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INFECTION 2026

10TH EDITION OF WORLD CONGRESS ON

INFECTIOUS DISEASES

"New Frontiers in Infectious Diseases: Diagnosis, Treatment, and Control"

June 25-27, 2026
Barcelona, Spain

EXHIBITOR

bertin Life Sciences
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Hotel Alimara
Carrer de Berruguete, 126,
Horta-Guinardó, 08035 Barcelona, Spain

10TH EDITION OF

WORLD CONGRESS ON INFECTIOUS DISEASES

HYBRID EVENT

25-27 JUNE 2026

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ID-FISH Technology, USA

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University of Kentucky College of Medicine, United States

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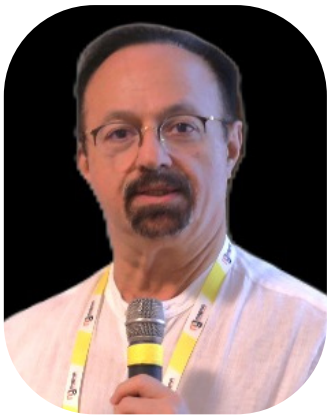
N.D. Zelinskii Institute for Organic Chemistry of the Russian Academy of Sciences, Russian Federation

Vincenzo Pennone

IRCCS Galeazzi Sant'Ambrogio Hospital, Italy

Xiaoyun Zhao

Tianjin University Chest Hospital, China



Yazdan Mirzanejad

University of British Columbia, Canada

Welcome Message

Masafumi Seki MD, PhD

Division of Infectious Diseases and Infection Control,
Saitama Medical University International Medical Center,
Japan

Dear Colleagues and Friends,

It is our great pleasure to invite distinguished speakers and researchers to the Infection 2026 on June 25-27, 2026 at Barcelona, Spain.

Sciences of infectious diseases field make unprecedented progress today since the pandemics of novel influenza 2009 and COVID-19. Furthermore, RS virus and other respiratory virus are also found to induce severe diseases not only in children, but also in elderly people.

Recently, we found new issues, including 'subclade K' in influenza as a 'new kid on the block', and pneumococcal vaccines have been developed to cover the wider serotypes as 'number games'.

This opens new opportunities to achieve higher treatment and prevention efficiency, and to introduce intelligent, differentiated methods to works against these infectious diseases. It is obvious that both basic and clinical research could go together, and these studies based of precise microbiological and clinical evidence will be the future basis for success.

Welcome Message

Pedro Plans-Rubió

College of Physicians of Barcelona, Spain

Dear Conference Attendees,

It is an honor and great pleasure to write a few welcome notes for the 10th Edition of World Congress on Infectious Diseases. We are living in the era of great research and innovations regrading the diagnosis, treatment, prevention and control of infectious diseases. This congress aims to cover a wide array of topics under the unifying theme of "New Frontiers in Infectious Diseases: Diagnosis, Treatment, and Control," including clinical aspects of infectious diseases, antimicrobial resistance, epidemiology of infectious diseases, pandemic preparedness, new treatments against infectious diseases, genomics, one health approach to infectious diseases, vaccines and prevention and control strategies of infectious diseases. The program is designed to cover all topics and facilitate comprehensive discussions, networking, and the sharing of new research insights among professionals. The congress sessions will provide a great opportunity for participants including young and senior researchers, scientists, clinicians and academicians to gain knowledge with the up-to-date research on infectious diseases.

Welcome Message

Ranjan Ramasamy

ID-FISH Technology, United States

Dear Participants,

It is a privilege to welcome you to the 10th World Congress on Infectious Diseases, June 25–27, 2026 being held in the beautiful city of Barcelona, Spain. Although there have been many advances in their diagnosis, treatment, epidemiology and prevention, infectious diseases continue to cause high levels of illness and fatalities in the world. They are capable of springing surprises with serious consequences, e.g. the COVID-19 pandemic of 2019. The many exciting in-person and online presentations on various aspects of infectious diseases that have been scheduled will make this an enjoyable and productive Congress.

Welcome Message

Saurabh Chattopadhyay

University of Kentucky, Country: USA

Dear Infection-2026 Attendees,

It is our honor to invite you to participate in Infection-2026. Infectious diseases continue to pose profound challenges to human and animal health, as highlighted by recent events such as the COVID-19 pandemic. Progress in this field depends on strong global collaboration and the sharing of new ideas. This conference will bring together scientists and clinicians to highlight recent discoveries and advances across the broad landscape of infectious disease research.

Welcome Message

Dr. Sergey Suchkov MD, PhD

Professor in Medicine & Immunology and Director for Center for Biodesign of N.D. Zelinskii Institute for Organic Chemistry of the Russian Academy of Sciences, Moscow, Russia
R&D Director, InMedStar, Russia-UAE

Senior Scientific Advisor of China Hong Kong Innovation International Business Association, Hong Kong
Member, New York Academy of Sciences, USA
Member: EPMA (European Association for Predictive, Preventive and Personalized Medicine), Brussels, EU
Member, ISPM (International Society for Personalized Medicine), Japan
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Member, AMEE (Association for Medical Education in Europe), Centre for Medical Education, Dundee, Scotland
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Member, AHA (American Heart Association), Dallas, TX, USA
Member, ARVO (The Association in Research in Vision & Ophthalmology), Rockville, MD, USA
ISER (International Society for Eye Research), Anchorage, AK USA
Secretary General, United Cultural Convention (UCC), Cambridge, UK

Dear Conference Attendees,

It is an honor and great pleasure to write a few welcome notes for the 10th Edition of World Congress on Infectious Diseases.

We are in an era of incredible opportunities, thanks to the progress in OMICS-driven immune therapies and vaccination prevention, and in design-inspired technological medicine applied to infectious disease. In this context, this Event would stimulate an enhanced understanding how to overcome the obstacles to the creation of effective personalized therapeutics (including vaccines) to protect against pathogens, and would disclose clinically relevant biomarkers of protection, vaccine response heterogeneity, and our understanding of immunosenes-cence. In this context, the Conference promises to be an exceptional gathering of renowned experts, researchers, healthcare professionals, policymakers, and industry leaders from around the world.

