja[3]

[1]Honorary Professor and Research Advisor, Sardar Bhagwan Singh University, Barawala, Dehradun-248161 (Uttarakhand), India

[2]Former Professor and Chairman, Department of Microbiology, Kurukshetra University, Kurukshetra-136119 (Haryana), India

[3]Medical Officer, University Health Centre, Kurukshetra University, Kurukshetra, Haryana, India – 136119

Immunosuppression in COVID-19 patients and emerging fungal infections: Vaccines, diagnosis and strategies to treat comorbiditiesacy

The incidence of fungal infections, called mycosis, has dramatically increased in COVID-19 patients with predisposing factors. COVID-19, not over and still circulating worldwide, is a respiratory illness caused by strains of coronavirus SARS-CoV-2 (Severe Acute Respiratory Syndrome Coronavirus-2). It is a highly transmissible, contagious airborne, positive-sense single-stranded RNA virus. This disease was first of all reported in December 2019 from the city of Wuhan, China, and was declared as a pandemic on 11 March, 2020 by WHO and continued till May 2023. It has been ranked as the 5th deadliest pandemic or epidemic in the human history that caused over 7 million deaths of the 777 million people affected globally, as of 22 December 2024. The vaccination is widely credited for its role in reducing the transmission of infection, disease severity, creating herd immunity and saving millions of lives from COVID-19. The COVID-19 vaccines that were granted Emergency Use Authorization (EUA) by WHO during 2020-2021 include: Pfizer/BioNTech vaccine, COVAXIN Bharat Biotech, Covishield Oxford/AstraZeneca, Spikevax Moderna vaccine and Janssen Johnson & Johnson. Globally, 67% of the total population has been vaccinated with a complete primary series of a COVID-19 vaccine, creating herd immunity. As of 12 August 2024, 13.72 billion doses of vaccines have been administered worldwide. If vaccines could not have been developed in short duration of time and got emergency approval for usage from the WHO, there would have been billions of deaths and very few of us would have been here to see the new day.

COVID-19 has increased human fungal infections, because of its effect on the immune system leading to severe illness and death. Body's defences against fungal pathogens also lower due to COVID-19 treatments like steroids and other antiviral drugs. Comorbidities or fungal coinfections i.e., patients having both a fungal infection and COVID-19 at the same time, might have been missed or misdiagnosed resulting to death of several thousand patients. Symptoms of certain fungal infections (e.g., fever, cough and shortness of breath) are similar to COVID-19. For proper, effective and safe treatment of patients suffering due to comorbidities, laboratory diagnosis is of utmost importance to know whether a patient is suffering from a virus, a fungus, or a bacterium. The most common COVID-19-associated mycoses reported are: aspergillosis, invasive candidiasis (due to *Candida auris* and *C. albicans*), pulmonary mucormycosis (black fungus disease due to mucoraceous molds), cryptococcosis, and fungal pneumonias (histoplasmosis, coccidioidomycosis, blastomycosis). The need of the hour is to lay emphasis in identifying potential fungal coinfection with COVID-19 and other microbial infections that

can reduce diagnosis and treatment delays for preventing severe illness and deaths from such infections.

Biography

Dr. Aneja got his B.Sc., M.Sc. and PhD degrees from Kurukshetra University Kurukshetra. He has a vast research and teaching experience of 38 years in Botany, Microbiology and Biotechnology. He joined the teaching faculty in the same Institute and served as Professor & Chairman for 11years. He is the recipients of many Awards and Fellowships, the major one's are INSA-Royal Society Academic Exchange Fellowship, Best Citizens of India, Rashtriya Gaurav and ISWA lecture awards. He is the 2022 Lifetime Achievement Awardee and past President of the Mycological Society of India; Recorder of ISCA; Shiksha Rattan Samman, and 2023 Unnat Bharat Shewa Shree Award. He has supervised 23 PhD scholars & over 35 M.Phil. students; published 180 research papers/ reviews/chapters; over 50 abstracts, attended over 35 National and International Conferences, delivered lead lectures and chaired several sessions; authored/co-authored 15 books, edited 5 books, written2 manuals, and Proceedings of an International Conference published by International Publishers (04) and National Publishers (19). He served as the Governor's/Chancellor's nominee for Teacher's selection at Punjabi university, Patiala. Currently, he is serving as an Honorary Professor & Research Advisor in Sardar Bhagwan Singh University, Dehradun (Uttarakhand), a Member of the Research Advisory Committee of ICAR Weed Research Centre, Jabalpur, M.P, India and an Expert Member of the ICFRE, Dehradun.

Kapil Goel[1*], Vineeth Rajagopal[1], Vivek Sagar[1], Rahul Gupta[1], Kanika Paruthi[1], Amudhamozhi KS[1], Neeraj Arora[2], Arun K Aggarwal[1], Radha K Ratho[3]

[1]Department of Community Medicine and School of Public Health, PGIMER, Chandigarh, India
[2]Department of Microbiology, Civil Hospital, Panchkula, India
[3]Department of Virology, PGIMER, Chandigarh, India

From mystery to clarity: A public health investigation into unexplained deaths in the Himalayan foothills, India

Background: Acute Febrile Illness (AFI) is a major public health challenge in tropical and subtropical regions, particularly during monsoon seasons when vector-borne diseases such as dengue, malaria, and scrub typhus increase. During August-September 2022, an unusual cluster of sudden mystery deaths was reported in Kalka sub-division of Panchkula–the Himalayan foothills, amidst a rise in Acute Febrile Illness (AFI) cases. The absence of a definitive diagnosis led to an urgent investigation to identify the cause and assess its public health implications.

Methods: A cross-sectional observational study was conducted by the Department of Community Medicine and School of Public Health, PGIMER, Chandigarh, between August and September 2022. Verbal autopsies were performed using the standardized Sample Registration System (SRS) questionnaire with consent from the deceased's relatives. Medical case records were reviewed, and environmental and entomological assessments were conducted to identify potential vector breeding sites. Epidemiological data from the Integrated Disease Surveillance Programme (IDSP) were analyzed to assess trends in AFI cases. Data were analyzed using SPSS v22, with descriptive epidemiology presented in terms of time, place, and person variables.

Results: Verbal autopsies were conducted for 18 out of 26 reported deaths. The mean age of the deceased was 23.9 years (SD=13.4), with a male-to-female ratio of 1.57. The highest mortality (44%) was observed in the 15–29-year age group. Fever was present in all cases, along with symptoms such as nausea, vomiting, muscular pain, chills, and abdominal discomfort. Complications included shock (83%), multi-organ dysfunction (44%), and bleeding manifestations (22%).

Medical records confirmed that 13 deaths were caused by dengue and its complications, while 4 were categorized as probable dengue based on clinical and epidemiological evidence. Delayed diagnosis, inadequate clinical monitoring, and improper administration of intravenous fluids were identified as contributing factors. Entomological assessments revealed the presence of Aedes aegypti mosquitoes and active breeding sites in affected households. IDSP data indicated a sharp rise in dengue cases, with laboratory confirmation of Dengue virus serotype 2. Epidemiological linkage was established in 11 cases through the presence of confirmed dengue cases among family members or neighbours.

Conclusion: The study confirms that the mystery deaths in Kalka subdivision were due to dengue and its complications, primarily dengue shock syndrome and hemorrhagic manifestations. The findings highlight the need for improved AFI management, including early diagnosis, timely clinical intervention, and judicious fluid management. Strengthening epidemiological surveillance, enhancing healthcare preparedness, and promoting community-driven vector control measures are crucial for preventing future outbreaks and reducing dengue-related mortality.

Keywords: Acute Febrile Illness, Outbreak, Dengue, Verbal Autopsy, Epidemiological Investigation, Entomological Surveillance, Public Health.

Biography

Dr. Kapil Goel is an Assistant Professor of Epidemiology at PGIMER, Chandigarh, India with over 20 years of experience in public health. He holds an MD in Community Medicine from Manipal University and is an alumnus of India's Epidemic Intelligence Service. His expertise spans Epidemiology of communicable and non-communicable diseases, public health emergencies, disease surveillance, vaccinology, and maternal-child health. He has worked with WHO, UNICEF, and CDC, published over 80 research papers, and led 30+ projects. A mentor in prestigious programs like India EIS and WHO-AEP, he is a life member of several public health associations and a National level trainer of Epidemiology.

Kundoly Velayudhan Suseela

Department Microbiology, Amala Institute of Medical Sciences, Thrissur, Kerala, India

Increased incidence of nontyphoidal salmonella infections following COVID 19 outbreak: Is it an impact of the pandemic?

Infection by Nontyphoidal Salmonella (NTS) is considered a zoonotic food poisoning of animal and poultry origin.NTS gastroenteritis is a major cause of diarrheal illness worldwide, which is usually self limiting. NTS can also cause extraintestinal manifestations and serious complications such as septicemia, particularly in very young, elderly, and immunocompromised patients.

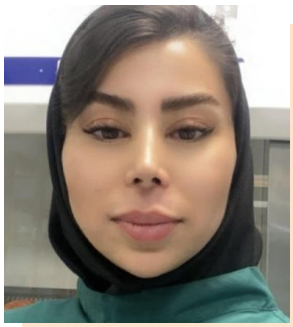
Following the relaxation of the COVID 19 Outbreak lockdown, in a tertiary care centre, admissions of NTS infection showed a two fold rise compared to pre COVID years.

We examined 2312 and 937 stool samples collected during the pre COVID and post COVID outbreak period, respectively. The number of samples collected during the outbreak (2020) was 273. During the pre COVID 19 period (2015–2019), the average annual isolation rate of NTS was 5.63%. During the lockdown of 2020, the corresponding rate was 5.49%. The isolation rate showed a significant rise (11.45%) during the relaxation of the lockdown ($P<0.001$). No significant change in resistance to antibiotics other than ciprofloxacin was noted. Malignancy was the leading comorbid condition (11.91%) followed by chronic liver diseases (10.31%).

The role of CD4 deficiency leading to NTS infection is well known. The long term impact of COVID 19 infection in the immune system leading to NTS diarrhea and septicemia should be studied in detail.

Biography

Dr. K V Suseela graduated from Gov. Medical College, Thrissur, Kerala, India and received MD degree in Microbiology from Govt. Medical College, Kozhikode, Kerala, India. Currently, she is working as Professor and Head of Microbiology department, Amala Institute of Medical Sciences, Thrissur, Kerala, India. She had published more than 20 research articles in peer reviewed national and International journals. Prof. Dr. Suseela has keen interest in bacteriology research.



Leila Salimi[1*], Reza Rahbarghazi[1,2]

[1]Stem Cell Research Center, Tabriz University of Medical Sciences, Tabriz, Iran

[2]Department of Applied Cell Sciences, Faculty of Advanced Medical Sciences, Tabriz University of Medical Sciences, Tabriz, Iran

Exosome-based vaccine for the therapy of cancer

In recent years, the extracellular vesicles have been used as theranostics in different pathological conditions. Extracellular vesicles include different subsets such as exosomes (these are the smallest of the extracellular vesicles, ranging from 30-150 nm in diameter. They originate from the endosomal pathway and are released via exocytosis), apoptotic bodies (these vesicles are the largest extracellular vesicles, with sizes ranging from 500-5000 nm. They are formed during programmed cell death), and microvesicles (these vesicles are larger than exosomes, typically ranging from 50-1000 nm. They are formed by budding directly from the plasma membrane) with different production machinery system. Besides, emerging data have indicated the potency of these nanosized particles to harbor parent cell antigens and metabolites. The metabolic status can alter the cargo sorting and sequestration of several factors into the luminal space. Therefore, any pathological conditions with a genetic and proteomic signature can be assessed using exosomes. So, monitoring these factors can help us to confirm the incidence and progression, and even follow up on the therapeutic protocols. Different studies confirm the integrity of cancer cell-associated antigens and distribution into various biofluids. Therefore, monitoring and studying cancer cell exosomes are valid tool for the early-stage diagnosis of tumors. It is also possible that the immunization of immune cells with cancer-associated exosomes is helpful to activate both cellular and humoral responses. Therefore, it is logical to use these particles as vaccination tools in sensitive individuals against different cancer types. Taken together, the future will witness the splendid progress in the application of cancer cell exosomes in cancer patients along with conventional therapeutic protocols.

Biography

Dr. Leila Salimi completed her Master's degree in Biochemistry at the University of Zanjan and Tabriz University of Medical Science jointly in Iran. Her academic performance was exceptional, as reflected in her GPA of 19.64 out of 20. She obtained a TOEFL degree, demonstrating her proficiency in English. She then joined the research group of Prof. Reza Rahbarghazi at the Stem Cell Research Center, Tabriz University of Medical Sciences, Iran. She joined Springer Nature as a peer reviewer. Currently, she is studying for a PhD degree in Regenerative Medicine (Stem Cell) at Tabriz University of Medical Sciences. She is proud to have successfully published papers and chapters with a 9 h-index.

Jerome Nyhalah Dinga[1], Leontine Kouemou Sinda[2*], Vincent P. K. Titanji [1,3]

[1]Biotechnology Unit, Faculty of Science, University of Buea, P.O. Box 63, Buea, Cameroon

[2]Department of Microbiology and Parasitology, Faculty of Science, University of Buea, P.O. Box 63, Buea, Cameroon, School of Medical and Biomedical Sciences SLHERF (Saint Leonard Health and Research Foundation) University Institute Limbe, P.O.box : 752 Limbe, Cameroon

[3]Faculty of Science, Engineering and Technology, Cameroon Christian University Institute, P.O. Box 5, Bali, Cameroon

Assessment of vaccine hesitancy to a COVID-19 vaccine in Cameroonian adults and its global implication

Since the outbreak of COVID-19 in December 2019, no global consensus treatment has been developed and generally accepted for the disease. However, eradicating the disease will require a safe and efficacious vaccine. In order to prepare for the eventual development of a safe and efficacious COVID-19 vaccine and to enhance its uptake, it is imperative to assess vaccine hesitancy in Cameroonians. After obtaining ethical clearance from the Institutional Review Board of the University of Buea, a questionnaire was administered (May–August 2020) to consenting adults either online or in person. A qualitative thematic analysis was done to analyze the participants' answers to the open questions. A déductive approach was used, that is, the codes and patterns according to the World Health Organization (WHO) Strategic Advisory Group of Experts (SAGE) working group matrix of déterminants of vaccine hesitancy. The number of consenting adult Cameroonians who completed the questionnaire were 2512 (Two thousand five hundred and twelve). Vaccine hesitancy to a COVID-19 vaccine was 84.6% in Cameroonians. Using the WHO recommended matrix of déterminant of Vaccine hesitancy, the most prominent determinants observed in this study were : Communication and Media Environment, Perception of pharmaceutical industry, Reliability and/or source of vaccine and cost. most Cameroonians agree that even though there are benefits of a clinical trial, they will prefer it should be done out of the continent and involving African scientists for eventual acceptance and uptake. The concerns of safety, efficacy and confidence has to be addressed using a public engagement approach if a COVID-19 vaccine has to be administered successfully in Africa or Cameroon specifically. Since this study was carried out following WHO standards, its result can be compared to those of other studies carried out in different cultural settings using similar standards.

Keywords: COVID-19 Pandemic, Vaccine Hesitancy, Vaccine Acceptance, Clinical Trials, Cameroon

Biography

Dr. Leontine Kouemou Sinda (PA, MS and PhD) is the Founder/CEO of Saint Leonard Health and Research Foundation (SLHERF) Founder/Rector of SLHERF University Institute Limbe, Cameroon. Team leader of mobile rural health Partner : Humanitarian Without Borders of Saint Leonard Health and Research Foundation Cameroon. Licensed Physician Assistant, Infectious Diseases specialist from the Faculty of Medicine and Biomedical Sciences University of Yaoundé 1. Expert in International Cooperation and Humanitarian Action from IRIC, University of Yaoundé 2. Reseacher on hospital acquired MRSA, antimicrobial resistance and COVID-19 vaccine hesitancy in Cameroon. She is a Dedicated community team worker with a focus on giving back to underserved, less privileged remote communities for the empowerment of more youths, women and childrenin who live remotely in Cameroon and Africa through health, education, entrepreneurship and skills acquisition with a vision for equal access to quality primary health care and higher education for all, justice, peace and sustainable development in Africa. With SLHERF multidisciplinary team Dr. Leontine Kouemou Sinda has strategically created an integrated, sustainable, and decentralized model which could revolutionize both healthcare capacity and delivery to the most vulnerable and elevate local nurses to providing care within remote communities, as such a foundation is laid for a continuously expanding community-based health system.

Manuel Sierra*, Juan Pablo Bulnes, Guimel Peralta, Sara Rivera, Alcides Vargas, Frances Durón, Gabriela Murillo, Gabriel Ortez, Gexy Mendoza Hernández, Melany Verónica Flores, Lisbeth Madrid, Mirna Hernández, Nicolle Suazo

Facultad de Ciencias de la Salud, Universidad Tecnológica Centroamericana, Tegucigalpa, Honduras

Post COVID-19 syndrome is associated with sex and severity of first COVID-19 episode in Honduras

Background/Introduction: COVID-19's pandemic has had a catastrophic global impact, with nearly one billion reported infections and seven million deaths worldwide. By the middle 2020, several studies described the so-called long COVID syndrome as an emerging and prevalent syndrome, with a highly diverse set of symptoms that persist long after a confirmed SARS-CoV-2 infection. There is a wide range in the frequency of Post-COVID-19 Syndrome (PCS), ranging 5%-90%. The purpose of the study is to estimate the prevalence of PCS and its association with sex and severity of first COVID-19 episode.

Methods & Materials: A cohort of last-year medical students from the Faculty of Medical Sciences (UNITEC) assigned by the Ministry of Health to Primary Health Clinics (PHC), during 2022-2023, participated in the study. The protocol was approved by UNITEC's Bioethical Committee. Only subjects that were diagnosed with COVID-19, usually by a RT-PCR test during years 2020-2021 were included. A convenience sample of adults that consecutively attended PHC participated. Date of first COVID-19 episode was established as well as the severity of disease. A 12-week-period after the first COVID-19 symptom appeared was estimated and subjects were asked for the presence and duration of PCS' symptoms by body organ and systems.

Results: A total of 2967 participated, 59.6% female, 20.3% 51 or more years of age, 71.6% overweight-obese, 17.4% hypertension and 12.2% diabetes mellitus. For first COVID-19 episode: 29.6% asymptomatic, 60.8% mild disease, 6.6% hospitalized, 2.0% severe disease and 0.4% admitted to intensive care unit. PCS' Prevalence was 51.5% (95% CI: 49.7%-53.3%), prevalence was higher for females 55.6% (95% CI: 53.3%-57.9%, $p<0.001$) than males 45.4% (95% CI: 42.7%-48.3%). For subjects with Mild-Asymptomatic disease PCS' Prevalence was lower: 47.2% (95% CI: 45.3%-49.1%) compared to persons that reported Hospitalized-Severe disease 92.2% (95% CI: 88.4%-94.9%, $p<0.001$).