A multidisciplinary approach linking basic, clinical and personalized health research is crucial to advance our understanding of the growing pandemic of infectious diseases. In this context, the Program will feature plenary lectures from internationally renowned experts, in-depth symposia, interactive workshops and seminars, and state-of-the-art poster sessions, designed to highlight the latest breakthroughs in microbial pathogenesis, vaccine development, antimicrobial resistance, emerging infections, digital health innovations, and strate-gies to advance health equity worldwide.

This Event will provide a dynamic platform for the exchange of knowledge, ideas, and in-sights into the latest developments in the field of infectious diseases and preventive and prophylactic immunization, as well as to develop international networks in order to advance their research, teaching and clinical practice.

We look forward to welcoming you to Infection 2026, as we come together to explore the fu-ture of the trends and their impact on global health.

Welcome Message

Xiaoyun Zhao

Tianjin University, Chest Hospital, China

Dear Conference Attendees,

It is an honor and great pleasure to write a few welcome notes for the World Congress on Infection Disease in 2026. We are living in an era of rising severe infections, where infection-related Acute Respiratory Distress Syndrome (ARDS) remains a major cause of mortality worldwide. A multidisciplinary approach linking stem cell biology, immunology, and translational medicine is urgently needed to understand how Mesenchymal Stem Cells (MSCs) and their exosomes (MSC-Exo) modulate inflammation and promote lung repair. Our session covers key topics: (1) Pathophysiology of infection-related ARDS; (2) Immunomodulation by stem cells in sepsis/pneumonia; (3) MSC-Exo as cell-free therapies; (4) Preclinical models of ARDS; (5) Clinical trials of stem cell interventions; and (6) Future translational challenges. This is a great opportunity for all WOC participants-intensivists, infectious disease specialists, stem cell biologists, and clinicians-to gain up to date knowledge on stem cell therapies for infection induced ARDS.

Welcome Message

Yazdan Mirzanejad

University of British Columbia, Canada

Dear colleagues and participants,

It is a great pleasure to welcome you to Barcelona for this conference devoted to the growing intersection between climate change and antimicrobial resistance. We are gathered here as clinicians, scientists, and public health professionals who share a common responsibility to address one of the most significant challenges facing global health today. Antimicrobial resistance, particularly Extensively Drug-Resistant (XDR) pathogens, continues to threaten the effectiveness of the therapies on which modern medicine depends. Increasingly, we recognize that this crisis does not exist in isolation. Climate change is reshaping ecosystems, influencing patterns of infection, and intensifying environmental pressures that contribute to the emergence and spread of resistant organisms. Responding to these interconnected threats requires broader collaboration across disciplines and sectors. The One Health perspective reminds us that human, animal, and environmental health are deeply linked. I hope this meeting encourages meaningful dialogue, strengthens partnerships, and helps advance strategies to preserve antibiotics for future generations.

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About
Magnus Group

About

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

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

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

About
Infection 2026

About

We are delighted to announce the **10th Edition of the World Congress on Infectious Diseases (Infection 2026),** taking place from **June 25–27, 2026, in Barcelona, Spain, and virtually.** This prestigious hybrid event will unite leading experts, researchers, healthcare professionals, and academicians from around the world to exchange knowledge and discuss the latest advancements in infectious diseases.

Under the theme **"New Frontiers in Infectious Diseases: Diagnosis, Treatment, and Control,"** the congress will serve as a dynamic platform for interdisciplinary collaboration and scientific innovation. Infection 2026 aims to address current global health challenges by promoting discussions on emerging infectious diseases, prevention strategies, novel therapies, public health policies, and advanced diagnostic technologies.

The scientific program will feature keynote lectures, plenary sessions, panel discussions, oral presentations, and interactive networking opportunities. Participants will gain valuable insights into groundbreaking research, clinical practices, epidemiology, immunology, and disease management approaches that are shaping the future of infectious disease care.

Infection 2026 promises an engaging and inspiring environment for learning, collaboration, and professional growth. We warmly invite you to join us in Barcelona or virtually to contribute to meaningful discussions and help advance the global fight against infectious diseases.

About Exhibitor

About

bertin Life Sciences

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Bertin Life Sciences, a brand of Bertin Technologies, provides innovative laboratory solutions for life sciences, pharmaceutical and biotechnology research. Our expertise spans three key areas: Sample preparation (sample homogenization and grinding), control of air-borne contamination (biological air sampler) and biomarker assay kits designed to ensure the reliability of analytical results. Through this broad portfolio and recognized scientific expertise, Bertin Life Sciences supports researchers and industry professionals throughout the entire analytical workflow.

Developed by Bertin Life Sciences, the Coriolis® range offers a high-performance and versatile solution for biological air sampling in both indoor and outdoor environments. Thanks to its cyclonic technology, this solution enables the efficient collection of airborne biological particles, regardless of their nature (bacteria, viruses, pollen, and more). The collected samples can be directly used for microbiological and molecular analyses, thereby facilitating rapid characterization of air contamination. In the context of infectious disease surveillance and outbreak response, the Coriolis® is a key tool for environmental monitoring and pathogen detection.

Contact Information:

Website: www.bertin-technologies.com

Email: sales-life@bertin.group

About
CPD Accreditation

About

Continuing Professional Development (CPD) credits are valuable for Infection 2026 attendees as they provide recognition and validation of their ongoing learning and professional development. The number of CPD credits that can be earned is typically based on the number of sessions attended. All the participants have an opportunity to avail 1 CPD credit for each hour of Attendance.

Some benefits of CPD credits include:

Career advancement: CPD credits demonstrate a commitment to ongoing learning and professional development, which can enhance one's reputation and increase chances of career advancement.

Maintenance of professional credentials: Many professions require a minimum number of CPD credits to maintain their certification or license.

Increased knowledge: Attending Infection 2026 and earning CPD credits can help attendees stay current with the latest developments and advancements in their field.

Networking opportunities: This Conference provide opportunities for attendees to network with peers and experts, expanding their professional network and building relationships with potential collaborators.

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25-27 JUNE 2026

KEYNOTE PRESENTATIONS

Claudia Ferreira MD, PhD

Sorbonne Université Paris, France

Biography: Claudia Ferreira MD, PhD, is graduated in medicine from the University of Cordoba in Argentina, followed by a fellowship from the Harvard AIDS Institute and the University of Texas Health Science Center in Houston, TX, USA. Dr. Ferreira has dedicated the last 25 years of her career to the fields of infectious diseases, tropical diseases, and gastroenterology. Dr. Ferreira was also a medical editor of a web portal related to community awareness for bioterrorism after 9/11. Dr. Ferreira also worked as an investigator for the National Agency for AIDS Research, a branch of the National Center for Research Science, and for several pharmaceutical laboratories in France. She helps international agencies and private organizations manage emerging infectious diseases, pandemic preparedness and-response planning. Currently she is the Medical Director of Biophytis, at the University of Sorbonne in France.

Bioterrorism through the ages: Historical perspective, emerging threats, and medical countermeasures

Bioterrorism is defined as “the intentional release or threat of release of biologic agents-viruses, bacteria, fungi, or their toxins-to cause disease or death in humans, animals, or crops”. Bioterrorism remains a significant and evolving threat to public health. Though often associated with modern terrorism, bioterrorism has deep historical roots spanning over 2,000 years-from the contamination of water sources in ancient warfare to the deliberate spread of smallpox during colonial campaigns.

In the 21st century, this threat has expanded, with over 1,200 known biological agents identified for their potential use as weapons of mass destruction. The convergence of biotechnology, synthetic biology, and accessible genomic tools has lowered the technical barriers to developing these agents. Notably, the 2001 anthrax letter attacks in the United States highlighted the devastating impact a relatively small-scale bioterrorist act can have on public trust, healthcare systems, and emergency response networks.

The historical trajectory of bioterrorism and its clinical manifestations, drawing from documented outbreaks and intentional releases. Special attention should be paid to Category A agents (e.g., *Bacillus anthracis, Variola virus, Yersinia pestis*) recognized for their high mortality, ease of dissemination, and potential to cause public panic.

In this context, healthcare professionals play the vital role of in early recognition, triage, infection control, and the deployment of countermeasures, including vaccines, antibiotics, and antitoxins. In addition, the architecture of modern biodefense systems such as the Laboratory Response Network (LRN), syndromic surveillance programs, and interagency emergency protocols are important tools for the medical community.

The SARS-CoV-2 pandemic demonstrated that the urgency for integrated preparedness strategies is greater than ever. Medical professionals are not only first responders but also frontline defenders in identifying and mitigating biologic threats. By enhancing our clinical vigilance, investing in ongoing training, and strengthening interprofessional collaboration, we can fortify our healthcare systems against future bioterrorist events.

Masafumi Seki MD, PhD

Division of Infectious Diseases and Infection Control, Saitama Medical University, International Medical Center, Hidaka City, Saitama, Japan

Biography: Professor Seki has been graduated from Department of Medicine, Nagasaki University, as Medical Doctor, with the specialties including Internal Medicine, Infectious Diseases, and Infection Control. Later on he obtained his post-graduation, started working at Osaka University. After the professor of Tohoku Medical and Pharmaceutical University, presently he has been working at the Saitama Medical University International Medical Center, Hidaka City, Saitama, Japan.

Severe influenza and other related respiratory infection cases during Omicron era in Japan

Introduction: We had severe respiratory infection cases after COVID-19 pandemic in Japan. At first, three cases of severe influenza that required ventilator management in the 2024-2025 season, which was a major influenza season in Japan, are presented.

Case Series:

Case 1: A 54-year-old man with obesity developed lobar pneumonia as a result of severe Community-Acquired Pneumonia (CAP) secondary to methicillin-susceptible *Staphylococcus aureus*, as confirmed on sputum culture. The nasal swab was positive for influenza A antigen. Intravenous peramivir and piperacillin/tazobactam were administered for 2 days followed by lascufloxacin and linezolid for 2 weeks. Veno-venous Extracorporeal Membrane Oxygenation (ECMO) was also performed after intubated ventilator management.

Case 2: A 63-year-old man with multiple myeloma and chronic kidney disease developed severe pneumonia as a result of CAP. Although influenza A antigen was detected, no bacteria were isolated from blood cultures or respiratory specimens. He showed severe hypoxia and massive ground-glass opacities in both lung fields, but he recovered after administration of peramivir and levofloxacin with prednisolone for 2 days and 2 weeks, respectively, with non-invasive positive pressure support.

Case 3: A 43-year-old man without any related medical history developed severe heart failure with mild bronchopneumonia and was admitted to our hospital; influenza A antigen was detected from the nasal swab. Acute heart failure caused by myocarditis and CAP were suspected and were effectively treated with peramivir and percutaneous ventricular assist device (IMPELLA), which involved an auxiliary circulating pump with veno-arterial ECMO for 1 day and 2 weeks, respectively, with intubated ventilator management.

Conclusions: In three middle-aged patients, influenza virus may have accelerated the secondary bacterial pneumonia, pure viral pneumonia, and myocarditis. All three patients had not received influenza vaccines and were not elderly. Although most of all vaccines have been made light after the COVID-19 pandemic appears to have subsided, we should reinform the importance of influenza vaccines and improvement of critical care protocols, including other respiratory infections, such as COVID-19, RS virus infection, and *Pneumococcal pneumonia*.