Discussion: There are very few studies of Post-COVID-19 Syndrome (PCS) in low-and middle-income countries. Convenience sampling, while it's a quick and cost-effective method, it comes with limitations, mainly the potential for sampling bias. Our sample may not represent the entire population affected by COVID-19 accurately. Taking into account this limitation, our study provides insightful evidence on the prevalence of PCS in Honduras and the association with sex and severity of first COVID-19 episode.

Conclusion: PCS' prevalence was 51.5% and it was higher for females (55.6%) and for individuals who reported Hospitalized-Severe disease for the first COVID-19 episode (92.2%).

Biography

Dr. Manuel Sierra graduated from T Chen Harvard School of Public Health obtaining an MPH in epidemiology and a PhD with concentration in Tropical Pubic Health and Infectious Diseases. Dr. Sierra was called to assess the national response to the pandemic. He has published several articles and a couple of books related with COVID-19. Dr. Sierra coordinates research at the Faculty of Health Sciences (UNITEC).

Matheus de Oliveira Nogueira[1*], Nadielle Castro Pereira[2], Adrya Suellen dos Santos Souza[2]

[1]Afya Faculty of Medical Sciences, Manacapuru, Amazonas, Brazil

[2]Coordination of Graduate Studies, Research, Extension, Innovation and Internationalization, Afya Faculty of Medical Sciences, Manacapuru, Amazonas, Brazil

Water quality and intestinal health: Assessment of access to treated water and the prevalence of endoparasitosis in Manacapuru, interior of the Amazon Region

Background: Parasitic infections persist as a global public health challenge, with the Brazilian Amazon region showing an alarmingly high prevalence of cases. This situation is particularly critical in the interior areas of Amazonas state, where the precariousness of basic sanitation exacerbates the problem. The scarcity of scientific studies in these remote locations hinders a comprehensive understanding of the real impact of parasitic infections on local populations. Consequently, there is an urgent need for research in this area to inform effective public health interventions and significantly improve the health conditions of these vulnerable communities.

Objective: Analyse the impact of access to treated water and the source of water used for consumption on the prevalence of parasitic infections in Manacapuru, a municipality with a population of 101 thousand inhabitants located in the interior of Amazonas state, Brazil. Evaluate the prevalence of intestinal endoparasitosis through spontaneous sedimentation and questionnaire.

Methods: The research will be conducted at the Central Laboratory of Clinical Analysis in Manacapuru, Amazonas, Brazil, between October 2024 and February 2025. It will involve 300 volunteer patients who will respond to a detailed questionnaire about access to and quality of consumed water. Concurrently, parasitological analysis of fecal samples from these patients will be performed using the spontaneous sedimentation method.

Results: The research results will provide a comprehensive analysis of the relationship between water access, consumption patterns, and the transmission of parasitic infections in Manacapuru. Data analysis will reveal the correlation between water quality and parasitosis prevalence, highlighting the most common parasites in the municipality.

Conclusion: The research will contribute to understanding risk factors and developing effective strategies for prevention and control of parasitic infections, while the results will guide sanitation and health policies aimed at reducing parasitic diseases in the region.

Biography

Matheus Nogueira is a third-year medical student at Afya Faculty of Medical Sciences in Manacapuru, Amazonas, Brazil. He demonstrates a great interest in medical research, driven by the belief that scientific inquiry can directly improve patient care and benefit society at large. Currently, Matheus is actively engaged in the Scientific Initiation program at Afya Faculty of Medical Sciences, focusing his research efforts on the field of parasitic diseases. His dedication to this area of study reflects his commitment to addressing significant public health challenges prevalent in the Amazon region.

Meseret Girma[1,2*], Prof. Tefera Belachew[1,3], Dr. Zelaem Tafesse[2]

[1]School of Public Health. Arba Micnch University, Ethiopia
[2]School of Nutrition & food Science Technology, Hawassa University, Ethiopia
[3]Nutritionand Dietetics Department, Faculty of Public Health, Jimma University, Ethiopia

Optimal complementary feeding practices and associated factors among children 6–23 months old in Konso Zone, South Ethiopia

Introduction: Despite the critical importance of complementary feeding, large proportions of children in developing countries are sub-optimally fed during 6–23 months of age. In Ethiopia, even though the government has been rolling out Infant and Young Child Feeding (IYCF) guidelines, the proportion of mothers adhering to the recommended optimal practices and its associated factors have not been assessed in Konso Zone Southern Ethiopia. Hence, the present study aimed to determine optimal complementary feeding practices, barriers and associated factors in Konso Zone, South Ethiopia.

Method: A community-based comparative cross-sectional study was conducted at Konso Zone in South Ethiopia among 337 randomly selected mothers having children 6 to 23 months of age from May 10 to June 30 /2024. Data were collected using a pre-tested interviewer-administered questionnaire. Data was collected using Kobo tool box and exported to SPPS Version 25 for analysis. Multivariable binary Logistic regression was used to predict the role of independent variables on optimal complementary feeding. Findings with a p-value <0.05 at a 95% Confidence Interval (CI) were considered statistically significant in the final model.

Result: The overall proportion of mothers with optimal complementary feeding practice was 14.8%. The timely initiation of complementary feeding, minimum meal frequency, minimum dietary diversity and minimum acceptable diet was 63.20% 92.60%, 20.50%. Age of mothers, exchange of food items from market and access to fruit and vegetables were significantly associated with optimal complementary feeding practices.

Conclusion: The findings showed that OCFP was low in study setting. Nutrition education and counseling should be provided to mothers focusing on promoting not only timely initiation of complementary feeding but adequate in diversity, appropriate frequency and consistency using variety of foods combination to accommodate the nutritional needs of the growing child while continuing breastfeeding.

Keywords: 6–23 Months of Age Children; Complementary feeding practice; Optimal.

Negar Seyed

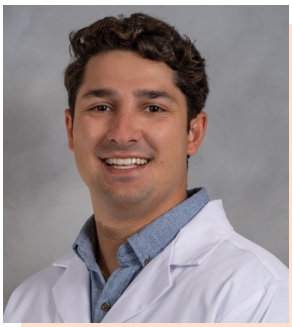
Pasteur Institute of Iran, Department of Immunotherapy and Leishmania Vaccine Research, Tehran, Iran

New biomarkers in *Leishmania major* vaccine development

Leishmaniasis (a sandfly0borne disease) is caused by the unicellular parasite from *Leishmania* genus and is already a major thread in tropical and subtropical regions of the world but the distribution map could shift to other regions due to climate change. Unfortunately, no vaccine for human is available in the market despite decades of labor-intensive experimental work. The underlying reason is the lack of knowledge around Leishmania-host-sandfly interplay which makes the vaccine design and development a complex issue. Very recently some new correlates of protection as biomarkers have been investigated including Ly6C+ T effector cells and Resident Memory T cells. These are the lessons learned form leishmanization with *Leishmania major* parasite in experimental C57BL/6 model. Our field experience has also confirmed that leishmanization remains the one and only effective vaccine formulation with the highest protection rate ever however the in-built drawbacks has hampered the general administration. Although many different vaccine formulations exist and almost every single protocol has been examined in the context of Leishmania, none has successfully passed to replace leishmanization except for live attenuated and live-nonpathogenic parasites and somehow DNA-based vaccines. This indicates that we need more investigation to further deconvolute the underlying molecular interactions at the single-cell genome/epigenome, transcriptome, proteome and metabolome level of early-stage infection to define the exact protection biomarkers before we could take steps toward effective vaccine.

Biography

Negar Seyed, an assistant professor of Medical Biotechnology in profession. She have a Bachelor of Science in Cellular and Molecular Biology from Tehran University and a Master of Science in Medical Immunology from Shahid Beheshti University of Medical sciences. She was a research assistant in Cellular and Molecular Research Center in Shahid Beheshti University of Medical Sciences for five years before she started her Ph.D in Pasteur Institute of Iran. She graduated in Medical Biotechnology mastering vaccine design and immediately started her career as assistant professor at Pasteur Institute of Iran in 2012. Since, country Iran is an endemic area for a parasitic disease known as leishmaniasis, She have focused on vaccine design against the cutaneous form of this disease right after winning the position. During the past years, she have trained master and Ph.D students on this subject and She continuously strive to inspire and empower interested people through her work. To this end, she is always seeking new challenges and opportunities for thriving.



Nikolas Minanov[1*] M.S., Yusuke Terasaki[2] M.D.

[1]Wayne State University School of Medicine, Department of Cardiothoracic Surgery
540 E. Canfield St, Detroit MI 48201

[2]Detroit Medical Center Harper University Hospital, Department of Cardiac Surgery
3990 John R Street Detroit, MI 48201

A case of aortic root abscess and repeated prosthetic aortic valve dehiscence in the setting of rare infection with *Cellulosimicrobium cellulans* and *Corynebacterium tuberculostearicum*

Cellulosimicrobium cellulans and *Corynebacterium tuberculostearicum* are commensal skin flora that rarely cause human infection. Due to their ubiquitous nature, blood and tissue cultures identifying these organisms are regularly dismissed as contaminants, delaying appropriate antibiotic treatment. However, over the past two decades, there have been increasing instances of infection from these organisms and are associated with significant mortality.

A 60-year-old female with a history of ventriculoperitoneal shunt and congestive heart failure from severe aortic regurgitation presented with dyspnea on exertion. After appropriate workup, she was admitted to cardiac surgery and underwent aortic valve replacement and coronary artery bypass grafting. During the procedure a non-purulent aortic root abscess was noted and debrided. Blood cultures taken at this time returned negative. She had uncomplicated postoperative course and was discharged on post-operative day 23. Approximately four months after the procedure, the patient presented to an outside hospital with acute shortness of breath. Echocardiogram showed valve dehiscence and she was emergently taken to the operating room where the valve was found to be circumferentially dehisced. The aortic root annulus was repaired and a valve replacement performed for the second time. The patient was discharged on post-operative day 18 to subacute rehab. Four months after the second operation, the patient returned to the primary hospital with left sided chest pain and shortness of breath. Echocardiogram showed severe aortic regurgitation secondary to a recurrent valve dehiscence. The patient was taken to the operating room for an aortic root replacement and again tissue cultures remained negative. Due to repeated valvular dehiscence the patient was started on empiric ceftriaxone and vancomycin and intra-operative tissue cultures were sent out for Polymerase Chain Reaction (PCR) testing. The PCR identified *Cellulosimicrobium cellulans* and *Corynebacterium tuberculostearicum* as the infectious agents and the patient was continued on appropriate treatment following sensitivity studies. She was discharged in stable condition on one month of daily vancomycin with planned lifetime Bactrim prophylaxis.

Cellulosimicrobium cellulans and *Corynebacterium tuberculostearicum* are exceedingly rare drivers of infections in humans. As such, these organisms are routinely discarded as contaminants of blood and tissue cultures. Through this case, we show that these organisms should be taken into consideration in cases of prolonged culture negative infection, especially in patients harboring foreign bodies or in immunocompromised states.

Biography

Nikolas Minanov, M.S. is a medical student at Wayne State University School of Medicine in Detroit, Michigan. He completed his Master of Science in Molecular and Integrated Physiology. He is clinically interested in surgical and post-operative infections.

Niranjan Nayak[1*] MBBS, MD; Dharm Raj Bhatta[2] PhD; Niraj Thapa[3] MS, MCh; Supram HS[4] PhD, Rajani Shrestha[4] MBBS, MD; Deependra Hamal[5] BDS, MD; Kamana Chhetri[6] MBBS; Sampada Subba[6] MBBS; Shishir Gokhale[7] MBBS, MD

[1]Professor and Head, Dept of Microbiology, Pokhara Manipal College of Medical Sciences, Pokhara, Gandaki, Nepal

[2]Professor, Dept of Microbiology, Pokhara Manipal College of Medical Sciences, Pokhara, Gandaki, Nepal

[3]Professor, Dept of Urology, Pokhara Manipal College of Medical Sciences, Pokhara, Gandaki, Nepal

[4]Assistant Professor, Dept of Microbiology, Pokhara Manipal College of Medical Sciences, Pokhara, Gandaki, Nepal

[5]Lecturer, Dept of Microbiology, Pokhara Manipal College of Medical Sciences, Pokhara, Gandaki, Nepal

[6]Postgraduate student, Dept of Microbiology, Pokhara Manipal College of Medical Sciences, Pokhara, Gandaki, Nepal

[7]Professor, Dept of Microbiology, and Principal, Pokhara Manipal College of Medical Sciences, Pokhara, Gandaki, Nepal

Bacteria or kidney stones: Which came first?

Background: Urinary Tract Infection (UTI) due to *Salmonella typhi* is uncommon, though there are scanty reports of bacteriuria caused by nontyphoidal Salmonellae and other gram negative bacilli. However, cases of bacteriuria with UTI due to nontyphoidal Salmonellae were more frequently reported in the past, among individuals having urolithiasis.

Case study: We, herein, report a case of *Salmonella typhi* bacteriuria with urolithiasis in a woman aged 35 years, having poor socio-economic background and coming from the rural belt of western Nepal with inadequate and hygienically unsatisfactory drinking water facility.

Results: Multiple renal stones were detected in the Ultrasonography (USG) of the abdomen and pelvis advocated as part of the investigations in the management of multiple episodes of bleeding Per Vagina (PV), the woman was complaining of.

Bacterial culture of both the stone and urine sample showed the growth of *Salmonella typhi* with similar antibiogram profile.

Conclusion: Our report highlighted the association of renal stone with urinary excretion of Salmonella Typhi. Isolation of the organism from the crushed out material of the renal stone as well as from the urine could suggest the persistence of the organism in the stone matrix being excreted from time to time giving rise to intermittent bacteriuria.

Based upon the clinical radiological and laboratory findings in the present case, an attempt has been made to unravel the poorly understood mechanism of urinary career state in *Salmonella typhi* infection.

Keywords: Salmonella, Urinary stones, Biofilm, Typhoid carrier.

Biography

Dr. Niranjan Nayak, Professor and Head of Microbiology at the Manipal College of Medical Sciences, a 500 bedded teaching hospital in Pokhara, Nepal is a retired Professor of Microbiology from the All India Institute of Medical Sciences (AIIMS) New Delhi, India. He has 107 research publications to his credit. He participated in more than 35 national/international conferences, where he presented his research and/or chaired scientific sessions. He supervised the thesis works of a number of PhD and MD students in Microbiology. He regularly teaches MBBS and postgraduate (MSc and MD) students. He devotes time in teaching, research, patient care.

Omar Malik[1*] BSA; Ernesto G. Miranda-Morales[2] PhD; Jorge R. Fernandez[2] MD; Sara Dann[3] PhD; Ashok K. Chopra[4] CSc, PhD; Xiang Fang[1,2,5] MD, PhD, FAAN, FANA

[1]John Sealy School of Medicine, The University of Texas Medical Branch, Galveston, TX, USA

[2]Department of Neurology, The University of Texas Medical Branch, Galveston, TX, USA

[3]Department of Internal Medicine, The University of Texas Medical Branch, Galveston, TX, USA

[4]Department of Microbiology and Immunology, The University of Texas Medical Branch, Galveston, TX, USA

[5]Moody Brain Institute, The University of Texas Medical Branch, Galveston, TX, USA

Infectious disease risk among patients prescribed amoxapine or trifluoperazine: A retrospective cohort study using real-world data

Rising rates of antimicrobial resistance combined with the lack of new antibiotic development has brought new focus to drug repurposing strategies. Early evidence suggests that certain centrally acting psychotropic drugs, including Trifluoperazine (TFP) and Amoxapine (AXPN), may have antimicrobial or immuno-modulatory properties. However, their effects on infection risk in human populations remain poorly understood. The current study aims to evaluate whether exposure to TFP or AXPN is associated with altered risks of infectious illnesses and of systemic inflammation compared to fluoxetine, a commonly prescribed antidepressant which has been shown to have some benefits in these settings.

To evaluate potential differences in rates of infectious diseases and inflammation, a retrospective cohort study was conducted by collecting human data via TriNetX, a federated network of de-identified electronic health records that together cover over 75 million patients across multiple healthcare systems. Study data included patients aged 18-90 who received a TFP, AXPN, or fluoxetine prescription. Eligible candidates were identified and classified into mutually exclusive, non-overlapping cohorts. Age- and sex- matched cohorts between TFP and fluoxetine, and between AXPN and fluoxetine, were compared on six outcomes, including: C. difficile infection, pneumonia, sepsis, COVID-19, neutrophilia, and increased C- reactive protein. Risk Ratios (RR), Odds Ratios (OR), 95% confidence intervals, and p-values were calculated to evaluate differences between fluoxetine cohorts and their corresponding age- and sex-matched treatment groups. Outcomes that achieved statistically significant differences between groups were analyzed further using Kaplan-Meier survival analysis.

Study results showed that TFP use was associated with a significantly lower risk of *C. difficile* infection (p=0.007), COVID-19 (p=0.002), and higher levels of CRP (p=0.045) when compared to that prescribed fluoxetine. On the other hand, statistical differences in incidences of pneumonia, sepsis, or neutrophilia were not found between TFP and fluoxetine users.

Additionally, Kaplan-Meier analyses supported a lower cumulative incidence of COVID-19 and *C. difficile* in patients treated with TFP compared to fluoxetine controls. In contrast, when AXPN users were compared to fluoxetine users, AXPN did not show significant differences in incidence for any of the six outcomes examined.

As a retrospective observational study, the results of the study are limited due to residual confounders and therefore do not support causal inferences. Data limitations preclude adjusting for adherence to medications, dosing, or risk behavior, which could not be controlled for in this observational study. Additionally, the analysis relied on coded diagnosis, which may have been variably reported across health systems.

Nevertheless, in comparison to those prescribed fluoxetine, patients receiving TFP were associated with reduced incidence of severe infectious and inflammatory conditions, suggesting potential repurposing opportunities in infection treatment. These findings call for further mechanistic and clinical investigations to evaluate TFP's therapeutic role under infectious disease conditions. Although AXPN may still be associated with benefits of infectious or inflammatory conditions, it showed no such differences in incidence of these outcomes when compared to the standard treatment drug, fluoxetine.

Biography

Omar Malik is a second-year medical student at the University of Texas Medical Branch (UTMB). He graduated from The University of Texas at Austin with a BSA in Neuroscience and a BA in Health and Society, earning the university-wide Distinction in Research for his work investigating art therapy's pain modulation effects in orthopedic populations. During medical school, he joined the clinical research team of Dr. Xiang Fang, Chair of Clinical Research in the Department of Neurology. He currently works with professors in UTMB's Departments of Internal Medicine, Microbiology, and Immunology to assess antibiotic drug repurposing potential of psychotropic medications.