Michele Mishto

The Francis Crick Institute, UK
King's College London, UK

Biography: Prof. Michele Mishto is Professor in Immunobiology at the King's College London and Senior Group leader at the Francis Crick Institute in London (UK). PhD in Medical Biotechnology at University of Bologna (ITA) and a long post-doc and project leader experience at the Institute of Biochemistry at Universitätsmedizin Charite' Berlin (GER). His research focuses on antigen presentation and proteasomes. He particularly contributed to the identification and characterisation of noncanonical peptides such as proteasome-generated spliced peptides, investigating their antigenicity and immunogenicity in cancer and infections.

Pathogen-derived noncanonical epitopes: Are they valuable targets for novel vaccinations and shall we be concerned about autoimmune responses?

MHC class I complexes can present antigenic peptides that derive from canonical proteins as well as have a sequence produced by post-translational mechanisms such as proteasome-generated peptide splicing. Few pathogen-derived proteasome-generated spliced epitopes have been investigated for their immunogenicity so far. We developed several pipelines to identify and predict both canonical and noncanonical epitopes derived from pathogens, which are freely available. In addition, we tested the immunogenicity and the potential for therapeutical applications for those associated to various forms of infections. During my lecture I review the work done my team and others on the identification of pathogen-derived noncanonical epitopes, I discuss the risk of autoimmune response triggered by them and their potential relevance for future development on vaccines.

Nathalie Silvestre*, Jean-Baptiste Marchand, Patricia Kleinpeter, Véronique Koerper, Christelle Remy, Hakim Makhloufi, Bérangère Marie-Bastien, Clémentine Spring-Giusti, Geneviève Inschauspé, Emmanuelle Dochy, Maurizio Ceppi

Transgene SA, France

Biography: Nathalie Silvestre is Head of the Vectorology Laboratory at Transgene, where she leads activities focused on the design, engineering, and characterization of viral vectors for therapeutic applications. With extensive experience in virology and molecular biology, she plays a key role in advancing Transgene's platform technologies, including vaccinia-based vectors. Nathalie works at the interface of research and development, supporting both preclinical innovation and translational readiness. Her expertise contributes to the development of novel immunotherapies in oncology and infectious diseases, helping to drive scientific excellence and foster collaborations within the biotech ecosystem.

Robust protection against monkeypox virus mediated by a novel cell-line–derived MVA vaccine (TGMVAcL)

Monkeypox (mpox) is a zoonotic disease caused by the Monkeypox Virus (MPXV). Recent global outbreaks in non-endemic countries demonstrated their significance as a threat to public health. The main approved and widely used vaccine to fight MPXV infection, MVA-BN®, is based on the Modified Vaccinia Ankara (MVA) produced on primary cells (chicken embryo fibroblast - CEF). To respond to the critical and unmet need for vaccine stockpiling preparedness, we have used an easily scalable and transposable cell line-based manufacturing process to produce a novel generation of MVA-based mpox vaccine, the TG-MVACL manufactured on cell line. Safety, immunogenicity (specific of Vaccinia Virus (VACV) and/or MPXV and prophylactic protection against MPXV clade Ia lethal infection studies) were carried out in mice and Non-Human Primates (NHP) to compare both cell-line manufactured TG-MVACL and its counterpart produced in CEF (TG-MVACEF) with MVA-BN®.

VACV-specific responses were analyzed in BALB/C mice in which all three vaccines developed similar levels Neutralizing antibodies (Nab), specific T-cells by ELISPOT which were detected in 70-100% of vaccines.

Stringent, infectious challenge was applied using the MPXV clade Ia (Zaïre 79 strain) in established mice and NHP models. The three vaccines induced very high, comparable protection in CAST/Ei mice (100%) and NHP (88%) in contrast to control groups displaying 100% mortality. Whether in mice or NHP, both the kinetics and level of transient weight loss

observed post-challenge, were similar for all vaccine groups.

In the NHP prophylactic model, only a limited number of lesions (< 42) were observed in the vaccines versus up to 400 in control animals indicating that vaccination strongly protected against mpox-

induced lesion development and substantially blunted the severity of clinical skin disease following challenge. Following MPXV intratracheal challenge, controls developed rapid and high-magnitude viremia. In contrast, all vaccinated cohorts exhibited markedly attenuated systemic viral burden in the blood and in throat swabs. At immunogenicity peak (D42), all vaccinated animals demonstrated broad vaccine-induced binding antibody responses against both major VACV and MPXV antigens tested. Moreover, neutralizing antibody responses against VACV, MPXV Clade II, and to a lesser extent to MPXV Clade I were also detected in the vaccinated animal. ELISPOT data showed detection of an overall peptide pool with specific response in 30-70 % of the vaccinees.

Overall safety based on clinical signs, local reactogenicity, hematology and biochemistry were good with comparable safety profile across the three MVA-based vaccines, regardless of the manufacturing process.

In conclusion, TG-MVA produced on a continuous cell line (TG-MVACL) or on CEF (TG-MVACEF) induced robust humoral and cellular immune responses, comparable to those elicited by MVA-BN®. Prophylactic protection and safety of TG-MVACL strongly support its clinical development in the fight against MPXV and more broadly against Orthopoxviruses.

Pedro Plans-Rubió

College of Physicians of Barcelona, Spain

Biography: Pedro Plans-Rubió has been Responsible for Health Registries, Public Health Agency of Catalonia, Barcelona, Spain. MD from the School of Medicine, University of Barcelona; PhD from the School of Medicine, University of Barcelona; MSc in Health Economics from the School of Economics, University of Barcelona. Specialist in Preventive Medicine and Public Health. Member of the Group of Prioritization of Treatments (GIP), Heath Emergency Preparedness and Response (HERA), European Commission. Member of the Non-communicable diseases risk factor Collaboration (NCD-RisC) research group. Editor-in Chief of Section "Vaccine Advancement, Efficacy and Safety" of journal Vaccines. Member of the Editorial Board of journal Pharmacoeconomics Open, Elsevier.

Measles vaccination coverage indicators in 2023 and advance towards measles elimination and eradication by 2030

The Immunization Agenda 2030 (IA2030) proposed by the 73rd World Health Assembly in 2020 committed to eliminating measles in at least five of the six WHO regions by 2030. Mean percentages of vaccination coverage with two, one and zero doses of measles vaccine in WHO regions in 2023 were calculated using data from the WHO/UNICEF global and regional immunization information system. The study found that in 2023, the two-dose measles vaccination coverage was lower than 95% in all WHO regions and anti-measles herd immunity levels were sufficient to block the transmission of measles viruses with greater transmissibility (R_o of 15) only in the Western Pacific and European WHO regions. All measles vaccination-coverage-related indicators worsened from 2019 to 2023. The global two-dose measles vaccination coverage decreased by 3.7%, the global zero-dose measles vaccination coverage increased by 7.8%, and the prevalence of vaccine-induced protected individuals (target population) decreased by 0.6%. In 2023, the zero-dose measles vaccination coverage and number of zero-dose measles children observed were not on track to achieve the AI2030 objective. To advance towards measles elimination from WHO regions and measles eradication worldwide it is necessary to develop ambitious strategies to increase routine two-dose measles vaccination coverage in all WHO regions, and to prevent measles transmission among different WHO regions.

Ranjan Ramasamy

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

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

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

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

Saurabh Chattopadhyay

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

Biography: Saurabh Chattopadhyay Ph.D., is an associate professor in the Department of Microbiology, Immunology, and Molecular Genetics at University of Kentucky (UK) College of Medicine, Lexington, Kentucky, USA. His group studies virus infection and its interaction with host immune responses. Research in his laboratory is funded by the National Institutes of Health, Ohio Department of Health, Center for Disease Control, and American Heart Association.

New paradigms of IRF biology in virus infection

Interferon Regulatory Factors (IRFs) are classically viewed as transcription factors that induce interferons and antiviral genes during viral infection. Our work reveals that IRF biology extends beyond transcriptional control to include non-canonical functions that shape host responses. We identified a transcription-independent activity of IRF3 that promotes apoptotic elimination of infected cells (RIPA), providing an alternative antiviral effector mechanism. We further uncovered a distinct pathway in which IRF3 suppresses NF-κB-dependent inflammatory gene expression, thereby limiting excessive cytokine responses during respiratory viral infection (RIKA). Notably, IRF7 contains a homologous NF-κB-binding motif and similarly represses inflammatory gene expression, suggesting that this anti-inflammatory function represents a broader regulatory module within the IRF family. Together, these findings redefine IRFs as multifunctional regulators that coordinate antiviral defense while restraining pathological inflammation during viral infection.

Sergey Suchkov[1-13*], Robert Langer[14], Shawn Murphy[15,16], David Smith[17], Hiroyuki Abe[6,18]

[1]Professor in Medicine & Immunology and Director for Center for Biodesign of N.D. Zelinskii Institute for Organic Chemistry of the Russian Academy of Sciences, Moscow, Russia

[2]R&D Director, InMedStar, Russia

[3]Senior Scientific Advisor of China Hong Kong Innovation International Business Association, Hong Kong

[4]Member, New York Academy of Sciences, USA

[5]Member: EPMA (European Association for Predictive, Preventive and Personalized Medicine), Brussels, EU, Belgium

[6]Member, ISPM (International Society for Personalized Medicine), Japan

[7]Member, PMC (Personalized Medicine Coalition), Washington, USA

[8]Member, AMEE (Association for Medical Education in Europe), Centre for Medical Education, Dundee, Scotland

[9]Member, ACS (American Chemical Society), Washington, DC, USA

[10]Member, AHA (American Heart Association), Dallas, TX, USA

[11]Member, ARVO (The Association in Research in Vision & Ophthalmology), Rockville, MD, USA

[12]ISER (International Society for Eye Research), Anchorage, AK, USA

[13]Secretary General, United Cultural Convention (UCC), Cambridge, UK

[14]MIT, Cambridge, MA, USA

[15]Harvard Medical School, USA

[16]MGH, Boston, MA, USA

[17]Mayo Clinic, Rochester, MN, USA

[18]Tokyo Cancer Clinic, Tokyo, Japan

Biography: Sergey Suchkov was born in the City of Astrakhan, Russia, in a family of dynasty medical doctors. In 1980, graduated from Astrakhan State Medical University and was awarded with MD. In 1985, Suchkov maintained his PhD as a PhD student of the I. M. Sechenov Moscow Medical Academy and Institute of Medical Enzymology. In 2001, Suchkov maintained his Doctor Degree at the National Institute of Immunology, Russia. From 1989 through 1995, Dr. Suchkov was being a Head of the Lab of Clinical Immunology, Helmholtz Eye Research Institute in Moscow. From 1995 through 2004-a Chair of the Dept for Clinical Immunology, Moscow Clinical Research Institute (MONIKI). In 1993-1996, Dr. Suchkov was a Secretary-in-Chief of the Editorial Board, Biomedical Science, an international journal published jointly by the USSR Academy of Sciences and the Royal Society of Chemistry, UK. At present, Dr. Sergey Suchkov MD, PhD, is: Professor and 1R&D Director, Centro de Estudios de la Fotosintesis Humana, Aguascalientes, Mexico. Member, The Russian Academy of Natural Sciences (RANS), Russia. Member, New York Academy of Sciences, USA. Secretary General, United Cultural Convention (UCC), Cambridge, UK. Dr. Suchkov is a member of the: American Chemical Society (ACS), USA; American Heart Association (AHA), USA; European Association for Medical Education (AMEE), Dundee, UK; EPMA (European Association for Predictive, Preventive and Personalized Medicine), Brussels, EU; ARVO (American Association for Research in Vision and Ophthalmology); ISER (International Society for Eye Research); Personalized Medicine Coalition (PMC), Washington, DC, USA.