Patrizia Russo[1,2*], Laura Vitiello[1,2], Dolores Limongi[1,2], Fabrizio Maggi[3], Guido Antonelli[4], Stefano Bonassi[1],

[1]Department of Human Sciences and Quality, Life Promotion San Raffaele University, Rome Italy

[2]IRCCS San Raffaele, Rome Italy

[3]Laboratory of Virology, National Institute for Infectious Diseases, Lazzaro Spallanzani IRCCS, Rome, Italy

[4]Department of Public Health and Infectious Diseases, Sapienza University of Rome, Rome, Italy

TTV-virome analysis for predicting immune dysfunction and clinical outcomes in COPD patients

Introduction: Torquetenovirus (TTV), the main representative of the Anelloviridae family, is a non-pathogenic virus whose blood viral load reflects immune competence. Elevated TTV levels (≥4 log10 copies/mL) have been associated with immunosuppression, clinical frailty, and poor outcomes in patients with Chronic Obstructive Pulmonary Disease (COPD). This study investigated the role of TTV viremia as a potential biomarker of immune status and prognosis in COPD.

Methods: Serum samples from 102 COPD patients were analyzed for TTV load by real-time PCR. Peripheral blood mononuclear cells were subjected to immunophenotypic analysis of T lymphocyte subsets (CD3, CD4, CD8, and regulatory T cells [CD25+ CD127–]). Statistical analyses included Fisher's exact test, Mann– Whitney test, and Spearman's rho coefficient (SPSS v23).

Results: TTV viremia >4 log10 copies/mL was detected in 62.75% of patients. Higher TTV load was significantly associated with reduced CD3+, CD4+, and Treg lymphocytes and with lower 5-year survival probability, likely related to Treg depletion.

Conclusions: COPD patients with TTV levels ≥4 log10 copies/mL showed impaired immune function and reduced survival. TTV viremia may represent a novel biomarker of poor prognosis in COPD and could contribute to the development of personalized rehabilitation strategies based on immune status.

Biography

Prof Patrizia Russo, PhD in Microbiology, works at San Raffaele University in Rome as an Associate Professor of Pathology and History of Medicine. She is UO (Operational Unit) responsible for the grant: TTV-virome prediction of dysregulated immunity and clinical differential diagnosis n. B53D2300376006/G53D23000700001 AWARDED by MUR (Ministry of University and Research) in Rome, Italy, from 2023 to 2025. Her h-index is 39 according to Scopus, and she has 187 published works. Her Scopus Author ID is 57192333601, her ORCID ID is 0000-0003-1745-7827, and her RESEARCH ID is J-8767-2016.

Pawandeep Kaur[1]* MD, Jose Arriaga Flores[1] MD, Lee Connor[2] MD

[1]Internal Medicine Resident Physician, Hamilton Medical Center, Dalton, Georgia, US

[2]Infectious Disease Specialist, Hamilton Medical Center, Dalton, Georgia, US

Unveiling the uncommon pathogenesis of *Streptococcus gallolyticus* subspecies pasteurianus bacteremia and its link to gastric pathology

Background: While *Streptococcus gallolyticus* subsp. gallolyticus has a well-known association with colorectal cancer, an epidemiological association between *S. gallolyticus* subsp. pasteurianus and hepatobiliary diseases has been suggested. Herein, we present a unique case of S. gallolyticus subsp. pasteurianus bacteremia in a patient with a complex medical background, including autoimmune hepatitis, liver cirrhosis, and multiple potential gastrointestinal sources. A detailed gastrointestinal evaluation also revealed a bleeding gastric polyp and colonic tubular adenomas. With evolving understanding of its association with gastrointestinal pathologies beyond colorectal cancer, it opens an intriguing area for future research into its potential link to gastric conditions.

Case Presentation: A 73-year-old female with a past medical history of autoimmune hepatitis on azathioprine, chronic anemia, COPD, type 2 diabetes mellitus, paroxysmal atrial fibrillation, and hypertension presented with complaints of let foot swelling for one day, generalized weakness, and back pain for the past two weeks. Approximately one week prior, she was admitted to an outside hospital with similar complaints of back pain. MRI scans of the lumbar spine and pelvis revealed degenerative changes throughout the lumbar spine and possible compressive pathology at the L5 nerve root on the left. Thereafter, she was discharged with pain medications and muscle relaxants.

Upon arrival at our facility, her vital signs were as follows: temperature 37.6°C, heart rate 82, and blood pressure 114/83. Physical examination was notable for a grade 2 systolic murmur over the precordium, erythema and warmth over the lateral aspect of the left foot, and tenderness to palpation. Laboratory results on admission showed a white blood cell count of 6.3, hemoglobin 8.1 g/dL, platelets 251, CRP 9.1 mg/L, proBNP 614 pg/mL, ESR 104 mm/h, and lactate 1.5 mmol/L. Iron studies revealed an iron level of 16µg/dL, TIBC 202 µg/dL, iron saturation 8%, and ferritin 75 ng/mL suggestive of iron deficiency anemia. The patient was started on IV ceftriaxone every 24 hours for suspected foot cellulitis, and gastrointestinal consultation was requested to evaluate the anemia for possible GI etiology. Blood cultures obtained on admission grew *Streptococcus gallolyticus* subspecies pasteurianus on both aerobic and anaerobic broths after two days of incubation, and the patient was continued on ceftriaxone 2g every 24 hours per susceptibility testing. A transthoracic echocardiogram revealed a possible vegetation on the anterior mitral valve leaflet and a prior finding of mild mitral valve regurgitation. A

transesophageal echocardiogram confirmed the presence of a small vegetation on the posterior mitral valve leaflet, measuring 5 mm x 6 mm near the commissure. The EGD revealed a 10 mm semi-pedunculated hyperplastic polyp with active bleeding in the gastric cardia, which was removed, clipped, and injected with epinephrine. Colonoscopy revealed seven tubular polyps which were removed. Her repeat blood cultures were negative. While all this was ongoing, the patient continued to have lower back pain which continued to worsen, especially with movement. A repeat MRI of the lumbar spine and pelvis showed findings concerning for L4/L5 discitis with adjacent mild osteomyelitis of L3 and L4, and a small epidural abscess spanning the L4 vertebral body. Due to the need for neurosurgical intervention, she was transferred to a higher-level facility. There, she underwent laminectomy with drainage of the epidural abscess, but the cultures from the abscess did not reveal any growth. Her antibiotic regimen was changed to Penicillin G 24 million units IV daily via continuous infusion to complete a total of six-week course of antibiotics. A repeat TEE, performed 11 days after the prior one, revealed no valvular vegetation's. Azathioprine was withheld for the course of her infecHon.

Conclusion/Discussion: Numerous studies have established a strong association between *S. gallolyticus* subsp. pasteurianus bacteremia and underlying hepatobiliary disease, as well as, though much less frequently, colonic pathology. Notably, our patient had a long-standing history of liver cirrhosis secondary to autoimmune hepatitis. Immunosuppressive therapy with azathioprine and prednisone could have also played a role.

Unlike the well-established link between *S. gallolyticus* subsp. gallolyticus (formerly bovis biotype I) and colorectal carcinoma, there is limited information on S gallolyticus subsp. pasteurianus bacteremia and its connection to gastrointestinal pathology. With no specific treatment guidelines available, a colonoscopy is recommended if the source of infection remains unidentified. Apart from association with colorectal carcinoma, a few cases have also reported S. gallolyticus bacteremia originating from other seemingly benign sources, such as cellulitis or colonic adenomas.

In our case, apart from multiple risk factors as discussed above, the potential sources of infection could include intestinal adenomas or a bleeding gastric polyp. Existing literature primarily focuses on the association with colonic pathology, and there is no documented link between gastric polyps and S. gallolyticus bacteremia. This presents an intriguing area for further research and exploration to better understand potential associations with gastric pathologies. The need for upper GI endoscopy apart from thorough colonic and hepatobiliary–pancreatic assessment should also be considered in appropriate clinical settings.

Biography

Dr. Pawandeep Kaur completed her MBBS from Government Medical College, Patiala, India in 2021. She then joined the Internal medicine residency program at Hamilton Medical Center, Dalton, Georgia in 2023. Dr. Kaur has a deep interest in the field of infectious diseases and is currently pursuing her medical career with a focus on this specialty.

Percival C. Dilla MD
Conner District Hospital, Philippines

Association between cardio metabolic risk factors and COVID-19 severity in patients of a rural tertiary hospital

Background: The COVID-19 pandemic has had a significant impact on the world leading to significant morbidity and mortality. The disease was caused by the SARS-CoV-2 virus and can caused severe respiratory illness, as well as a range of other complications depending on presence of cardio metabolic risks. These factors included a range of conditions such as obesity, high blood pressure, high cholesterol, and states of insulin resistance. People with these risk factors are hypothesized to more likely experience severe COVID-19 symptoms and have worse clinical outcomes.

Objective: To determine the association between cardio metabolic risk factors and the development of severe COVID-19 patients in rural tertiary hospital in Bayombong, Nueva Vizcaya.

Methods: We reviewed the medical records of patients aged 19 years or older with A Real-Time Polymerase Chain Reaction (RT-PCR)–confirmed COVID-19 hospitalized at the Region II Trauma and Medical Center in Bayombong, Nueva Vizcaya. A retrospective correlation design was utilized for the study, using a review of the medical records of patients from March 2020 to December 2022. Fasting Plasma Glucose (FPG), Low Density Lipoprotein-Cholesterol (LDL-C) levels, Hypertension, BMI, Waist to hip ratio and demographic characteristics of the patients were recorded. A simple and multiple ordinal logistic regression was done to checked the association between COVID-19 and different independent variables. All analyses were performed using STATA SE 18.0, with a p-value of less than 0.05 as the cut-off to determine statistical significance.

Result: We enrolled 1,582 participants; most were 50 to 59 years old (24.3%), Male (57.7%) and unvaccinated. When we compared our patients' Hyperlipidemia, FBS and Hypertension directly correlate with length of stay while Myocardial Infarction, Atrial Fibrillation and waist to hip ratio inversely correlate with length of stay measured during the pandemic and the pre-pandemic period, we found a statically significant increased (<0.05). Specifically, older patients, with hyperlipidemia, those with confirmed diabetes and elevated BP had a higher probability of staying in the hospital for more than a week while those with MI, AF, and higher WHR tend to stay shorter. In- hospital mortality, COVID patients with Myocardial Infarction 27.3 times (OR: 27.3, p<0.001), Atrial Fibrillation 5.8 times (OR: 5, p<0.001), and high 2 BP 10.4

times (OR: 10.4, p=0.007) odds of dying compared when they don't have these conditions. Crudely, vaccination decreased the odds of having severe COVID-19, while the rest of the predictors, aside from sex, type 1 DM, and obesity increase the odds. On multiple ordinal logistic regression analysis, however, only vaccination status was associated with decreased severity of COVID-19. Specifically, a vaccinated patient has 53% less odds of having severe COVID-19.

Conclusion: This study demonstrates the consequences of Diabetes Mellitus, Hypertension, Hyperlipidemia and Cardiovascular Disease showed significant associations with mortality and Clinical Severity of patients. Moreover, Age, Male, and Co-morbidities were significant confounders for the associations of Cardio metabolic Risk Factors on COVID-19 mortality and clinical severity.

Percival C. Dilla MD
Conner District Hospital, Philippines

A rare case of meningitis and septicemia due to *Streptococcus acidominimus*

Background: *Streptococcus acidominimus* is mainly recognized as a veterinary pathogen; however, it can lead to severe infections in humans, especially in those with pre-existing health issues. Proper identification and timely treatment are essential for effectively managing these infections. To date, only a limited number of cases have been documented regarding bacterial meningitis caused by *S. acidominimus.* Furthermore, there are no recorded instances of bacterial meningitis or septicemia attributed to *S. acidominimus* in the Philippines. In this report, we present a case of bacterial meningitis and septicemia resulting from *S. acidominimus,* which exhibited sensitivity to beta-lactams, in a 37- year-old male employed as a swineherd.

Keywords: *Streptococcus acidominimus*, Meningitis, Septicemia

Rachana R*, Aadhaar Kohli

Department of Biotechnology, JIIT Noida, Sec-62, Noida, UP, India

Yeast-derived exosomes as a transformative platform for next-generation vaccine development

The persistent global demand for safer, more effective, and rapidly scalable vaccine platforms has driven innovations beyond traditional formulations. Exosomes, a class of nanosized Extracellular Vesicles (EVs), represent a revolutionary approach owing to their inherent biocompatibility, stability, and crucial role in intercellular communication. While the primary focus has been on exosomes derived from mammalian cells, exosomes released by yeast (YEVs) share fundamental characteristics with their mammalian counterparts, including a lipid bilayer and a similar size range of 25–250 nm, but exhibit unique advantages rooted in their host organism. The yeast cell wall contains powerful immunomodulatory components, such as β-glucan and mannoproteins, which are incorporated into YEVs. These components function as natural adjuvants, activating innate immune cells, such as macrophages and dendritic cells, and upregulating key maturation markers, such as CD40, CD80, and CD86. A recent study reported a 2-5-fold upregulation of these markers after exposure to YEVs, demonstrating their intrinsic adjuvanticity. This unique property can eliminate the need for separate immune-boosting additives, thereby streamlining vaccine design. This effect is mediated by the binding of yeast-derived β-glucans to Dectin-1 receptors on antigen-presenting cells, a well-characterized pattern recognition mechanism that triggers a potent downstream inflammatory and pro-immunogenic cascade. Furthermore, yeast's well-established industrial bioproduction infrastructure offers a clear pathway for scalable manufacturing, which is a critical bottleneck for other EV platforms. The ability to genetically engineer yeast to express and package specific vaccine antigens into YEVs further enhances the versatility and precision of this platform. Although challenges remain, particularly in standardizing isolation protocols and deciphering non-canonical biogenesis pathways in yeast, the synthesis of biological and industrial advantages positions YEVs as a highly promising avenue for developing effective, easily administered, and potent vaccines, particularly for oral delivery.

Keywords: Exosomes, Yeast, Vaccines, Extracellular vesicles, Adjuvants.

Biography

Professor Rachana has been with the Department of Biotechnology at Jaypee Institute of Information Technology since June 2009. Previously, she worked at SPTM, NMIMS University, Mumbai. She completed her postgraduate studies in Biotechnology at IIT Roorkee (1998) and earned her PhD from IIT Bombay (2006). She qualified NET-LS and GATE, topping the Kanpur zone. She holds two Indian patents, authored 3 textbooks, and contributed to 60 international publications. A fellow of Biotechnology Society of India, her work focuses on molecular mechanisms of plant-based treatments for diseases like ARDS, asthma, diabetes, cancer, and Alzheimer's.

Dr. Rakshand Shetty[1*], Griffin Stinson[2] BS

[1]KMC Hospital, MAHE, Manipal, Karnataka, India

[2]University of Florida College of Medicine, Gainesville, Florida

Management of infected aortobifemoral bypass graft with ureteral fistula in a patient with complex vascular history: A case report

Introduction: Aortobifemoral (ABF) bypass grafting is a standard surgical approach for severe aortoiliac occlusive disease, though Vascular Graft Infections (VGIs) remain a serious, albeit rare, complication. VGI can lead to life-threatening outcomes such as sepsis and fistula formation. Aorto-Ureteral Fistulas (AUFs) in particular are notoriously difficult to diagnose, often presenting with hematuria and associated with delayed diagnosis due to inconclusive imaging. This case highlights the diagnostic and therapeutic complexity of a VGI complicated by AUF.

Case Presentation: A 46-year-old man with a complex history including diabetes, IV drug use, peripheral artery disease, and prior rectal cancer surgery underwent ABF grafting for severe aortoiliac disease. Postoperative complications included a femoral artery pseudoaneurysm, left foot gangrene, and multiple amputations. The patient endured several wound infections, including MRSA and ESBL-producing *Klebsiella pneumoniae*, and required repeated antibiotic regimens. Ten months' post-surgery, he developed a persistent groin wound and gross hematuria, raising concern for VGI.

On transfer, imaging confirmed thrombosed and infected graft with suspected AUF. Surgical exploration revealed a fistula between the graft and the left ureter, necessitating left nephrectomy, graft removal, and complex vascular reconstruction using a femoral vein conduit. Intraabdominal cultures grew *Candida glabrata*, prompting antifungal therapy with micafungin, later transitioned to fluconazole. Subsequent surgeries addressed wound dehiscence and suspected bowel involvement. After a multidisciplinary effort, including psychiatric support and infectious disease consultation, the patient stabilized and was discharged on a prolonged antibiotic regimen.

Discussion: This case underscores the critical importance of recognizing AUF as a potential complication of VGI, particularly in patients with prior pelvic surgeries, ureteral stenting, or immunocompromising conditions. Diagnosis is often clinical, as imaging may be non-revealing. Early surgical consultation is essential given the high mortality risk. Antibiotic regimens must cover gram-positive cocci, gram-negative bacilli, and fungi, with adjustments based on culture data. The management of biofilm-associated infections on prosthetic material is particularly challenging and often requires combined surgical and medical strategies.

AUFs are often precipitated by friction, fibrosis, or ischemia caused by indwelling stents, vascular grafts, or radiation therapy. Although nephroureterectomy is a rapid solution, it may not be viable in patients with compromised renal function. In this case, the use of a venous conduit and tailored antifungal therapy led to favorable recovery.

Conclusion: This case illustrates the need for heightened suspicion of AUF in patients with hematuria and prior vascular or urologic surgery. A multidisciplinary approach involving vascular surgery, urology, infectious disease, and critical care teams is vital for effective treatment of complex VGI cases. Prompt surgical intervention and targeted antimicrobial therapy can significantly improve outcomes in these life-threatening conditions.

Biography

Dr. Rakshand Shetty is an MBBS graduate from the 2022 batch of SDM Medical College, India. He has two years of clinical experience in rural hospitals and tertiary care centers, with significant involvement in managing patients during the COVID-19 pandemic. He has completed four months of U.S. clinical experience, including a rotation with the Program Director of Infectious Diseases at the University of Florida, which deepened his interest in infectious diseases and clinical case reporting. Currently, he serves as a Research Associate at Kasturba Medical College, Manipal. He also mentors students and contributes to medical education and competitive exam preparation for medical students in India.

Veronika Kholodovych, Rakshand Shetty*, Chilsia Shaffi, Shehla Islam

[1]Division of Infectious Diseases and Global Medicine, Department of Medicine, University of Florida, Gainesville, Florida

[2]KMC Hospital, MAHE, Manipal, Karnataka, India

Multifocal invasive syphilis in an HIV-positive male mimicking septic emboli and testicular malignancy: A diagnostic and therapeutic challenge

Background: Syphilis, a sexually transmitted infection caused by *Treponema pallidum*, remains a diagnostic challenge due to its diverse clinical presentations and ability to mimic various infectious and malignant conditions. In immunocompromised patients, particularly those with HIV, its manifestations can be even more atypical and aggressive. We present a rare and complex case of multifocal tissue-invasive syphilis involving the bone, testis, lungs, and central nervous system in a newly diagnosed HIV-positive male, initially suspected to have septic emboli and metastatic testicular cancer.