Personalized and Precision Medicine (PPM) as a unique healthcare model to secure the human healthcare, wellness and biosafety through the view of public health, network driven healthcare services and lifestyle management

Personalized and Precision Medicine (PPM) is being the Grand Challenge to forecast, to predict and to prevent is rooted in a big and a new SCIENCE generated by the achievements of (i) Systems & Synthetic Biology; (ii) Biodesign-driven Translationa applications and Biotech-driven Biomanufacturing; (iii) Bioindustry and Biomarketing of the next step generation. The latter, being a Grand Brick laid into the frame of National Bioeconomy, says and confirms that the efficiency and efficacy of the Bioeconomy are determined and dictated by the innovative trends, generated by fresh knowledge and their transfer into the scientific, bioindustrial and social areas to maintain the national stability and extensive development of the country.

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

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

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

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

PPM-guided public health systems are essential for preventing and controlling the spread of infectious diseases. They provide the framework for identifying, tracking, and responding to disease outbreaks through surveillance, early detection, and effective treatment. Strengthening public health systems is essential for effective infectious disease control in the modern world. By investing in robust surveillance systems, expanding personalized vaccination programs, improving healthcare infrastructure, engaging communities, and fostering international collaboration, countries can better prevent and respond to outbreaks of infectious diseases. While challenges such as limited resources, vaccine hesitancy, and emerging diseases. remain, a concerted effort to build resilient public health systems can significantly reduce the global burden of infectious diseases.

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

PPM has indeed arrived for the diagnosis of infectious diseases. More than that, it has arrived once and for all in the areas of clinical microbiology, molecular epidemiology and many other areas. With the current capabilities, cost, and speed of sequencing technologies, the field has finally reached a point where rapid genomic surveillance and analysis can start to become a standard part of the response to infectious disease outbreaks. Just as broadscale human genome sequencing revolutionized the treatment of many noncommunicable diseases, pathogen genome data are poised to drive a similar revolution in the response to infectious diseases.

In this context, the network links hospitals to allow them to view guidelines developed by institutions across the globe, access their epidemiological datasets and subscribe to updates. Hospitals can adapt and use those guidelines, and the system can help them communicate with frontline healthcare providers through their mobile devices and computers. The system also provides hospitals with a real-time feed of emerging evidence, information and guidelines, as well as predictive and research data from other sources. It will also include platforms that enable discussion within the hospital and with other health organizations.

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

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Biography: Dr. Vincenzo Pennone is a microbiologist specializing in antimicrobial resistance, biofilm-associated infections, and the testing of novel antimicrobial compounds. After earning his degrees in Biology and completing a Ph.D. on foodborne pathogens in Ireland, he gained international experience through postdoctoral and European research fellowships. He is currently a senior researcher at the IRCCS Ospedale Galeazzi–Sant'Ambrogio in Milan (Italy), where his work focuses on antimicrobial peptides and innovative strategies to prevent and treat orthopedic infections. His research integrates microbiology, genetics, omics technologies, and translational approaches to better understand and combat persistent bacterial infections.

From bench to preclinical evaluation: LL-37-derived peptides for combating orthopedic infections

Orthopedic implant-associated infections, frequently caused by *Staphylococcus* species, remain a major clinical concern due to biofilm formation and the growing threat of antimicrobial resistance. Antimicrobial Peptides (AMPs), derived from the human cathelicidin LL-37, represent a promising alternative approach, offering potent antimicrobial activity and low susceptibility to resistance. This study aimed to design, characterize, and validate LL-37-derived synthetic peptides and their integration into silk fibroin-based biomaterials as delivery compounds to locally treat orthopedic infections.

Truncated analogues of LL-37 were synthesized and evaluated for antimicrobial activity against multi-drug resistant *Staphylococcus aureus* and *Staphylococcus epidermidis* reference and clinical strains. MIC, MBC, and biofilm eradication assays were conducted alongside cytotoxicity and hemolytic tests to determine efficacy and safety. The two most effective peptides, FK-16 and GF-17, were incorporated into Silk Fibroin (SF) and osteoinductive peptide-enriched Silk Fibroin (PSF) scaffolds. Structural and release characterizations,

swelling behaviour, and time-kill assays were performed to analyse their delivery performance against methicillin-resistant *Staphylococcus* strains. Systemic in vivo toxicity studies were conducted in mice by intravenous injection of FK-16 and GF-17.

FK-16 and GF-17 exhibited potent antimicrobial and antibiofilm activities, with MIC values ranging from 2.34-18.75µg/mL and a minimal cytotoxicity at concentrations below 75µg/mL for GF-17 and 150µg/mL for FK-16. Hemolytic activity was negligible (<1%) at antimicrobial doses. FK-16 showed superior release and bactericidal performance when incorporated into SF and PSF scaffolds, particularly against methicillin-resistant *S. epidermidis.* PSF matrices improved peptide retention and antibacterial efficacy relative to unmodified SF. In vivo systemic administration in mice revealed no signs of toxicity, confirming the safety of both peptides for further translational research. Importantly, a preclinical trial is currently underway in a rat model of septic nonunion infected with a clinical isolate of methicillin-resistant *S. epidermidis* to evaluate the therapeutic potential of FK-16-based local treatments.

LL-37-derived peptides, especially FK-16, display strong antimicrobial efficacy, low cytotoxicity, and successful integration into silk fibroin-based delivery systems. The combination of FK-16-loaded PSF scaffolds represents a promising strategy for localized prevention and treatment of multi-drug resistant orthopedic infections. The absence of systemic toxicity and ongoing preclinical evaluations in an infected nonunion model underscore the translational potential of this AMP-based therapeutic approach for the management of orthopedic infections.

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Biography: Dr. Xiaoyun Zhao studied Clinical Medicine at the Nankai University and got his MM degree in 2004, and then received his MD degree at the Tianjin Medical University. His fellowship was supervised by Dr. Richard Castriotta at the Texas University Health Science Center at Huston. Now he serve as the chief doctor and the discipline leader of National Respiratory Medicine Clinical Key Specialty at Tianjin Chest Hospital. Also he serve as a professor of Clinical Medicine and Biomedical Engineering at the Tianjin University, Tianjin Medical University and Tiangong University, China. He has published more than 100 articles in various journals.

Mechanisms of mesenchymal stem cells and MSC-Exo in therapy of infection-related ARDS

Mesenchymal Stem Cells (MSCs) and their Exosomes (MSC-Exo) are promising for treating infection-induced Acute Respiratory Distress Syndrome (ARDS), mainly via paracrine effects involving immunomodulation, anti-inflammation, antimicrobial activity, and tissue repair, rather than direct cell replacement.

Infections (e.g., bacterial pneumonia, sepsis) cause ARDS, whose pathology involves uncontrolled inflammatory cytokine storms and disrupted pulmonary endothelial-epithelial barriers, leading to edema and respiratory failure. Their core mechanisms are as follows:

I. **Immunomodulation and Anti-Inflammation:** This is the key mechanism. MSCs and MSC-Exo promote M1-to-M2 macrophage polarization via miRNAs (e.g., miR-223, miR-146a), inhibit neutrophil infiltration/NETosis, suppress pro-inflammatory Th1/Th17 cells while enhancing regulatory T cells, and reduce pro-inflammatory cytokines (e.g., TNF-α, IL-6) via soluble factors (e.g., PGE2, TGF-β), elevating anti-inflammatory IL-10.

II. **Antimicrobial Activity:** They enhance pathogen clearance by boosting M2 macrophage phagocytosis, secreting antimicrobial peptides (e.g., LL-37), transferring mitochondria to restore cellular energy and bactericidal capacity, and upregulating endogenous antimicrobial peptides via MSC-Exo miRNAs.

III. **Tissue Repair:** They promote alveolar fluid clearance via VEGF/KGF, protect endothelial/epithelial cells from apoptosis, upregulate tight junction proteins (e.g., occludin), stimulate alveolar type II cell proliferation, and inhibit pulmonary fibrosis via TGF-β1/Smad pathway modulation.

IV. **MSC-Exo Advantages:** As cell-free mediators, they avoid live cell risks (e.g., embolism, rejection), target injured sites specifically, protect cargo (miRNAs, proteins) via lipid bilayers, with miRNAs as core components regulating inflammation and barrier function.

Preclinical studies and early clinical trials (I/II) confirm safety and efficacy. Key challenges include optimizing cell sources/dosing, standardizing exosome production, and addressing efficacy heterogeneity across ARDS etiologies. In summary, MSCs and MSC-Exo treat infection-induced ARDS via synergistic effects: Suppressing inflammation, combating infection, and repairing tissue.

Yazdan Mirzanejad

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Biography: Dr. Yazdan Mirzanejad is a highly respected Infectious Diseases specialist with formal certification in Tropical Medicine, and a Clinical Professor in the Division of Infectious Diseases at the University of British Columbia (UBC). He currently leads Undergraduate Medical Education at UBC's Surrey Campus and holds an adjunct faculty appointment with the Simon Fraser University (SFU) Medical School. Dr. Mirzanejad also serves as Co-Site Director of the CDC-GeoSentinel Global Surveillance Network (Vancouver site), a prestigious international initiative monitoring emerging and travel-related infectious diseases. Over the course of his distinguished career, he has authored and contributed to more than 50 peer-reviewed publications, advancing knowledge in the diagnosis, management, and prevention of infectious and tropical diseases. Renowned for his academic leadership, clinical expertise, and global health perspective, Dr. Mirzanejad has been a driving force in shaping the education of future physicians and in promoting excellence in infectious diseases care. His work has had a significant impact on public health policy, clinical training, and research both nationally and internationally. As a frequent keynote speaker and contributor at international conferences, he continues to influence the evolving landscape of infectious diseases through research, collaboration, and education. Dr. Mirzanejad practice and teaches in Surrey, Fraser Health, located in the South of Vancouver, British Columbia.

Extensively drug-resistant bacterial infections: Confronting a global crisis with urgent solutions in prevention, surveillance, and treatment

Extensively Drug-Resistant (XDR) bacterial infections represent a growing global crisis with profound impacts on morbidity, mortality, and health system sustainability. These pathogens, resistant to nearly all available antibiotics, are rapidly outpacing our therapeutic options and spreading across international borders through healthcare systems, travel, and community networks. Major culprits include *Klebsiella pneumoniae, Acinetobacter baumannii, and Pseudomonas aeruginosa,* as well as strains of *Mycobacterium tuberculosis* with extensive drug resistance. The rising burden of XDR infections is driven by antibiotic overuse, global antibiotic supply chain vulnerabilities, limited infection prevention practices, and gaps in antimicrobial stewardship, particularly in resource-limited settings. This presentation will explore the critical challenges in controlling XDR bacterial infections, including diagnostic delays, high mortality rates, and limited effective treatments. At the same time, it will highlight emerging opportunities: Novel antimicrobial agents, phage therapy, microbiome-based approaches, enhanced global surveillance networks, rapid molecular diagnostics, and the critical role of infection prevention and control. Collaborative international efforts,

sustained investment in antibiotic research and development, and strengthening public health infrastructure are essential to turn the tide. Confronting this crisis demands urgent, coordinated global action to prevent further spread and safeguard the effectiveness of remaining therapeutic options.

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ORAL PRESENTATIONS

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From oral flora to embolic disease: A case of *Streptococcus salivarius* endocarditis presenting with splenic infarction in a young patient

Background: *Streptococcus salivarius* is a viridans group streptococcus that forms part of the normal oral flora and is a rare cause of Infective Endocarditis (IE). Cases are typically associated with poor dentition, dental procedures, or underlying structural cardiac disease. Splenic infarction is an uncommon presentation of IE and may delay diagnosis when an embolic source is not immediately recognised.