Case Presentation: A 39-year-old male with no significant medical history presented with right foot pain of several weeks' duration and progressive right testicular swelling over several months. Imaging revealed destructive bony lesions, a heterogeneous testicular mass, and multiple pulmonary nodules. Initial differentials included septic emboli, disseminated fungal infection, or metastatic malignancy. Serological testing revealed a new HIV diagnosis (viral load: 124,443 copies/mL; CD4: 312/μL) and a high-titer reactive RPR (1:1024). CSF analysis confirmed neurosyphilis (reactive VDRL 1:8), and testicular ultrasound revealed a 2.8 cm mass suspicious for malignancy. CT and bone scans further supported a multifocal process.

He was treated with 14 days of intravenous penicillin G followed by intramuscular benzathine penicillin. Remarkable clinical and radiographic improvement was noted, including regression of the testicular mass, thus avoiding an unnecessary orchiectomy. Histopathology of a biopsied lymph node showed reactive plasmacytosis without evidence of malignancy or treponemal organisms. Broad-range PCR testing on lymph tissue later returned negative for *T. pallidum*.

Discussion: This case underscores the protean nature of syphilis and its capacity to mimic oncologic, septic, and granulomatous diseases, especially in HIV-positive individuals. In the setting of syphilitic orchitis, misdiagnosis may lead to unwarranted radical surgeries such as orchiectomy. While urologic guidelines recommend orchiectomy for suspicious testicular masses, a testicular-sparing approach is increasingly recognized as appropriate in high-risk STI populations. The diagnostic conundrum is further complicated by low sensitivity of histological staining and occasional false negatives on PCR assays. Hence, clinical acumen, high suspicion, and therapeutic trials may be crucial in diagnosis. Additionally, this case highlights the under recognized prevalence of syphilitic bone involvement and the potential role of advanced imaging in identifying atypical lesions.

Conclusion: Clinicians should maintain a high index of suspicion for syphilis in immunocompromised patients presenting with systemic, multifocal lesions mimicking malignancy or embolic disease. A conservative and multidisciplinary approach can avert unnecessary invasive procedures and improve outcomes. This case exemplifies the evolving landscape of syphilis in the HIV era and reinforces the importance of integrating infectious disease perspectives in the evaluation of complex systemic presentations.

Biography

Dr. Rakshand Shetty is an MBBS graduate from the 2022 batch of SDM Medical College, India. He has two years of clinical experience in rural hospitals and tertiary care centers, with significant involvement in managing patients during the COVID-19 pandemic. He has completed four months of U.S. clinical experience, including a rotation with the Program Director of Infectious Diseases at the University of Florida, which deepened his interest in infectious diseases and clinical case reporting. Currently, he serves as a Research Associate at Kasturba Medical College, Manipal. He also mentors students and contributes to medical education and competitive exam preparation for medical students in India.

Ranjan Ramasamy*, Jyotsna S. Shah

ID-FISH Technology and IGeneX Laboratory, 556 Gibraltar Drive, Milpitas, CA 95035, USA

Recent advances in the serodiagnosis of tick-borne borreliosis

Spirochete bacteria of the genus Borrelia termed Lyme Disease Borreliae (LDB) cause Lyme disease (LD) while other related Borrelia species termed Relapsing Fever Borreliae (RFB) cause Tick-Borne Relapsing Fever (TBRF). LD is widely prevalent in the USA. Because symptoms are mainly non-specific, the clinical diagnosis of LD relies mainly on serodiagnosis that until recently relied on a cumbersome two-tier test procedure. We recently described Immunoblot Tests (IBs) with recombinant proteins from LDB and RFB for the serodiagnosis and differentiation of LD and TBRF, which that showed many suspected LD patients to have TBRF in different continents. We have also developed a US FDA-approved one-step IB test for IgM and IgG antibodies in LD. Both findings significantly advance the serodiagnosis of LD and TBRF.

Biography

Ranjan Ramasamy graduated in 1971 and then obtained a PhD in 1974, both from the University of Cambridge, UK. He was the Chairman of the National Science Foundation of Sri Lanka, Professor of Life Sciences at the Institute of Fundamental Studies in Kandy in Sri Lanka, Professor of Biochemistry in the University of Jaffna in Jaffna Sri Lanka, Professor of Immunology in the University Brunei Darussalam Medical School and has held institute appointments at the Babraham Institute, Cambridge, UK and Scripps Clinic and Research Foundation, La Jolla, USA. He was also a member of the Committee for Scientific Planning and Review (CSPR) of the International Council for Science (ICSU), and the Governing Board of the International Centre for Genetic Engineering and Biotechnology (ICGEB). He has more than 280 publications.

Satya Chitturi[1*] MD, Vidya Atluri[2] MD

[1]Internal Medicine Department, Charles Drew University, Los Angeles, CA, USA

[2]Department of Infectious Disease, University of California Irvine, Irvine, CA, USA

From myositis to mycosis: Invasive aspergillosis in a patient treated for presumed autoimmune disease

We present a diagnostically challenging case of Disseminated Invasive Aspergillosis (DIA) in a 71-year-old male with recent E. coli bacteremia, Acute Kidney Injury Requiring Hemodialysis (AKI-D), and autoimmune myositis treated with high-dose corticosteroids. The patient was initially hospitalized for progressive bilateral lower extremity weakness and was treated empirically for Guillain-Barre Syndrome (GBS) and inflammatory myopathy, receiving IVIG, methylprednisolone (1g daily x5), and a prednisone taper. Extensive imaging and serologic workup, including negative myositis panel and muscle biopsy, failed to confirm a unifying diagnosis. The patient's course was complicated by persistent thrombocytopenia, recurrent hypotension, and transfusion-dependent anemia. Despite serial Transthoracic Echocardiograms (TTEs) showing no evidence of endocarditis, a Transesophageal Echocardiogram (TEE) was deferred due to profound thrombocytopenia, delaying the evaluation for fungal endocarditis or embolic disease. After multiple admissions, he developed distributive shock and was found to have evidence of disseminated aspergillosis involving the lungs, spleen, liver, and myocardium, confirmed postmortem. This case highlights how prolonged immunosuppression and diagnostic inertia in a complex host may contribute to missed opportunities for early detection of opportunistic infections. Earlier TEE, empiric antifungal consideration, or tapering of immunosuppression in the absence of definitive autoimmune disease may have altered the clinical trajectory.

Biography

Dr. Chitturi received her MD degree from Michigan State University College of Human Medicine and is currently a first year Internal Medicine resident at Charles Drew University. Her clinical interests include infectious diseases, diagnostic reasoning in complex cases, and management of complex immunocompromised patients. She is committed to a career that looks to clinical inquiry as a tool for improving patient outcomes.

Zhiwei Li[1,2], Zhiqian Ma[1,2], Shuqi Xiao[1,2*]

[1]State Key Laboratory for Animal Disease Control and Prevention, College of Veterinary Medicine, Lanzhou University, Lanzhou Veterinary Research Institute, Chinese Academy of Agricultural Sciences, Lanzhou, Gansu, China

[2]Gansu Province Research Centre for Basic Disciplines of Pathogen Biology, Lanzhou, Gansu, China

Mapping virulence attenuation sites in PEDV genome: Implications for rational vaccine design

Porcine Epidemic Diarrhea Virus (PEDV) continues to cause substantial economic losses in the global swine industry, highlighting the urgent need for rationally designed attenuated vaccines. This study systematically characterizes specific virulence-attenuating mutations in both the Spike (S) and Envelope (E) proteins, providing a molecular blueprint for precision vaccine development.

Utilizing reverse genetics systems, we generated a series of recombinant PEDV mutants with specific abolishment's of key N-linked glycosylation sites on the S protein (rPEDV-Smut62, rPEDV-Smut381, rPEDV-Smut722). The replication kinetics of these mutants were characterized in Vero cells. Our results demonstrate that the loss of specific glycan's (rPEDV-Smut62 and rPEDV-Smut722) significantly attenuated viral replication efficiency, while the replication kinetics of rPEDV-Smut381 was comparable to the wild strain. Mutations at S protein glycosylation sites Smut62 and Smut722 significantly attenuated viral pathogenicity while maintaining robust immunogenicity. In contrast, the Smut381 mutation caused attenuation but significantly compromised immunogenicity, as demonstrated by reduced neutralizing antibody titters in immunized piglets. Parallel studies revealed that the E protein contributes to virulence through dual mechanisms: triggering inflammatory responses and suppressing IFN production. Both the rPEDV-EΔaa23-aa29 and rPEDV-EN13A represent defective replication efficiency. Deletion of residues 23-29 partially attenuated the viruses by enhancing IFN responses and protected against wild virus challenge in pigs, while the EN13A point mutation markedly attenuated inflammatory and virulence.

Our findings identify S protein glycosylation sites (N62 and N722) and E protein functional domains (residues 13 and 23-29) as precise genetic targets for virulence attenuation. This study provides a strategic framework for developing next-generation PEDV vaccines through rational modulation of viral immunomodulatory elements.

Biography

Professor Shuqi Xiao earned a Master of Agriculture degree from the College of Animal Science and Veterinary Medicine, Jilin University in July 2007, and a Ph.D. in Science from the School of Life Sciences, Sun Yat-sen University in June 2010. From July 2010 to June 2012, he conducted postdoctoral research at the State Key Laboratory of Biocontrol, School of Life Sciences, Sun Yat-sen University. He is currently conducting research on the vaccine and pathogenesis of PRRSV and PEDV at Lanzhou University and Lanzhou Veterinary Research Institute of CAAS. To date, he has published more than 40 research papers in SCI (E) journals.

Simone Hunter[1*], Robert Reid[2]

[1]Department of Pediatrics, Joe Dimaggio Children's Hospital, Hollywood, Florida, United States of America

[2]Department of Pediatric Infectious Disease, Joe Dimaggio Children's Hospital, Hollywood, Florida, United States of America

Recurrent *Plasmodium falciparum* infection in a pediatric traveler following artemisinin-based combination therapy

Transmitted primarily through the bite of a female anopheles mosquito, malaria is a potentially fatal disease that is endemic throughout most of the tropics. Cases in the United States are rare and are usually the result of international travel to areas such as Sub-Saharan Africa and parts of South America and Southeast Asia. Despite control strategies such as vector management and chemoprophylaxis, malaria remains a global health challenge with relapse being a major contributor to the burden and transmission of the disease. *Plasmodium vivax* and *Plasmodium ovale* are the most common culprits of this, but even more unusual, is the recurrence of *Plasmodium falciparum* malaria despite Artemisinin Combination Therapy (ACT).

We report a seventeen-year-old male who presents with recurrent malaria after being treated with ACT in Akwa Ibom, Nigeria. The patient clinically improved after initial treatment, however, a month after, he presented with recurrent symptoms such as fever, malaise, abdominal pain and diarrhea. Blood smear revealed 3% parasitemia and subsequent testing by the state lab confirmed Plasmodium Falciparum. P falciparum is highly endemic to Sub-Saharan Africa and accounted for 97% of cases worldwide in 2023. Despite rare reports of recurrence in this strain, a high level of suspicion is crucial in patients with travel to this endemic region.

Recurrence within 4-6 weeks after ACT raises concern for recrudescence and emerging resistance, though reinfection remains possible in travelers with prolonged exposure. In this case, reinfection was favored, supporting reuse of the same ACT. However, concerns about resistance underscore the importance of case-by-case evaluation, regimen selection and collaboration with public health authorities.

Biography

Dr. Simone Hunter received her medical education at the University of the West Indies in Jamaica and graduated with her MB, BS degree in 2016. She spent time working in the Emergency Department of Spanish Town Hospital and in the Intensive Care Unit at Bustamante Children's Hospital in Jamaica, before beginning pediatric residency with Memorial Healthcare Systems in 2024. She is currently a second-year resident at the Joe DiMaggio Children's Hospital.

Solange Whegang Youdom
Department of Public health, Faculty of Medicine and Pharmaceutical Sciences, University of Dschang, Cameroon

Beyond coverage estimates: Leveraging analytical approaches from Cameroon's Multiple Indicators Cluster Survey (MICS) to strengthen future immunization planning

Background: In Cameroon, vaccination coverage remains below national and global targets, partly due to Missed Opportunities for Vaccination (MOV) and delays in timely immunization. While household surveys such as the Multiple Indicator Cluster Survey (MICS) provide valuable data, older ones can be used to develop statistical analysis plans that can be applied to more recent or future datasets. This study uses the MICS 2014 dataset to explore MOV and vaccination timeliness, not to inform present-day vaccination strategies directly, but to propose an analytical framework that can be reused in future surveys to better interpret vaccination data and guide targeted improvements in immunization services.

Methods: Children aged 12–35 months with documented vaccination histories (from cards) were included. MOV was defined as the failure to receive eligible vaccine doses during health system contacts, identified using recorded vaccination dates in relation to visit history, and simultaneously estimated with all the antigens involved. Vaccination timeliness based on the national immunization schedule, with doses classified as early, timely, or delayed. Timeliness-to-completeness identifies how many children were protected on time. MOV descriptive statistics and disaggregated analyses by different MICS variables, and decision tree for a call to action.

Results: A total of 2214 alive children aged 12 to 35 months were surveyed, and 1447 (65.3%) had cards seen with dates. A percentage of 66.3 of children were completely vaccinated. Vaccination timeliness was all below 80% and ranged from 34.7% for BCG to 61% for Penta1 and PCV1. Timely and completeness for dose specific ranged from the lowest of 27%for BCG, 50% for Polio 3, 52% for MCV1, 46.1% for Penta3, and 48.1 for the Yellow Fever vaccine. The national prevalence of MOV for simultaneous vaccines was 90%; 95% confidence interval (CI)=84%-94%. Within this prevalence, 61% (95% CI=53-69) had previous missed vaccines uncaught. MOV was an issue in all regions and more prevalent in rural areas that urban areas. MOV was more prevalent for yellow fever. Significant differences between proportions of MOV were found for place of residence, mother's education, wealth index, prenatal consultation, vitamin A contact, domestic violence, religion, and the number of vaccination contact. Dose specific MOV ranged from the lowest of 4% (56/1413) for BCG, to the highest of 53.04% for the yellow fever, to 57.1% for polio vaccines. Significant interactions between boys and girls were

found. Decision tree revealed the importance of attaining all scheduled visits to reduce the risk of uncaught vaccines.

Conclusion: Although this work provides results from a distant past, it highlights a methodology for survey data analysis and demonstrates how findings can be obtained on both vaccination timeliness and combined timeliness and completeness, along with missed opportunities for vaccination (MOV). It also identifies research topics to explore, suggesting that such an approach should be considered in the conduct of future surveys.

Keywords: Timeliness, Mics, Analytics and Insights, Domestic Violence, Vaccination Timeliness, Mov, Children, Health System Performance, Cameroon.

Biography

Dr. Solange Whegang Youdom is a Cameroonian statistician and Senior Lecturer at the Faculty of Medicine and Pharmaceutical Sciences, University of Dschang. She holds a PhD in Epidemiology and has recognized expertise in data analysis and statistics, with a specialization in public health and scientific research. Her work focuses on developing statistical methods for analyzing health data, with a strong interest in vaccination, particularly through the secondary analysis of survey databases. She has made significant contributions to scientific research and has authored several publications aimed at advancing knowledge in the field. Passionate about capacity building, she is also actively involved in training initiatives designed to increase the number of women in Francophone Africa who are proficient in statistical tools.

Som E[1*], Adjogoua E[2], Tia M[3], Pierre W[4], Otshudiandjeka J[4], Tiembre I[5]

1. Angré University Hospital
2. Pasteur Institute of Côte d'Ivoire
3. Expending Programme Immunisation
4. AFENET
5. National Institute of Public Hygiene

Epidemiological profile Acute Flaccid Paralysis, Côte d'Ivoire 2021-2023

Introduction: Acute Flaccid Paralysis (AFP), a major symptom of poliomyelitis, is caused by the poliovirus. According to the WHO, in 2022, 21,143 cases of AFP were reported worldwide, with 30 cases (%) of wild poliovirus (WPV1) and 828 cases (%) of vaccine-derived poliovirus (cVDPV). In Africa, 5,588 AFP cases were reported, with 8 cases of WPV1 and 657 cases (%) of VDPV. In 2023, 2 cases of cVDPV2 were reported in Burkina Faso and 6 cases in Côte d'Ivoire (CIV). analysis of AFP in order to understand the progression and make decisions.; The objective of the To describe the Acuite Flaccid Paralysis cases in person, in time,in place

Methods: This was a descriptive cross-sectional study conducted from 2021 to 2023. The study population consisted of Children of under 15 years .The WHO target for the non-polio AFP rate in children under 15 years of age is 3/100,000. Data were extracted in Excel format and cleaned to search for duplicates, missing data, and outliers. EPI info version 7.2 software was used to perform the analyses and calculate proportion and rate, and QGIS version 3.10.7 software was used to create the maps.

Results: Clinical characteristic of the AFP cases was 2,463 AFP cases, 2097(80%) stool samples were of good quality, Stool analysis revealed 2,419 (98.2%) non-polio AFP cases and 7 (0.3%) cVDPV2 cases.
The description of AFP cases revealed that males were more numerous 1,325(54%), with a sex ratio (male/female) of 1.16.Children aged 1 to 4 years were the most numerous, with 1,675 (68%), and the average age was 3.5 years with a standard deviation of 3.2. More than 4 doses of OPV (oral polio vaccine) were administered to 1,038 (42%) AFP cases, and 652 (26%) received 1 to 3 doses of OPV.
Fever at the onset of paralysis was the most common symptom (78,8%). The rates of non-polio AFP per 100,000 children under 15 years of age per year were 6/100,000 (2021), 6/100,000 (2022), and 7/100,000 (2023). The northern part of the country was most affected by cVDPVs, with the districts of Bouna (36.36%), Doropo (18.18%), and Kong (18.18%) respectively.

Conclusion: The PFA database exists with good quality data and samples, children aged 1 to 4 and male were the most numerous. The detection rate of non-polio PFA per 100,000 children under 15 years per year significantly exceed the target of 3/100,000 according to WHO surveillance guidelines.

Biography

Dr. Som Estelle Dipielte, born September 7, 1986, Medical Biologist and Epidemiologist, FETP graduate of Côte d'Ivoire. She currently works at the Angré University Hospital (CHU) where she serves as a Medical Biologist and Quality Manager. She is also a member of the surveillance committee for diseases under epidemiological surveillance. As an intermediate FETP participant, she analyzed the database of Acute Flaccid Paralysis (AFP) in Côte d'Ivoire from 2021 to 2023; she evaluated the AFP surveillance system in the Abidjan region.

Dr. Sukesh Gerard*, Dr. Soumya Umesh
Internal Medicine, St John's Medical College Hospital, Bangalore, Karnataka, India

Tb or not Tb - A cryptic case of pleural effusion in an immunocompromised host

Cryptococcosis, a fungal infection, represents a significant and potentially life-threatening condition primarily seen in individuals with compromised immune systems worldwide. The presence of pleural effusion as the sole clinical manifestation is one of the rarest clinical presentations of cryptococcal infection in cases of pulmonary cryptococcosis.

A 29-year-old man was admitted to the hospital presenting with fever and breathlessness that had persisted for over one month. The chest X-ray revealed a slight left pleural effusion, with no observable abnormalities in the pulmonary parenchyma. A test result for HIV was positive.

The pleural fluid exhibited exudative characteristics with elevated ADA levels. He was initially empirically initiated on ATT in view of high clinical suspicion, exudative nature of pleural fluid and elevated ADA however the result for CBNAAT was negative. In view of persistence of fever beyond 48hrs after initiation of ATT other alternative diagnosis was sought. On day 14 of admission, the pleural fluid yielded a positive culture for cryptococcus neoformans. Consequently, the patient received a diagnosis of cryptococcal pleural effusion and ATT has been discontinued. The patient was administered Amphotericin B and fluconazole, resulting in a positive response with resolution of fever. Elevated serum CMV PCR copies were observed, and patients were treated with valganciclovir. The patient showed improvement and was discharged to continue follow-up on an outpatient basis for the initiation of HAART, which commenced after a period of three weeks. He has responded positively to therapy and is currently doing well.

Conclusion: An exudative pleural effusion accompanied by an elevated ADA level in a patient with immunosuppression although highly suggestive of, may be incorrectly identified as tuberculosis. Cryptococcal infection, while uncommon, warrants consideration. Timely identification and treatment with antifungal medications are crucial to avoid unfavourable results.

Keywords: Cryptococcosis, Cryptococcus Neoformans, Retro Positive, Multilocus Sequence Typing (Mlst), Pleuritis.

Biography

Dr. Sukesh Gerard did his medical school training and residency at the St John's Medical College and Hospital, Bangalore and graduated as MD in 2023. He then joined the department of Internal Medicine. He has since worked in the department over the last two years and was part of the research mentorship for undergraduates' team. He has worked with several subspecialities and closely with the Infectious Disease Unit at the Institute and is part of the team analyzing the prevalence of Vaccine Preventable Infections in the state, a joint effort by the institute and the World Health Organization. He has several case reports detailing the rare presentations of multiple infectious diseases.

Vianey J. Del Mercado González*, Santiago Saavedra Alonso, Pablo Zapata Benavides, Moises F. Molina Armides, M. Cristina Rodríguez Padilla

Immunology and Virology Laboratory, Faculty of Biological Sciences, Autonomous University of Nuevo León (UANL), San Nicolás de los Garza 66450, Nuevo León, MX

In silico and experimental evaluation of the immunogenic efficacy of a DNA-WT1 vaccine in a murine model

This paper reports the development and expression of a DNA vaccine targeting WT1overexpressed in many solid and hematologic tumors. This vaccine incorporates immunogenic epitopes, guaranteeing broad demographic representation (99.26.26% worldwide and 98.37% in Mexico) via prominent HLA alleles such as A*02:01 and DRB1*04:07. Structural predictions revealed 86.21% of random coli, enhancing epitope accessibility and facilitating optimal antigen processing. The construct also showed no expected allergenic or toxic repercussions fortifying its immunogenic potential. In vitro studies confirmed the vaccine's capability in induce cytotoxic responses, particularly in WT1 expressing mouse models (4T1 and B16F10). In vivo evaluations revealed that the non-adjuvant DNA-WT1 vaccine group demonstrated significantly superior prophylactic effectiveness and reduced tumor growth compared to their adjuvant counterparts, suggesting that Incomplete Freund's Adjuvant (IFA) might stifle T cells and the injection site, resulting in fatigue and apoptosis instead of robust anti-tumor responses as demonstrated previously. Together, these insights underscore the vaccines capacity to provoke targeted cytotoxic T-cell responses unhindered by IFA-induced T-cell entrapment. Finally, these results suggest that the DNA-WT1 vaccines exhibited safety, immunogenicity, and the capacity to induce cytotoxic responses while limiting tumor development, making it a potential prophylactic vaccine.

Biography

MS. Vianey Jetzabel Del Mercado González graduated as MS in Immunobiology in 2025 and started her PhD at the Autonomous University of Nuevo León. She has worked developing cancer vaccines as an alternative for immunotherapy in the Immunology and Virology Laboratory of the Faculty of Biological Sciences at the Autonomous University of Nuevo León.

Xiaojun Shen*, Hua Luo
MICU, Peking University Shenzhen Hospital, Shenzhen, China

Sepsis or HLH? Solving the diagnostic puzzle in multiorgan failure

Sepsis and Hemophagocytic Lymphohistiocytosis (HLH) are two critical and life-threatening conditions that often share overlapping clinical features, leading to diagnostic challenges. However, their underlying pathophysiology and treatment approaches differ significantly, making accurate differentiation crucial.

Sepsis is an immune dysregulation syndrome triggered by infection, characterized by a systemic inflammatory response that can progress to multiple organ dysfunction. In contrast, HLH is a severe immune system disorder marked by abnormal activation of immune cells and a cytokine storm, leading to multiorgan failure.

This presentation will explore the diagnostic process through a shared case study of a patient admitted with fever and multiorgan dysfunction. Initially suspected of sepsis, the clinical course and investigations pointed towards HLH. Key diagnostic indicators such as persistent fever, hepatosplenomegaly, cytopenias, hyperferritinemia, hypertriglyceridemia, and hypofibrinogenemia were instrumental in differentiating HLH. Additional confirmation came from bone marrow examination, which revealed hemophagocytosis.

Through this case, we will delve into the critical differences in clinical features, laboratory findings, diagnostic criteria (e.g., HLH-2004 criteria), and therapeutic strategies between sepsis and HLH. By highlighting the nuances in their pathophysiology and management, this presentation aims to provide clinicians with practical guidance on distinguishing between these conditions, thereby improving diagnostic accuracy and treatment outcomes.

Biography

Dr. Xiaojun Shen, MD, is the Attending Physician in Critical Care Medicine at Peking University Shenzhen Hospital specializing in the diagnosis and management of severe infectious diseases and immune-related critical illnesses. With over a decade of clinical experience, Dr. Xiaojun Shen has developed expertise in the differentiation and management of complex cases, particularly in sepsis and HLH. She frequently shares insights and research findings at international conferences to promote better clinical practices.

Yair Lara Blanco[1,2*], Alexandra Villalpando Solorzano[3], Ashley Marieth Ramirez Diaz[3], Jose Giovanni Navarro Rangel[3], Francisco Ramos Pillado[3], José Román Chavez Méndez[1,3], Genaro Rodriguez Uribe[1,2]

[1]Department of Pharmacogenetics, Autonomous University of Baja California, Tijuana, Baja California, México

[2]Faculty of Medicine and Psychology, Autonomous University of Baja California, Tijuana, Baja California, México

[3]Faculty of Health Sciences Valle de las Palmas, Autonomous University of Baja California, Tijuana, Baja California, México

Clinical relevance of the 516 G>T polymorphism in CYP2B6 and its effects on efavirenz concentrations in patients with HIV and tuberculosis: A meta-analysis

Introduction: Efavirenz is a long-acting antiretroviral drug that has been available for several decades. Despite being an older medication, it remains widely used in certain regions due to its low susceptibility to resistance. However, its use is associated with frequent adverse effects, mainly due to toxicity, particularly when coadministered with rifampicin in patients with HIV-TB coinfection. The most common adverse effects include hepatotoxicity and Central Nervous System (CNS) disturbances. The enzyme CYP2B6 plays a crucial role in the metabolism of efavirenz and has been directly linked to these adverse effects.

Objective: This study aims to analyze the impact of polymorphisms in the CYP2B6 gene, specifically the 516 G>T variant, on efavirenz metabolism. We intent to evaluate differences in plasma efavirenz concentrations among the GG, GT, and TT genotypes.

Methods: A systematic review was conducted using PubMed, Embase, and Cochrane databases to identify studies published up to March 2025 that examined the effects of the CYP2B6 516 G>T polymorphism on efavirenz treatment. The primary outcome of interest was plasma efavirenz concentration. Data were analyzed using pooled relative Risk Ratios (RR) and Mean Differences (MD) with 95% Confidence Intervals (CI), applying random-effects models.

Results: Five studies including a total of 373 patients met the inclusion criteria. Compared with the GG and GT genotypes, individuals with the TT genotype exhibited significantly higher plasma efavirenz concentrations. The mean differences in plasma concentration between the GT-TT and GG-TT subgroups were 5.65 µg/mL (95% CI: 2.90–8.40) and 6.41 µg/mL (95% CI: 3.52–9.30), respectively, both statistically significant ($p<0.05$). No significant difference was observed between the GG and GT subgroups.

Conclusion: These findings suggest that individuals with the TT genotype of the CYP2B6 516 G>T polymorphism are at a higher risk of experiencing toxic effects due to elevated plasma efavirenz concentrations. This underscores the importance of pharmacogenetic testing to optimize efavirenz dosing and minimize toxicity, particularly in patients carrying the TT genotype. The observed heterogeneity among studies may be attributed to ethnic variability and differences in sample sizes.

Biography

Professor Yair studied medicine at the Naval Medical School in Mexico, where he earned his degree in 2018. He subsequently completed a master's degree in hospital and health services administration at the Autonomous University of Guadalajara in 2024. He is currently pursuing a postgraduate degree in Medical Sciences at the Autonomous University of Baja California, Mexico, where he is part of the Department of Pharmacogenetics. He has contributed to the publication of book chapters in both the medical and teaching fields.

Ying Wan[1*], Walter Wasylaschuk[1], Joseph Straub[2], Wei Xu[1], Nicole Lepo[3], Patricia M Egan[1], Jillian Acevedo-Skrip[1], Elizabeth Thoryk[1], Megan Mackey[1]

[1]Analytical Research and Development, Merck & Co., Inc., West Point, PA, USA

[2]Global Science & Technology Services, Merck & Co., Inc., West Point, PA, USA

[3]Regulatory CMC, Global Regulatory Affairs & Clinical Safety, Merck & Co., Inc., West Point, PA, USA

Establishing a platform method for physical appearance assessment of new parenteral pharmaceuticals

Physical Appearance (PA) is an attribute indicating the quality of parenteral pharmaceuticals. It is routinely evaluated during release and stability testing and included in regulatory filings. PA assessment of liquids involves three tests: visible particulates, clarity, and color. For each test, compendial general method chapters are available requiring minimal modification. This allows for a platform PA method approach, streamlining method readiness for new test articles. However, selecting the appropriate method is challenging, as no method suits all test articles, and pharmacopeias do not specify suitable condition(s) for each method. Improper method selection can lead to inappropriate specification setting and unreliable results. The need for guidance is especially urgent for vaccines, which often exhibit a wide range of PA attributes due to complex delivery systems and adjuvants that boost immunogenicity.

This presentation addresses this challenge by explaining method suitability and presenting a decision table for PA method selection based on the appearance properties of pharmaceuticals. A case study involving a yellow-turbid vaccine adjuvant is presented to demonstrate the practical application of the decision table. When color and turbidity make visual comparison to reference liquids difficult, instrumental clarity and visual qualitative methods are suitable options. The manuscript provides valuable insights on PA method selection and setting specifications for new parenteral pharmaceuticals. Furthermore, the decision table enables platform methods for test articles sharing similar appearance properties, eliminating the need for individual methods, reducing document preparation time for method and verification protocol, and enhancing the consistency and efficiency of GMP testing for PA.

Biography

Dr. Ying Wan received her PhD from the University of Missouri and completed postdoctoral training at the Vaccine Analytics and Formulation Center, University of Kansas, under Drs. David Volkin and Sangeeta Joshi. She joined Merck in 2020 and is an Associate Principal Scientist in Vaccines Analytical R&D GxP Laboratories. Dr. Wan has published in journals such as PNAS and AAPS and spoke at the PDA Annual Meeting. She has extensive expertise in vaccine analytics, formulation, and GMP testing for various vaccine candidates and is a subject matter expert in compendial methods including visible particulates, color, clarity, volume of fill, and container closure integrity methods.

Zamina Bi Yourou Guillaume*, Issaka Tiembre, Pierre Wilnique, Joseph Otshudiandjeka, Moussa Soro, Ricks Philip, Benie Bi Vroh Joseph

AFENET, Cote d'Ivoire

Seroprevalence of COVID-19 among people aged 12 and over, in a silent district, case of Zoukougbeu, Ivory Coast, April 2023

Introduction: In March 2020, Ivory Coast recorded its first case of Covid-19. First, located in Abidjan, in the economic capital, the disease gradually spread within the country, affecting almost all health districts, thus testing the entire surveillance system. However, until October 2022, around 20 health districts in the interior of the country out of 113 remained without a confirmed case of Covid-19. This study was carried out with the aim of estimating the seroprevalence of Covid-19 in the Zoukougbeu health district and assessing knowledge of the disease in the population.

Methods: A descriptive cross-sectional study was carried out. This was a three-stage cluster random sampling. Included in this study w, ere subjects aged 12 and over residing in Zoukougbeu for more than six months who agreed voluntarily and free of charge to participate in the survey. People who had received vaccination against Covid-19 and who were unable to answer the questions were excluded. Blood samples were taken and ELISA tests were carried out at the laboratory of the Institute Pasteur de Côte d'Ivoire. Approval from the National Ethics Committee for Life and Health Sciences was obtained. Measures of central tendencies, frequencies or proportions were calculated using Epi-Info 7.2.0 software.

Results: 398 people were interviewed. The female gender was in the majority in 54% (215/398) and the median age was 32 years (range: 18-75 years). The respondents had respectively a secondary (37%), primary (33%), no level (28%) and higher (2%) education level. 69% of respondents responded that they had traveled outside the Zoukougbeu department during the Covid-19 period. Almost all respondents (97%) had heard about Covid-19 through television (67%), radio (50%), social networks (13%) and health workers (10%). Among those surveyed, 46% knew the signs of Covid-19 and 89% were aware of its seriousness. 79% were of the opinion that vaccination was a means of protection against the disease. According to serological analyses, 99.23% of respondents had IgG antibodies and 6.38% had IgM positive antibodies.

Conclusion: High seroprevalence of COVID-19 in Zoukougbeu district. Need to strengthen epidemiological surveillance and for the population to respect hygiene measures and barriers to prevent possible epidemics.

Keywords: Seroprevalence, Covid-19, Zoukougbeu, Ivory Coast.

Zeynep Burcin Yilmaz
Inonu University, Turkey

A case of possible CMV pneumonia after liver transplantation and management of CMV infection

Cytomegalovirus (CMV) infection remains a leading cause of illness and death after Liver Transplantation (LT). According to current international guidelines, the two most effective strategies to prevent post-transplant CMV infection are antiviral prophylaxis and pre-emptive therapy. CMV-IgG serology is the standard tool for pre-transplant screening of both donors and recipients.

Because the clinical manifestations of CMV infection and disease are highly variable, clinicians must maintain a high level of suspicion, particularly during the first year after transplantation or in the setting of intensified immunosuppression. Optimizing outcomes depends on tailoring preventive and therapeutic strategies to each patient, balancing the risks of infection and disease with the degree of immunosuppression required.

Despite preventive measures, CMV disease can still develop in up to 50% of high-risk patients. The purpose of my presentation is to highlight the importance of CMV infection consultations both before and after liver transplantation. To illustrate this point, I will discuss a case of suspected CMV pneumonia following liver transplantation.

Biography

Zeynep Burcin Yilmaz is 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 have been working as an assist. prof. at Inonu University for one year. She have 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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POSTER PRESENTATIONS

Agata Bancerz-Kisiel[1*], Klaudia Kończyk-Kmiecik[1], Karolina Lipczyńska-Ilczuk[1], Aneta Nowakiewicz[2]

[1]Department of Epizootiology, University of Warmia and Mazury, Olsztyn, Poland

[2]Sub-Department of Veterinary Microbiology, Department of Preclinical Veterinary Sciences, University of Life Sciences, Lublin, Poland

Assessment of the role of free-living forest mammals as a potential source of *Yersinia enterocolitica* infection

Free-living animals are an important environmental reservoir of the pathogens dangerous for other animal species and humans. One of those is *Yersinia (Y.) enterocolitica*, the causative agent of yersiniosis – foodborne, enzootic disease, significant for public health. *Y. enterocolitica* has been divided into six biotypes based on its specific biochemical features (1A, 1B, and 2 – 5), and more than 70 serological groups have been identified based on chemical variations in the thermostable somatic antigen O. The objective of this study was to identify the bioserotypes and virulence markers of *Y. enterocolitica* strains isolated from different species of free-living forest mammals: red foxes (*Vulpes vulpes*), European hares (*Lepus europaeus*), European hedgehogs (*Erinaceus europaeus*), European beavers (*Castor fiber*) and European rabbits (*Oryctolagus cuniculus*). Sixteen Y. enterocolitica strains have been found in samples obtained from red foxes, while the pathogen has not been isolated from other species. Eight strains were isolated from warm enrichment (ITC), and eight from cold enrichment (PSB). 1A/NT (not-typable) was the most common Y. enterocolitica bioserotype. It was detected in 6/16 (37.5%) isolates. The remaining strains were represented by bioserotypes: 1A/O:8 – 3/16 (18.75%), 1B/NT – 2/16 (12.5%); 2/NT – 2/16 (12.5%); 1A/O:3 – 1/16 (6.25%); 1A/O:5 – 1/16 (6.25%) and 3/O:3 – 1/16 (6.25%). Presence of amplicons corresponding only to ystB gene fragments was demonstrated in 12 of examined Y. enterocolitica strains. Amplicons corresponding to ail and ystB genes were noted in 3 *Y. enterocolitica* biotype 1A strains and one *Y. enterocolitica* biotype 3 strain. Ail-positive strains belonging to biotype 1A are extremely rare. Research has shown that red foxes may be the carriers, shedders and potential source of *Y. enterocolitica* infections for other animal species and indirectly for humans. Funded by the Minister of Science under the “Regional Initiative of Excellence Program”.

Biography

Agata Bancerz-Kisiel has completed her PhD in 2009, and habilitation in 2016. Since December 2023 she is a full professor of veterinary sciences. Her scientific interests focus on Yersinia enterocolitica bacterium. She is the author or co-author of approximately 100 scientific papers and 209 newly defined nucleotide sequences and 234 protein sequences published in GenBank NCBI. The sum of her citations, according to the Web of Science Core Collection database, exceeds 400. She has implemented several scientific projects and was the leader of three of them. She supervised two master's students, two doctors of veterinary sciences, and reviewed doctoral theses and habilitation proceedings eight times.

Ali Ejaz MD[1*], Fatima Abdulle MD[1], Carrie Freed PharmD[2], Dhatri Kotekal DO[3]

[1]Department of Internal Medicine, Cleveland Clinic Akron General/Resident Physician, PGY-2, Akron, Ohio, United States

[2]Department of Infectious Diseases, Pharmacy Clinical Specialist Akron, Ohio United States

[3]Department of Infectious Disease, Cleveland Clinic Akron General/Attending Physician, Akron, Ohio, United States

Uncommon complications of invasive *Streptococcus pneumoniae* post dental care

The gram-positive cocci *S. pneumoniae*, is the most common cause of pneumonia, with more than 500,000 cases reported each year in the United States (US). Rarely, S. pneumoniae may present as an invasive infection with a reported incidence of 8.6 cases per 100,000 people in the US. “Austrian Syndrome” first described by Osler in 1881, is a rare triad of pneumococcal endocarditis, meningitis, and pneumonia. Here, we present a case of invasive streptococcus pneumoniae infection with uncommon complications and resulting transient gammopathy.

A 54-year-old previously healthy male with past medical history of tobacco use disorder presented in late September with upper respiratory tract symptoms, acute mental status change and headache. He was admitted to the Intensive Care Unit (ICU) for concerns of meningitis given his acutely altered state. Computed Tomography (CT) scan of his brain did not show any acute etiology. Thus, he was initiated on empiric antibiotics to cover for bacterial meningitis and his mentation improved. Subsequently, he was stable for regular nursing floors. Blood cultures showed *S. pneumoniae*, antibiotics were continued. However, his hospital course was complicated by ongoing back pain and progressive confusion. Thus, he underwent a lumbar puncture which revealed *S. pneumoniae* as well. Despite appropriate antibiotics therapy, he developed worsening diffuse back pain and headache, with no neurological deficits. A Magnetic Resonance Imaging (MRI) of the spine was completed showing cervical osteomyelitis/discitis and epidural abscess with canal stenosis. MRI of the brain was notable for left parietal lobe abscess. A Transesophageal Echocardiogram (TEE) was also obtained which showed mitral valve thickening, consistent with infective endocarditis in the setting of underlying rheumatic valve disease. Given the spine findings orthopedic surgery was consulted and the patient underwent C2-C6 posterior spinal fusion and C3-4 laminectomy for stabilization and no cultures were sent from the procedure. Given the aggressive nature of his infection, HIV testing, immunoglobulin levels, complement levels, and Serum Protein Electrophoresis (SPEP) were completed. He was found to have gammopathy with multiple M spikes. Hematology was consulted.

Given the overall improvement in his clinical status, he was eventually discharged on high dose IV Ceftriaxone for an 8-week course with plans to follow-up with infectious disease and hematology/oncology.

Subsequently, follow-up SPEP showed normal protein levels, with no unusual spike. The lack of a definitive respiratory process coupled with the infection's aggressive nature makes for an unusual presentation for streptococcus bacteremia. Given the overall clinical course, the most likely trigger for his infection may have been the underlying undiagnosed rheumatic mitral valve lesion, emphasizing the need for a broad work-up to identify possible source in the setting of *S. pneumoniae* bacteremia.

Biography

Dr. Ejaz is a 2nd year internal medicine resident at Cleveland Clinic Akron General. He completed his medical studies at C.M.H Lahore Medical College, Pakistan and graduated in 2020. Going through his rotations here at Akron General, infectious disease, has piqued his interest, inclining him to pursue further training in this subspecialty.

Asha Kumari Verma[1*], Manoj Kumar[2], Harshad V. Murugkar[2], Shanmugasundaram Nagarajan[2], Chakradhar Tosh[2], Pushpendra Namdeo[2], Rupal Singh[2], Suman Mishra[2], Subbiah Kombiah[2], Senthilkumar Dhanapal[2], Vijendra Pal Singh[2]

[1]Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya (Faizabad)- 224229, Uttar Pradesh, India

[2]ICAR- National Institute of High Security Animal Diseases, Bhopal (MP)- 462 022

Experimental infection and in-contact transmission of H9N2 avian influenza virus in crows

Low-pathogenicity avian influenza A (H9N2) viruses are enzootic in poultry populations in Asia and has undergone extensive genetic reassortment along with various co-circulating subtypes of avian influenza viruses, including highly pathogenic avian influenza H5N1 virus and H7N9 viruses. These mutations have permitted H9N2 virus to cross intra-species barrier to cause sporadic human infection. Herein, we have investigated the potential of H9N2 avian influenza virus to cause disease and intra-species transmission in house crows (*Corvus splendens*). A Group of six crows were intranasally inoculated with $10^{6.0}$ EID_{50} of H9N2 virus A/chicken/India/01OR17/2021 and 24-hour post inoculation six naïve crows were introduced to assess in-contact transmission. Crows were observed for 14 days for any overt signs of illness. Oropharyngeal and cloacal swabs were collected up to 14 days to assess virus excretion. No apparent clinical signs were observed in either infected or in-contact crows. Virus excretion was inconsistent through oropharyngeal and cloacal routes and was observed only in infected birds up to 7 days' post- infection (dpi). All six infected crows seroconverted to H9N2 virus at 14 dpi whereas all in-contact crows remained negative to H9N2 virus antibodies. At 14 dpi all crows were humanely euthanized at tissues were collected for virus isolation. No virus could be isolated from tissues *viz*., lung, liver, kidney, pancreas, small intestine and large intestine. Although, crows became infected with H9N2 virus however, transmission of virus was inefficient to contact group. However, virus excretion through oral and cloacal swabs from infected crows suggests a potential threat for inter-species transmission including humans. Crow being a common synanthrope species might have some role in influenza virus transmission to poultry and humans which can be explored further.

Biography

Dr. Asha Kumari Verma studied Veterinary Public Health at the ICAR-IVRI, India and post graduated as Bachelor of Veterinary Public Health in 2018. She completed her Ph.D. working at Biosafety level 3 (BSL3) facility at ICAR-NIHSAD, Bhopal, India. Her research work focused on transmission studies of avian influenza viruses mainly H5N1 and H9N2 viruses in crows. Currently she is working as Assistant professor in Department of Veterinary Public Health and Epidemiology, College of Veterinary Science and Animal Husbandry, ANDUAT, India.

Attahir Abubakar[1*], Umar Yahaya[2], Hauwa Aliyu Sani[1], Almustapha Alinkilo[3], Comfort K. Randa[4], Musa H. Dauda[5]

[1]Department of public health, faculty of basic and applied biological sciences, ahmadu bello university, Samaru Zaria

[2]Department of community medicine ahmadu bello university, Samaru Zaria

[3]Department of disease control, zamfara state primary healthcare board

[4]Ta-connect Abuja Nigeria

[5]SAP America IT Project Consultant 3500 Lenox Rd NE Ste T12 Atlanta, GA 30326

Awareness and acceptability of rotavirus vaccine among mothers of under-five children in Gusau and Bungudu communities of Zamfara State, Northwestern Nigeria

This study examines the awareness and acceptability of the rotavirus vaccine among mothers of children under five in Gusau and Bungudu, Zamfara State, Nigeria. Employing a comparative cross-sectional design, the research utilized quantitative surveys and qualitative focus groups discussions with 429 respondents from both urban (Gusau) and rural (Bungudu) areas. A systematic sampling technique ensured diverse representation across socio-demographic backgrounds. Findings revealed that 92.5% of mothers in Gusau were aware of the rotavirus vaccine, compared to 83.9% in Bungudu, indicating a significant association between awareness and urban residency (p=0.007). The sources of vaccine awareness were notably different, with Gusau mothers having greater exposure to health programs (p=0.006). Income levels also varied significantly; 74.3% of Gusau respondents were in the middle-income bracket, versus 65.8% in Bungudu (p=0.003). Education played a crucial role, as 60.4% of mothers in Gusau completed secondary education, while Bungudu had higher rates of mothers with no formal education (30.4%) or only primary education (25.5%) (p=0.0001). Additionally, the study found differences in perceptions of vaccine safety, with urban respondents expressing fewer concerns compared to those in rural areas, who often cited fears of side effects and cultural beliefs. Despite these barriers, rotavirus vaccine acceptability was high in both locations, with 81.4% in Gusau and 73.2% in Bungudu willing to vaccinate, largely due to trust in healthcare providers. The research highlights the socio-economic and educational disparities affecting vaccine uptake, recommending enhanced healthcare access and educational outreach in rural areas. Strategies such as mobile health clinics and community involvement are suggested to improve awareness and ultimately reduce rotavirus-related morbidity in Zamfara State.

Biography

Attahir Abubakar studied Physiology from Karolinska Institutet Sweden in 2003 and proceed to Ahmadu Bello University Zaria to study MSc Physiology and MPH, from there he joins the developmental space working with various international nongovernmental organization in area of immunization, family planning, malaria and health system strengthening. He received his PhD degree in 2024 at the same institution.

D. Edwards[1*], R. Reid[2]

[1]Department of Pediatrics, Joe DiMaggio Children's Hospital, Hollywood, FL, USA

[2]Division of Infectious Diseases, Department of Pediatrics, Joe DiMaggio Children's Hospital, Hollywood, FL, USA

Delayed diagnosis of measles in an unimmunized child

Background: Measles was declared eliminated in the United States in 2000 due to widespread administration of the 2-dose Measles-Mumps-Rubella (MMR) vaccine. However, this vaccine preventable disease has reemerged in recent years due to declining vaccination rates and increased international travel. In 2025, the United States reported the highest number of measles cases in over three decades, with 1,281 confirmed cases as of July 7. Delayed diagnosis is common as early symptoms overlap with other pediatric illnesses. This leads to multiple healthcare encounters, protracted courses, and as a result, increased risk of both community and nosocomial transmission. We present the case of a partially immunized 5-year-old girl with delayed diagnosis of measles.

Case Presentation: A 5-year-old girl with incomplete immunization and recent travel to Russia presented multiple times to the Emergency Department (ED). On initial presentation she had five days of fever, sore throat, nasal congestion and conjunctivitis. Rapid streptococcal testing was negative but early otitis media was suspected, and she was discharged on oral amoxicillin and a topical ophthalmic antibiotic. On day 8 of illness, she returned with persistent fevers and a new cough; a respiratory viral panel was negative and she was again discharged with supportive care. On day 9 of fever, she returned to the ED with a diffuse maculopapular rash, bilateral non exudative conjunctivitis and red/cracked lips. Review of her vaccination records revealed that she had not received any MMR vaccines. The differential diagnosis included atypical Kawasaki disease and measles and thus she was admitted to a negative pressure room. Due to morbidity associated with untreated Kawasaki disease, she was treated with IVIG and underwent echocardiography, which was normal.

On day 11, urine and nasopharyngeal PCR confirmed acute measles infection. She improved clinically, received oral vitamin A supplementation, and was discharged to continue isolation for one more day and supportive care at home. Appropriate post exposure prophylaxis was offered to all unimmunized and immunocompromised exposed patients the moment measles was suspected, even prior to confirmatory tests.

Discussion: This case illustrates the diagnostic challenges of measles. Early nonspecific features mimic common viral infections, while later findings may resemble Kawasaki disease, potentially delaying diagnosis. In this patient, recognition of measles was not considered until the

third ED visit, highlighting the importance of maintaining a high index of suspicion, particularly in the context of international travel and incomplete vaccination. Delayed recognition increases the risk of transmission in the community and healthcare setting, emphasizing the critical role of rapid isolation and public health notification.

Conclusion: Measles should remain a key consideration in all children presenting with fever and rash, particularly those with a recent history of travel uncertain vaccination status. Early diagnosis, strict isolation, and timely reporting are essential to reduce transmission and prevent outbreaks. This case highlights the importance of careful vaccine history verification and vigilance in the current era as the incidence of measles continues to rise.

Biography

Dr. Edwards graduated from the University of the West Indies, Mona in 2019 and subsequently completed internship at May Pen Hospital in Jamaica in 2020. She then worked at Bustamante Hospital for Children and gained experience in care of pediatric patients. She is currently a second year pediatric resident at Joe DiMaggio Children's Hospital, with an interest in pediatric hematology/oncology.

David S. Buchinsky[1]*; Halimat Olaoluwa[2] MD, MPH; Hari Polenakovik[3] MD

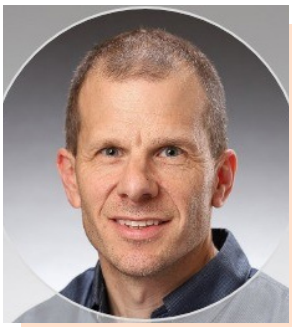
[1]Wright State University Boonshoft School of Medicine, Dayton, OH
[2]Department of Urology, University of Washington, Seattle, WA
[3]Dayton VA Medical Center, Dayton, OH

From gut to bladder: Fecal microbiota transplant for *C. difficile* yields surprising UTI remedy in immunosuppressed patient

Recurrent Urinary Tract Infections (UTIs) present significant management challenges, especially when caused by Multidrug-Resistant (MDR) bacteria, due to the limited availability of effective oral and Intravenous (IV) antibiotics. Patients with these infections often undergo multiple courses of antibiotics, which increases the risk of *Clostridioides Difficile* Infection (CDI). We report the case of a lung transplant recipient who experienced recurrent UTIs caused by Extended-Spectrum Beta-Lactamase (ESBL) producing *Klebsiella pneumoniae*. This patient developed recurrent CDI, which necessitated a Fecal Microbiota Transplant (FMT). Following the FMT procedure, the patient experienced resolution of both the CDI and UTIs for nearly two years, despite ongoing antimicrobial treatment primarily for respiratory tract infections. However, two years later, he again developed recurrent CDI and UTIs, for which he underwent two additional courses of FMT to control the CDI. As of two years after the repeated FMT, the patient remains free of both UTI and CDI. Our findings show that FMT is a safe and effective treatment when administered on three occasions to an immunosuppressed patient, providing protection against recurrent CDI and UTIs for nearly two years. Further research is needed to evaluate the efficacy of FMT in managing recurrent UTIs caused by multidrug-resistant (MDR) pathogens.

Biography

David S. Buchinsky is an MS3 at Wright State University Boonshoft School of Medicine originally from the suburbs of Cleveland, OH. He attained undergraduate degrees in Anthropology: Global Health and the Environment and Biology from Washington University in St. Louis. He is a Global Health Scholar Candidate as part of his medical studies. He enjoys researching in the fields of urology, oncology, and infectious disease. In his free time, he enjoys running, playing tennis and spending time with friends and family.



Eric Kemp*, Walter Wasylaschuk, Malini Mukherjee

Merck & Co., Inc./ MRL/ Analytical R&D/West Point, PA 19486 USA

Overcoming biophysical characterization challenges of small antigens in dilute vaccine formulations

The large-scale manufacturing of vaccines is a complex series of steps that demands significant effort in process, formulation, and analytical development. One notable challenge in the vaccine manufacturing process is aggregation. Interfacial & shear stress, freeze/thaw and formulation components can all lead to aggregate formation. Aggregation can occur across different viral families, encompassing both enveloped and non-enveloped viruses, as well as segmented and non-segmented viruses, including DNA and RNA viruses. Aggregation is an established phenomenon that can compromise the quality, safety, and efficacy of biotherapeutics. Aggregation can have a substantial effect on both the physical and chemical stability of vaccine formulations. Aggregation can have unknown outcomes on immunogenicity and needs to be carefully controlled and monitored in vaccine development. Regulatory considerations in vaccine development highlight the critical importance of quality control, especially in relation to the characterization of aggregates in vaccine products.

Regulatory agencies require a thorough understanding of aggregate formation, size distribution, and their potential impacts on safety and efficacy. Virus particles are inherently smaller than the size of the cells they infect. Several common viral pathogens are less than 100 nm in size, including adenovirus (90 nm), papillomavirus (55 nm), norovirus (40 nm) and poliovirus (30 nm). To maximize immunogenicity and safety, vaccine antigens would ideally have all the properties of the native pathogens except for the ability to cause disease. Vaccine antigens are often designed to mimic key properties of the native pathogens, including size, shape, and surface properties. However, based on current analytical technologies, analysis of particles less than 100 nm in size can be challenging even at moderate concentration levels.

There are numerous instruments available for the analysis of particles in parenteral formulations spanning the range of submicron to visible particulates. This work will focus on the analysis of small therapeutic antigens less than 80 nm in diameter and their submicron sized aggregates in both drug substance and drug product. A comparison of more established techniques, such as AUC, DLS and NTA will be made against the emerging technology of Nano flow cytometry (Beckman Coulter Cytoflex Nano). Techniques will be evaluated for the ability to measure primary antigen particles and the formation of aggregates, including the ability to resolve multimeric populations.

Biography

Eric Kemp studied chemistry at Bloomsburg (BS) & Lehigh Universities (MS) in Pennsylvania. Eric has spent 25 yrs as an analytical chemist in preclinical drug product development at Merck & Co., Inc. He has extensive expertise in analytical and biophysical characterization of small molecules, peptides, LNPs, RNA conjugates, mAbs and vaccines.

Israa Abdullah Malli[1] Ph.D, MMedEd; Sarah Ali Alqhtani[1]; Hannah Ghazi Abid[1*]; Norah Ali Alqhtani[2]; Ghaida Essa Alharbi[1]; Lamar Hassan Aboaljadiel[1]; Roza Khalid Alharbi[1]; Tala Habib Aletani[1]; Taif Mohammed Alamri[1]

[1]King Saud bin Abdulaziz University for Health Sciences, Jeddah, Makkah, Saudi Arabia

[2]Ibn Sina National College for Medical Studies, Jeddah, Makkah, Saudi Arabia

The outcomes of cryptococcal disease in HIV-positive individuals following COVID-19 infection: A systematic review and meta-analysis

Cryptococcal disease is considered a major cause of morbidity in individuals with HIV in resource-limited settings. The long-term effects of COVID-19 and cryptococcal coinfection among PLWHIV have not been thoroughly investigated. This study examined the incidence of cryptococcosis among HIV-positive individuals following COVID-19.

Methods: A thorough search was conducted across five databases on November 14, 2023, and updated on May 7, 2024. Observational and case reports on the clinical and pathological outcomes of cryptococcosis in HIV-positive individuals with COVID-19 were eligible. The authors extracted the study characteristics and main outcomes: mortality, prevalence, AIDS-defining diseases, combined cryptococcosis, and COVID-19 impact on hospitalization, in a standard Excel sheet.

Results: Of the 752 identified articles (40 in the initial search and six in the updated search), eight were selected. The minimum follow-up duration varied between the research periods, which was three months. The investigations comprised 5,751 people living with HIV: 3830 were COVID-19-positive, 130 developed cryptococcosis, and two case reports revealed individuals with concomitant HIV, COVID-19, and cryptococcal infections. The meta-analysis pooled Risk Ratio (RR) for incidence was 0.21 (90% Confidence Interval [CI]: 0.04–1.31) with high heterogeneity (I^2=98%), while the pooled risk for mortality was 1.49 (95% confidence interval: 0.60-3.72), with moderate heterogeneity (I^2 = 65%). The chi-squared test for heterogeneity (χ^2=125.62, p-value <0.00001) revealed considerable variation.

Conclusions: Cryptococcosis remains a rare but significant complication for people living with HIV following the COVID-19 infection. The data suggest a decrease in incidence risk while a probable increase in mortality. The observed heterogeneity and variability address the importance of enhanced surveillance and targeted interventions for this vulnerable population. Further research is essential to identify factors contributing to heterogeneity and develop effective strategies for managing cryptococcosis in people living with HIV.

Biography

Hannah Abid studied Biology at Middle Tennessee State University, USA, where she graduated with a Bachelor of Science in 2019. She is currently pursuing her medical degree at King Saud bin Abdulaziz University for Health Sciences in Saudi Arabia. Throughout her academic journey, Hannah has actively contributed to research projects across various specialties within the medical field, demonstrating a commitment to advancing healthcare and improving patient outcomes.

Hirotomo Dochi[1*], Janardhan Avilala[1], Joseph Wekselblatt[2], Adam Caro[3], Leslie Birke[3], Erik Flemington[1], Zhen Lin[1]

[1]Department of Pathology & Laboratory Medicine, Tulane University Health Sciences Center and Louisiana Cancer Research Center, New Orleans, Louisiana, USA

[2]California Institute of Technology, California, USA

[3]Louisiana State University Health Sciences Center, New Orleans, Louisiana, USA

Tree shrew: A new primate-like small animal for EBV research

Epstein-Barr Virus (EBV) is implicated in a wide range of human malignancies, including nasopharyngeal carcinoma, Hodgkin lymphoma, and gastric carcinoma. However, progress in elucidating the mechanisms of EBV-associated oncogenesis has been hampered by the absence of an in vivo model that accurately recapitulates human infection. In this study, we propose the tree shrew as a physiologically relevant and genetically tractable animal model for EBV research. Owing to their close evolutionary relationship to primates and a human-like immune system, tree shrews offer unique advantages for studying EBV biology in vivo. Our preliminary data demonstrate that EBV can successfully infect tree shrews, establish latency, and undergo lytic reactivation—mirroring key aspects of human EBV infection. These results represent a critical advancement in overcoming the species barrier in EBV modeling. The tree shrew system provides a promising platform for dissecting EBV-host interactions, evaluating therapeutic interventions, and developing immunotherapeutic strategies against EBV-associated malignancies.

Biography

Dr. Hirotomo Dochi earned his MD and PhD from Kanazawa University, Japan. He completed clinical training in otolaryngology and focused his PhD research on Epstein-Barr virus (EBV)-associated cancers. He is currently a postdoctoral fellow in Dr. Lin's lab at Tulane University and the Louisiana Cancer Research Center, where he studies EBV reactivation and host-virus interactions. Dr. Dochi has received multiple honors, including a travel award to present his work on EBV infection models at the 2024 International Symposium on EBV & KSHV. His goal is to advance translational oncology through a combination of clinical and molecular research.

Junmei Zhang*, Ke Li, Xiaoyu Li, Andy Ng

WuXi Biology, WuXi AppTec, Shanghai, China

Establishment of a high-throughput fluorescent antibody-to-membrane antigen assay to measure the humoral immune response against the varicella-zoster virus

Varicella-Zoster Virus (VZV) is a highly contagious alpha-herpesvirus that infects more than 90% of people worldwide. Primary VZV infection results in Chickenpox (varicella), predominantly affecting children. Reactivation of latent VZV leads to shingles (herpes zoster), which mainly occurs in people aged 50 years and above, often accompanied with intense neuralgia. It is estimated that about one third of those who have had chickenpox will develop shingles. To date, there is still no specific cure for VZV-induced diseases, thus VZV infection is still prevalent and accounts for a significant disease burden worldwide.

Vaccination is among the most cost-effective ways for preventing chickenpox and shingles. Therefore, measuring the specific immunogenicity induced by the varicella vaccine is very crucial. The Fluorescent Antibody to Membrane Antigen (FAMA) test is a cell-based assay that uses VZV glycoproteins expressed on the surface of VZV-infected cells as antigens. Due to its high sensitivity and specificity, the FAMA test is regarded as the gold standard for measuring protective antibodies against VZV and serves as a reference method for evaluating other assays' performance.

However, the standard FAMA procedure is semi-quantitative, low-throughput, labor-intensive, and requires evaluation by trained technicians, which limits its widespread application. To overcome these challenges and to increase the applicability and robustness of the test, we developed a High Content Screening (HCS) based FAMA assay, which is quantitative, high-throughput, and overcomes the issue of subjectivity of observers in the standard FAMA test. Furthermore, we evaluated the stability of FAMA antigens under different storage conditions to find suitable conditions for stable storage of antigens from the same batch, thus reducing the lot-to-lot variation of FAMA antigens, as well as the time and labor required to prepare FAMA antigens.

Keywords: Varicella-Zoster Virus (VZV), Fluorescent Antibody-To-Membrane Antigen (FAMA), High Content Screening (HCS).

Dr. Karol Ann Stefanía Montúfar Melo*, Dr. Lina Paola Montaña Jiménez

Pontificia Universidad Javeriana (PUJ), Bogotá, Colombia

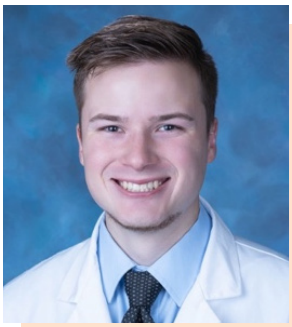
Cardiovascular complications associated with Human Immunodeficiency Virus in pediatric patients

Human Immunodeficiency Virus (HIV) infection can affect the pediatric cardiovascular system through various mechanisms, including chronic inflammation, endothelial dysfunction, and intestinal microbial translocation. These processes lead to complications such as an increased incidence of congenital heart defects, inflammatory vascular disease, cardiac contractility abnormalities, systolic and diastolic heart failure, dilated cardiomyopathy, and heart failure. Antiretroviral therapy (ART) can induce chronic inflammation, endothelial dysfunction, lipid abnormalities, insulin resistance, and lipodystrophy, contributing to accelerated atherosclerosis. This abstract explores the pathophysiology, complications, diagnostic methods, and prognosis of cardiovascular complications in pediatric HIV patients.

Methods: A specialized search was conducted in various databases at the Pontificia Universidad Javeriana using relevant keywords and MeSH terms, including: "Human Immunodeficiency Virus* Infection*", "HIV disease*", "HIV Infections (MESH)", "Human Immunodeficiency Virus* (EMTREE)", "AIDS Virus*", "Acquired Immune Deficiency Syndrome Virus", "Acquired Immunodeficiency Syndrome Virus", "human immunodeficiency virus HIV disease*", "human immunodeficiency virus HIV infection*", "Heart Diseases (MESH)", "Heart Disease (EMTREE)", "Cardiac Disease*", "Cardiac Disorder*", "Heart Disorder*", "cardiac anomaly", "cardiac disturbance", "cardiopathy", "heart deficiency", "heart deformity", "heart dysfunction", AND "Infant*", "Newborn*", "Newborn Infant*", "Neonate*", "Child[Mesh]", "Adolescent*", "Teen*", "Teenager*", "Youth*", and "Pediatric*". The findings were summarized in a narrative review.

Biography

Karol Ann Stefanía Montúfar Melo has special interest in pediatric cardiology, and pediatric infectious diseases. Her dedication lies in improving the health and well-being of newborns and children through clinical practice, research, and academic collaboration. She has developed her research focus on the intersection between infectious diseases and cardiovascular health in pediatric populations, aiming to generate new approaches for prevention, diagnosis, and treatment. Her approach integrates evidence-based medicine with multidisciplinary collaboration, shaped by her experience as a resident physician at the Pontificia Universidad Javeriana, where she combines patient care with academic development.



Kole Winebrenner[1*] OMS-IV, Madeline Manuel[2] OMS-IV, John Greene[3] MD

[1]Nova South-eastern University Dr. Kiran C. Patel College of Osteopathic Medicine, Clearwater, FL, USA

[2]Department of Internal Medicine, Division of Infectious Diseases, Moffitt Cancer Centre, Tampa, FL, USA

Emphysematous Cystitis in an Immunocompromised patient with Ovarian cancer: A case report

Background: Emphysematous Cystitis (EC) is a rare, potentially life-threatening urinary tract infection characterized by gas formation within the bladder wall or lumen. While most cases occur in older diabetic patients, EC may also develop in immunocompromised oncology patients, where overlapping risk factors complicate diagnosis and management.

Case Report: We present a 67-year-old female with high-grade serous ovarian carcinoma receiving carboplatin and paclitaxel chemotherapy, with additional risk factors of chronic corticosteroid use, poorly controlled hyperglycemia (blood glucose 322 mg/dL, A1c 8.1%), and opioid-associated urinary retention. She was admitted for evaluation of gastrointestinal bleeding but reported several months of intermittent dysuria, hematuria, and straining to void.

On admission, she was afebrile, hemodynamically stable, and pancytopenic. Urinalysis revealed significant glucosuria, proteinuria, hematuria, positive nitrites, and bacteriuria. Computed tomography angiography of the abdomen and pelvis, obtained for the suspected gastrointestinal hemorrhage incidentally demonstrated extensive intramural gas within the bladder wall consistent with EC. Urine culture grew *Klebsiella pneumoniae*, sensitive to ceftriaxone. She was managed conservatively with intravenous ceftriaxone for 14 days, bladder decompression via Foley catheter, and supportive care. Follow-up imaging during subsequent admissions showed resolution of the EC.

Discussion: This case highlights the diagnostic challenges of EC in non-diabetic immunocompromised hosts. Cytotoxic chemotherapy, corticosteroids, uncontrolled hyperglycemia, and urinary stasis created an ideal environment for gas-forming pathogens. While diabetes mellitus remains the most common risk factor, oncology patients undergoing chemotherapy may present atypically and require a high index of suspicion. Early cross-sectional imaging was pivotal in diagnosis; despite being ordered for an unrelated indication.

Conclusion: To our knowledge, this is the first reported case of EC in a patient receiving carboplatin and paclitaxel for ovarian cancer. Conservative management achieved full resolution. This case underscores the importance of considering EC in immunocompromised oncology patients presenting with even subtle urinary symptoms and highlights the role of early imaging and culture-guided antimicrobial therapy.

Biography

Mr. Kole Winebrenner is a fourth-year medical student at Nova Southeastern University Dr. Kiran C. Patel College of Osteopathic Medicine, currently pursuing a career in diagnostic radiology. His academic interests center on the integration of clinical medicine and imaging, with early contributions through case-based research in infectious diseases and radiology. He is particularly focused on case-based scholarship and collaborative projects that highlight the role of radiologic findings in guiding clinical management.

Tripathi Manish*, Rathore Sumit

Dept. of Biotechnology, All India Institute of Medical Sciences, New Delhi, India

Exploring a novel interaction between the human malaria parasite *Plasmodium vivax* and reticulocyte protein

The global burden of malaria remains significant despite concerted elimination efforts, with Plasmodium vivax presenting unique challenges due to its distinctive biology and invasion mechanisms. Despite progress in understanding Plasmodium falciparum, the molecular interactions governing P. vivax infection remain relatively obscure, particularly regarding its exclusive preference for reticulocytes. This study illuminates a critical host-parasite interaction that advances our understanding of P. vivax pathogenesis and opens new avenues for therapeutic intervention.

The research focuses on PvTRAg36.6, a member of the P. vivax-specific tryptophan-rich antigen family (Pv-fam-a). This protein represents an excellent candidate for investigation due to several key characteristics: it is consistently expressed during the merozoite stage, shows remarkable sequence conservation across geographically diverse parasite populations, and critically, elicits both cellular and humoral immune responses during natural infection. These properties suggest evolutionary importance and potential immunological relevance. Through meticulous biochemical analysis, we identified CD71 as the binding partner for PvTRAg36.6 on human reticulocytes. The investigation employed Liquid Chromatography-Mass Spectrometry (LC-MS) analysis of proteins recovered from pull-down assays, providing initial evidence of this interaction. The specificity of this receptor-ligand pairing was subsequently confirmed through multiple complementary approaches, including solid-phase binding assays and Surface Plasmon Resonance (SPR), and Bio-layer interferometry establishing a robust foundation for the findings.

Further characterization revealed that PvTRAg36.6 engages with CD71 through two discrete peptide regions. This molecular specificity suggests a highly evolved interaction that has been optimized throughout the parasite's evolutionary history. Functional assays demonstrated that this binding event plays a significant role in the invasion of reticulocytes by P. vivax merozoites, highlighting its biological relevance in the parasite's life cycle. The identification of CD71 as a receptor is particularly notable given its specific expression on reticulocytes. This aligns with P. vivax's strict tropism for these immature red blood cells and may partially explain this selective preference. The CD71 receptor is essential for iron uptake in developing erythroid cells and is progressively lost during red cell maturation, correlating with the window of susceptibility to P. vivax infection. The conservation of PvTRAg36.6 across parasite isolates suggests strong selective pressure to maintain this interaction, further emphasizing its importance for parasite

survival and propagation. Unlike some other invasion ligands that show high variability to evade host immunity, the relative conservation of PvTRAg36.6 may indicate either limited immune pressure on this protein or critical functional constraints that prevent extensive sequence variation. From an immunological perspective, the documented humoral and cellular responses against PvTRAg36.6 during natural infection present promising opportunities for vaccine development. Targeting conserved epitopes involved in CD71 binding could potentially disrupt this critical invasion pathway. Additionally, the identification of the specific peptide regions mediating this interaction provides focused targets for the development of inhibitory antibodies or small molecule inhibitors.

In conclusion, this study provides valuable insights into the molecular basis of P. vivax infection and highlights PvTRAg36.6 as a promising target for immunotherapeutic approaches. These findings advance our fundamental understanding of host-parasite biology while simultaneously offering practical directions for developing interventions against this persistent global health threat.

Biography

Manish Tripathi completed his post-graduation from All India Institute of Medical Sciences, New Delhi (2018), where he carried out his dissertation work in the Molecular Parasitology Laboratory. He is currently pursuing his Ph.D., with research focused on the characterization of parasite ligand–host receptor interactions in Plasmodium infection using a combination of proteomics-based approaches, in-silico techniques, and *Plasmodium vivax* culture systems. Through these approaches, he has successfully identified host receptors for *Plasmodium vivax* ligands and has published several research papers on host red cell–parasite interactions and malaria detection using aptamer-based diagnostic kits. In addition, his Ph.D. work extends to drug discovery, where he is actively involved in designing and screening potential drug molecules against P. falciparum and P. vivax. He has also authored two book chapters, reflecting his interest in malaria biology and therapeutic interventions.

Henry Nabeta[1] MD, Nicole Northover[2*], Neguemadji Ngardig Ngaba[1] MD, Swetha Doddi[1] MD, Amoa Akua[1] MD, Abel Akanyijuka[1] MD, Reina Raul[1] MD, Kalpana Uday[1] MD

[1]BronxCare Hospital System, Department of Internal Medicine, Bronx New York, USA

[2]American University of the Caribbean School of Medicine, St Maarten

A rare polymicrobial bloodstream infection in end-stage renal disease: Enterobacter cloacae, and dual achromobacter species in a hemodialysis patient

Bloodstream infections are a major source of morbidity and mortality among patients with End-Stage Renal Disease (ESRD) on hemodialysis, particularly when caused by uncommon and multidrug-resistant organisms. *Achromobacter xylosoxidans* and *Achromobacter denitrificans* are rare environmental pathogens that have emerged as opportunistic threats in immunocompromised hosts. However, co-infection with both species has not been previously documented in the hemodialysis population. We present a unique case of recurrent polymicrobial bacteremia involving *Enterobacter cloacae*, *A*. *xylosoxidans*, and *A. denitrificans* in a hemodialysis patient, highlighting critical challenges in diagnosis, management, and antimicrobial treatment.

A 51-year-old male with diabetes, hypertension, and end-stage renal disease presented to the emergency room with fever and chills that occurred during dialysis via a right chest Tunneled Dialysis Catheter (TDC). Two months' prior, a left forearm arteriovenous graft had been placed. Initial blood cultures at his dialysis center grew gram-negative bacilli, prompting treatment with vancomycin and gentamicin and transfer to the emergency room. A chest X-ray suggested pneumonia, hence antibiotics were changed to vancomycin and piperacillin-tazobactam. Due to concerns for TDC infection, a catheter change was recommended after several negative cultures. Enterobacter cloacae complex was later isolated, prompting a switch to meropenem. Following TDC removal and placement of a right femoral non-tunneled Central Venous Catheter (CVC), subsequent cultures identified *Achromobacter xylosoxidans* sensitive to meropenem. After negative cultures, he was discharged home three weeks later. One month after discharge, he developed a fever and shortness of breath during dialysis. Vancomycin and gentamicin were started, and he was transferred to the emergency room. He was admitted to the intensive care unit for worsening hypoxemia and placed on Bi-Level Positive Airway Pressure (BiPAP) ventilation. Oral vancomycin was initiated for *Clostridium difficile* colitis, following a positive Glutamate Dehydrogenase (GDH) antigen test and detection of toxin B. Blood cultures grew *A. xylosoxidans*, leading to meropenem treatment. The left Internal Jugular (IJ) TDC was removed. He experienced spontaneous bleeding at the graft site. *A contrast tomography* angiogram showed no pseudoaneurysm. An urgent graft excision revealed *A. xylosoxidans* in the resected arteriovenous graft, along with *A. denitrificans* in blood cultures. He developed transaminitis (likely due to meropenem use), leading to a switch to ceftazidime. After subsequent negative cultures, a left chest TDC was placed, and he was discharged.

This case underscores the clinical significance of environmental pathogens in healthcare-associated infections and the need for vigilance in immunocompromised populations. Polymicrobial bloodstream infections, particularly with rare and resistant organisms, pose diagnostic, therapeutic, and infection control challenges. Early source control, organism-directed therapy, and careful monitoring for antimicrobial toxicity are critical for favorable outcomes.

Presenting cases like this enhances clinician awareness of emerging pathogens, informs future approaches to vascular access management, and supports the urgent need for antimicrobial stewardship strategies in high-risk patients. Further case series and studies are warranted to guide best practices in managing polymicrobial infections in hemodialysis populations.

Biography

Nicole Northover is a medical student at the American University of the Caribbean School of Medicine (M.D., anticipated 2026). She holds a Master of Science in Health Administration from Fordham University and a Bachelor of Science in Molecular Biology from New York University. Nicole has published research in Substance Abuse: Research and Treatment and the Archives of Psychiatry Research, and has contributed to multiple conference presentations. Her research experience spans NYU Langone and Columbia University, focusing on addiction, wearable technologies, and biomedical engineering. She is a member of the American Psychiatric Association and Alpha Omega Phi Honor Society.

Pawandeep Kaur[1*] MD, Bugra Zengin[1] MD, Mansoor Rahman[1] MD, Lee Connor[2] MD

[1]Internal Medicine Resident Physician, Hamilton Medical Center, Dalton, Georgia, US

[2]Infectious Disease Specialist, Hamilton Medical Center, Dalton, Georgia, US

Clostridium difficile bacteremia in a case of acute appendicitis

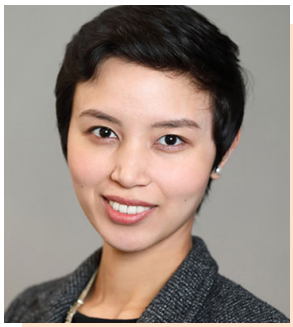
Background: *Clostridium difficile* is the principal agent of nosocomial diarrhea. *C. difficile* is not intrinsically invasive and rarely infects extra intestinal sites. The bacterium, therefore, is not commonly detected in blood cultures. Herein, we report a case of *C. difficile* bacteremia in a patient with acute appendicitis.

Case presentation: A 53-year-old female with past medical history of type 2 diabetes mellitus presented with same day onset of severe right lower quadrant pain. On admission, her vitals were temperature 37.1°C, heart rate 109, and blood pressure 166/93. Physical exam revealed significant right lower quadrant tenderness. Initial lab workup revealed WBC count of 21.8k and lactic acid 4.6. CT scan of the abdomen revealed appendicitis with appendicolith without evidence of perforation or abscess. The patient was started empirically on piperacillin-tazobactam and underwent laparoscopic appendectomy where appendicular perforation was noted which required extensive washout for contamination and lysis of adhesions. Blood cultures taken postoperatively, on day 3 of admission grew *Clostridium difficile* on anaerobic broth. Stool testing was also positive for *C. difficile* toxin. Interestingly, patient had no complaint of diarrhea. Antibiotics were switched from piperacillin-tazobactam to IV ceftriaxone and IV Flagel based upon culture results and susceptibility testing. On susceptibility testing, the strain was sensitive to Ampicillin/Sulbactam, Clindamycin, Meropenem, Metronidazole and resistant to Imipenem and Penicillin. Repeat blood cultures collected after two days were clear. She was discharged on a 14-day course of IV ceftriaxone and PO Flagel from the day of her washout.

Conclusion: *Clostridium difficile* bacteremia is rare but carries a high mortality rate, open occurring in the context of polymicrobial infections. Interestingly, this case presents a monomicrobial C. difficile bacteremia without the typical gastrointestinal symptoms such as diarrhea or colitis. Given that Clostridium species are normal inhabitants of the gastrointestinal tract, most extracolonic *C. difficile* infections are preceded by gastrointestinal events, such as *C. difficile* colitis or surgical and anatomical disruptions, of the colon. In our case, the bacteremia likely resulted from bacterial translocation following appendix perforation or surgical intervention, emphasizing the need to consider *C. difficile* as a potential pathogen in patients with gastrointestinal perforations or surgical disruptions, even in the absence of classic symptoms like diarrhea or colitis.

Biography

Dr. Pawandeep Kaur completed her MBBS from Government Medical College, Patiala, India in 2021. She then joined the Internal medicine residency program at Hamilton Medical Center, Dalton, Georgia in 2023. Dr. Kaur has a deep interest in infectious diseases and is currently pursuing her medical career with a focus on this specialty.



Ria T Caringal[1*], John M Hickey[1], Nitya Sharma[1], Kaushal Jerajani[1], Oluwadara Bewaji[1], Sarah Brendle[2], Neil Christensen[2], Saurabh Batwal[3], Mustafa Mahedvi[3], Harish Rao[3], Vikas Dogar[3], Rahul Chandrasekharan[3], Umesh Shaligram[3], Sangeeta B Joshi[1], David B Volkin[1]

[1]Department of Pharmaceutical Chemistry, Vaccine Analytics and Formulation Center, University of Kansas, Lawrence, KS, USA

[2]Department of Pathology, College of Medicine, Pennsylvania State University, Hershey, PA, USA

[3]Serum Institute of India Pvt. Ltd., Pune, India

A combined LC-MS and immunoassay approach to characterize preservative-induced destabilization of human papillomavirus virus-like particles adsorbed to an aluminum-salt adjuvant

During the multi-dose formulation development of recombinant vaccine candidates, protein antigens can be destabilized by Antimicrobial Preservatives (APs). The degradation mechanisms are often poorly understood since available analytical tools are limited due to low protein concentrations and the presence of adjuvants. In this work, we evaluate different analytical approaches to monitor the structural integrity of HPV16 VLPs adsorbed to Alhydrogel™ (AH) in the presence and absence of APs (i.e., destabilizing m-cresol, MC, or non-destabilizing Chlorobutanol, CB) under accelerated conditions (pH 7.4, 50 °C). First, in vitro potency losses displayed only modest correlations with the results from two commonly used methods of protein analysis (SDS-PAGE, DSC). Next, results from two alternative analytical approaches provided a better understanding of physicochemical events occurring under these same conditions: (1) competitive ELISA immunoassays with a panel of mAbs against conformational and linear epitopes on HPV16 VLPs and (2) LC-MS peptide mapping to evaluate the accessibility/redox state of the 12 cysteine residues within each L1 protein comprising the HPV16 VLP (i.e., with 360 L1 proteins per VLP, there are 4320 Cys residues per VLP). These methods expand the limited analytical toolset currently available to characterize AH-adsorbed antigens and provide additional insights into the molecular mechanism(s) of AP-induced destabilization of vaccine antigens.

Biography

Ria T. Caringal earned her BS in Molecular Biology and Biotechnology at University of the Philippines – Diliman in 2011. She spent the next few years working as an associate scientist in vaccine formulation and development for both private industry (MedImmune) and government labs (NIH/NIAID/Vaccine Research Center). In 2020, she started her PhD studies at the Department of Pharmaceutical Chemistry at University of Kansas, with a focus on vaccines under Drs. David Volkin and Sangeeta Joshi at the Vaccine Analytics and Formulation Center (VAFC).

Dr. Sukesh Gerard*, Dr. Anusha Hegde, Dr. Ratnamala Choudhury

Internal Medicine, St John's Medical College Hospital, Bangalore, Karnataka, India

The great masquerader strikes again. Neurosyphilis presenting as general paresis of insane and stroke like syndrome: A case report

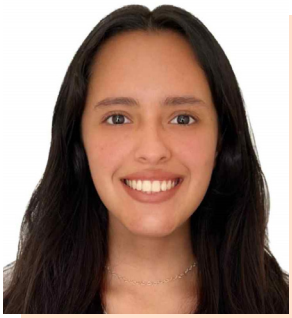
Introduction: Syphilis, often considered "the Great Imitator", due to its frequent atypical presentation with clinical phenotypes ranging from meningitis, meningovascular syphilis with strokes and in advanced stages as "general paralysis of the insane" to simple chancres. We present a case report of a young male with neurosyphilis presenting with a stroke-like picture and dementia.

Case report: 32-year-old unmarried gentleman, IT professional, known case of RHD and ankylosing spondylitis, presented with fever, slurring of speech, stiffness of limb, emotional lability, and memory impairment. Examination revealed punched out ulcers over the tongue and genital warts. The patient attenders did not report any promiscuous sexual relations. Neurological examination revealed bilateral upper and lower limb hypertonia with exaggerated DTRs- ankle and patellar clonus. He had a loud P2 and early diastolic murmur on auscultation. Neuroimaging was suggestive of right midbrain infarct. Due to the presence of cutaneous lesions he was tested for STIs and was positive for Hepatitis-B and serum TPHA. CSF was positive for VDRL and TPHA. A diagnosis of tertiary syphilis with general paresis of insane with vasculitic stroke was made. He was treated with Benzathine penicillin and oral glucocorticoids, SAPT and statins, antipsychotics for cognitive impairment and tenofovir alafenamide for Hepatitis-B. He was discharged on day 15 with significant neurological improvement.

Discussion: This case underscores the importance of early diagnosis of neurosyphilis, and initiation of antibiotics. It also emphasises the importance of evaluating infective or treatable causes especially in young-onset or rapidly progressive dementia. A high degree of suspicion is required with serological testing in cases with high index of suspicion.

Biography

Dr. Sukesh Gerard did his medical school training and residency at the St John's Medical College and Hospital, Bangalore and graduated as MD in 2023. He then joined the department of Internal Medicine. He has since worked in the department over the last two years and was part of the research mentorship for undergraduates' team. He has worked with several subspecialities and closely with the Infectious Disease Unit at the Institute and is part of the team analyzing the prevalence of Vaccine Preventable Infections in the state, a joint effort by the institute and the World Health Organization. He has several case reports detailing the rare presentations of multiple infectious diseases.



Valeria Gordillo Leo[1,2*], Sara Gavidia Verastegui[1,2], Diana Fernandez Merjildo[2,3], Coralith Garcia Apac[1,2,3]

[1]Instituto de Medicina Tropical Alexander von Humboldt, San Martin de Porres, Lima, Perú

[2]Universidad Peruana Cayetano Heredia, San Martín de Porres, Lima, Perú

[3]Hospital Nacional Cayetano Heredia, San Martín de Porres, Lima, Perú

Antibiotic resistantance pattern of the most frequently isolated bacteria of healthcare associated infections in patients in an intensive care unit before and during the COVID-19 pandemic

Introduction: During the COVID-19 pandemic, an increase in healthcare associated infections was observed. A 41% incidence was reported among critically ill patients infected with COVID-19, and 50% of those requiring hospitalization in the intensive care unit were found to be infected with multidrug resistant bacteria. The most frequently isolated bacterial species were *Staphylococcus aureus, Klebsiella pneumoniae and Streptococcus pneumoniae.*

Objectives: Compare and describe the antimicrobial resistance pattern of the most frequently isolated bacteria from healthcare associated infections in an intensive care unit before and during the COVID-19 pandemic in Lima, Peru.

Methods: A cross-sectional descriptive study conducted in the adult intensive care unit of Hospital Cayetano Heredia. The study was carried out in two distinct time periods. The pre-COVID-19 group data was collected from January 1st, 2019, to March 6th 2020, while the COVID-19 group data was collected between March 7th 2020 and December 31st 2020. The data was compiled into a Microsoft Excel database and analyzed using Stata version 4.

Results: Most of the isolated bacteria were Gram-negative. From the 42 bacteria isolates in the pre-COVID-19 group, *Pseudomonas aeruginosa* was the most frequent (14/42) followed by Klebsiella pneumoniae (9/42), while in the COVID-19 group from 129 isolates, Acinetobacter baumannii (46/129) was the most frequent followed by *Pseudomonas aeruginosa* (27/129). *Pseudomonas aeruginosa* showed similar resistance rates to carbapenems in both periods. The resistance rate to meropenem was 57,1% in the pre COVID-19 group and 55,6% in the COVID-19 group, while resistance to imipenem was 64,3% and 63%, respectively. Klebsiella pneumonia resistance to carbapenems increased from 11,1% in the pre COVID-19 group to 71,4% in the COVID-19 group. This bacterium also showed 66,7% resistance to amoxicillin-clavulanic acid and 33,3% resistance to cephalosporins, gentamicin, and ampicillin-sulbactam in the pre COVID-19 group. In contrast, the COVID-19 group showed that 95,2% of isolates were resistant to ceftriaxone, 90,5% to ciprofloxacin and 85,7% to cefepime. *Stenotrophomonas maltophilia* was an emergent bacterium in the COVID-19 group and showed resistance to ceftriaxone in 27,3% of isolates. 18,2% of isolates also showed resistance to carbapenems, aztreonam, ciprofloxacin, aminoglycosides, ampicillin-sulbactam, cefepime amoxicillin-clavulanic acid. Resistance to trimetropin-sulfametoxazol, the first line treatment, was observed in 9.1% of isolates.

Conclusion: Gram negative bacteria were the most frequently isolated during both periods. Acinetobacter baumannii and *Pseudomonas aeruginosa* showed similar carbapenem resistance in both periods, but Klebsiella pneumoniae showed an increase antimicrobial resistance to extended spectrum antibiotics, like carbapenems, aminoglycosides and third generation cephalosporins.

Keywords: Cross Infections, Drug Resistance, Bacterial, COVID-19, Intensive Care Units, (MeSH).

Biography

Dr. Valeria Gordillo Leo studied medicine at the Universidad Peruana Cayetano Heredia (UPCH) in Lima, Peru, and graduated as a Medical Surgeon in 2024. She then joined the research team at the Alexander von Humboldt Institute of Tropical Medicine in Lima, Peru, and is currently the coordinator of a multicenter *Salmonella* project conducted by the International Vaccine Institute, UPCH, and Harvard University.

Shu-Ling Yu[1], Ying-Chin Chen[1], Yen-Hung Chow[1,2*]

[1]Institute of Infectious Disease and Vaccinology, National Health Research Institutes, Zhunan Town, Miaoli County, Taiwan

[2]Graduate Institute of Biomedical Sciences, China Medical University, Taichung, Taiwan

Development of a broad-spectrum vaccine against enterovirus based on adenovirus expression viral-like particles

We study a potent valent vaccine based on adenovector expressing Enterovirus A71 (EV-A71) viral like particle (AdVLP) which elicits a multivalence against not only EV-A71 but also other coxsackieviruses such as A10. In young-aged Human Scavenger Receptor Class B, Member 2 –Transgenic ((hSCARB2-Tg) mice received two-dose of vaccine following challenge with EV-A71, CVA16, or CVA10, AdVLP immunization significantly reduced muscle, spinal cord, and brain's viral amounts and protected animal from disease occurrence. Passive immunization of Tg mice with serum from AdVLP-immunized subjects, following challenge with CVA10, demonstrated that the antibodies in the serum though lacking neutralizing capabilities but exhibiting viral-binding activity effectively protected against CVA10 infection. We also evaluated the efficacy of the Formalin-Inactivated CVA10 (FI-CVA10) vaccine against CVA10 infection. Serum from FI-CVA10-immunized subjects was found to elicit neutralizing antibodies and was subsequently tested in a passive immunization study, demonstrating its effectiveness in preventing CVA10 infection. Notably, passive immunization of Tg mice with AdVLP-immunized splenic lymphocytes, compared to lymphocytes depleted of Invariant Natural Killer T (iNKT) cells, revealed striking differences in outcomes following CVA10 challenge. Mice receiving iNKT-depleted lymphocytes experienced nearly complete mortality by challenge, whereas those receiving AdVLP-immunized lymphocytes achieved a 100% survival rate. In contrast, Tg mice passively immunized with FI-CVA10-immunized splenic lymphocytes showed no resistance to CVA10 challenge. These findings indicate that FI-CVA10 relies primarily on neutralizing antibodies, rather than cellular immunity, for protection against CVA10 infection. Conversely, AdVLP demonstrates multivalent efficacy against CVA10 by inducing iNKT cells and antibody-mediated cellular responses, which together serve as key protective mechanisms against CVA10 infection.

Biography

Dr. Yen-Hung Chow is a senior principal Investigator and professor at the Institute of Infectious Disease and Vaccinology (NIIDV), National Health Research Institutes (NHRI), Taiwan since 2019 until now. He received his PhD degree in 1997 at the Graduate School of Life Sciences, National Defense Medical Center, Taiwan. He then joined the research group of Prof. Dimitrov at the Laboratory of Experimental and Computational Biology, National Cancer Institute, National Institutes of health, USA in 2000-2002 for his postdoctoral fellow. He then moved to the Department of Infectious Disease, University of Georgia, Athens, GA, USA to be a senior postdoctoral fellow in 2002-2005. He obtained the position of an assistant Investigator at the NIIDV, NHRI in 2006. He has published more than 60 research articles in SCI journals.

Heba Tawfik[1] MD, DrPH; Fatima Khuram[2] BS; Radwa Emam[3] BS; Hufsa Arain[4] BS, MPH; Yomna Abdelghani[5*]

[1]College of Health Sciences and Public Policy, Walden University, Minneapolis, MN, USA

[2]Sam Houston State University College of Osteopathic Medicine, Conroe, TX, USA

[3]Texas A&M College of Medicine, Bryan, TX, USA

[4]McGovern Medical School, Houston, TX, USA

[5]University of Houston, Houston, TX, USA

Uncovering predictors of the 2025 measles resurgence in Texas: Ecologic determinants & risk patterns

Background: Despite measles elimination in the USA since 2000, recent outbreaks of measles have occurred in several Texas counties. The 2025 measles outbreak in Texas, with over 760 confirmed cases, marks the largest resurgence in over three decades. The last large outbreak in Texas occurred in 1992 and was driven primarily by limited vaccine availability and infrastructure gaps. This study explores risk factors for the current resurgence. Identifying county-level factors driving this resurgence is critical for targeted public health interventions.

Objective: This study aimed to identify key predictors of measles resurgence across Texas counties using data from the Texas Department of State Health Services and the CDC. The lessons learned from this resurgence can be useful in mitigating future outbreaks.

Methods: In this cross-sectional ecologic study, county-level data from 2024–2025 were compiled from public health sources namely the Texas Department of State Health Services and CDC. Multivariate linear regression was used to analyze associations between predictor variables, including social determinants of health, healthcare infrastructure metrics, vaccination coverage and the incidence of measles in Texas counties.

Results: As of August 2025, the Texas Department of State Health Services confirmed a total of 762 measles cases statewide, making it the largest outbreak in the state in over 30 years. Of those infected, 99 individuals required hospitalization, representing approximately 13% of all cases. There were two fatalities, both involving school-aged children. Neither had known underlying health conditions. At the individual level, vaccination status remained the most important predictor of contracting measles with 97% of individuals either unvaccinated or under-vaccinated. Linear regression was used to explore county-level risk factors. The adjusted regression model explained 66.1% of the variance in measles incidence (adjusted R^2=0.661, $p<0.001$). Higher measles incidence was significantly associated with lower vaccination coverage (β=-0.461, $p<0.001$) and higher percentages of individuals without high school education (β=0.542, $p<0.001$). In unadjusted analyses, increased provider density was associated with decreased measles incidence (β=-0.541, $p<0.001$), but this was not statistically significant in the final adjusted model. Other factors that were explored including rural/urban status, number of hospitals per county, population density, median income, and percentage of foreign-born residents, were not significant predictors of higher incidence of measles ($p>0.05$).

Conclusion: Measles resurgence in Texas was linked to lower vaccination rates and lower educational attainment. Areas with decreased immunization coverage have shown a higher incidence of outbreaks and lower educational attainment can be associated with reduced engagement in preventative healthcare practices, including childhood vaccinations. Individuals with limited formal education may be less likely to access credible health information or to recognize the importance of immunization in preventing highly contagious diseases like measles. These results highlight the importance of equity-focused vaccination efforts and education, alongside improving healthcare provider availability, to mitigate future outbreaks.

Biography

Yomna Abdelghani is a premedical student at the University of Houston majoring in Psychology with minors in Health and Biology. Passionate about research and public health, Yomna is particularly interested in infectious disease prevention, health disparities, and community-based interventions. As the President and Founder of the Health Outreach Society at the University of Houston, she leads initiatives that empower students to engage in health education and community service. Her work bridges academic knowledge and real-world impact, fostering student involvement in health awareness. With a strong commitment to medicine and community outreach, Yomna aspires to make meaningful contributions to healthcare, research and preventative education.

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