Case: A man in his twenties with bicuspid aortic valve and poor dentition presented with a one-month history of malaise, gastrointestinal symptoms, and worsening abdominal pain. Initial Computed Tomography (CT) demonstrated a splenic lesion suspicious for infarction. Subsequent magnetic resonance imaging confirmed multifocal splenic and left renal infarcts, including new lesions compared with the original CT, raising suspicion for an embolic process.

The patient re-presented one week later with worsening symptoms. Blood tests demonstrated elevated inflammatory markers, troponin, and D-dimer. Examination identified a loud ejection systolic murmur not documented previously. Repeated blood cultures isolated *Streptococcus salivarius*. Transthoracic echocardiography demonstrated vegetations on the aortic and mitral valves with moderate aortic regurgitation and suspicion of an aortic root abscess. Transoesophageal echocardiography subsequently confirmed an aortic root abscess, fulfilling Modified Duke criteria for infective endocarditis.

The patient was commenced on intravenous antibiotics and referred for cardiothoracic surgical management.

Discussion: This case highlights *Streptococcus salivarius* as a rare but clinically significant cause of infective endocarditis presenting with systemic embolisation. Although generally considered a low-virulence oral commensal, *S. salivarius* can cause severe invasive infection in patients with structural valve disease and poor dentition.

While viridans *Streptococci* are common causes of IE, *S. salivarius* represents only a small proportion of *Streptococcal endocarditis* cases and may therefore be overlooked as a contaminant. In this case, repeated positive blood cultures alongside echocardiographic findings confirmed clinically significant infection complicated by splenic and renal infarction and aortic root abscess formation.

This case also demonstrates the importance of considering infective endocarditis in patients presenting with unexplained visceral infarction, particularly younger patients with congenital valve abnormalities. Earlier echocardiography following identification of embolic infarction may expedite diagnosis and management.

Biography

Dr. Adam Bowden studied Medicine at the University of Manchester and graduated with MB ChB in 2021. Adam completed foundation training in York and Scarborough Teaching Hospitals NHS foundation trust, subsequently working as a senior house officer in emergency and acute medicine, with interests in infectious diseases and bacterial infections.

Ahmad Syibli Othman[1,2]*, Musa Ahmad Aminu[1], Chew Ching Hoong[1], Ahmed M. Salman[2], Blandine Franke-Fayard[3], Aneeq Ur Rehman[1]

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Assessment of vaccination with AMA1 of *Plasmodium knowlesi* expressed in *Pichia pastoris* against chimeric rodent malaria parasite

Introduction: Malaria continues to be one of the most significant infectious diseases globally. Its existence in various species complicates the development of an efficient broad-spectrum solution. One species that is gaining increased attention in Southeast Asia is *Plasmodium knowlesi,* a zoonotic parasite that has since 2018 been the sole cause of all indigenous malaria infections in Malaysia. To address the burden, this research was designed to evaluate the *P. knowlesi* Apical Membrane Antigen 1 (PkAMA1) as a malaria vaccine candidate.

Methodology: Recombinant PkAMA1 (DI-II and DI-II-III) was strategically expressed in *P. pastoris* (culture-induction-purification-characterization), followed by a pre-clinical study using a murine immunization-challenge model to assess the immunological efficacy of the protein on the chimeric rodent malaria parasite. This was elucidated in duplicate in 3 experimental groups. Under aseptic conditions, 50µg of purified rPkAMA1 (domain DI-II and DI-II-III) was administered to groups 1 and 2, respectively, via the intramuscular route (prime immunization), whereas group 3 was unimmunized (naïve). Fourteen days later, mice in immunized groups were boosted with the same antigen concentration. On day 14 after boost immunization, half of each group was sacrificed for comparative immunoassay, while the remaining half was challenged with 1.0 x10^3 blood-stage parasite expressing PkAMA1 antigen via the intraperitoneal route. After the challenge, parasitemia monitoring (patency=>2%) and survival time analysis were evaluated daily for 14 days. All data was analyzed using the GraphPad Prism software version 10.1.1(207). The biostatistical tests used in this study were ANOVA, Kaplan–Meier survival plot and log-rank (Mantel-Cox) test.

Result: Protein characterization and quantification demonstrated that the rPkAMA1 was rightly expressed and suitable for downstream application. rPkAMA1 DI-II was best expressed at 72 hours of 1% methanol induction and OD600 3, while rPkAMA1 DI-II-III was best expressed at 48 hours of 2% methanol induction and OD600. Immunization with both rPkAMA1 protects against the chimeric rodent malaria parasite expressing PkAMA1. For the protective efficacy experiment of the antigen, mice in the immunized groups exhibited reduced blood-stage parasitemia levels, remaining prepatent (number of days to reach a 0.5-2% parasitemia after challenge), whereas all unimmunized mice become patent before and on day 5. For the assessment of protection experiment, ELISA quantified parasite-specific IgG produced against the PkAMA1 antigen and the titers were statistically significant ($P<0.0001$). There was also a significant difference in survival rates observed between both immunized groups compared to the naïve group. Furthermore, the study demonstrated that the immune response generated by rPkAMA1 (DI-II) was equivalent in terms of antibody responses to that elicited by the complete rPkAMA1 protein (DI-II-III), highlighting the potency of the DI-II domain.

Conclusion: The immunological insights revealed by this study can aid the utilization of PkAMA1 as an efficacious blood-stage vaccine for *P. knowlesi*. Future research should focus on the assessment of cellular immunity and memory responses to further validate the antigen's potential. These would facilitate pre-clinical trials and the antigen's prospective role in malaria eradication.

Biography

Syibli Othman is currently a Postdoctoral Fellow at the Jenner Institute, University of Oxford, United Kingdom, and serves as a Senior Lecturer at the Faculty of Health Sciences, Universiti Sultan Zainal Abidin, Malaysia. Syibli has extensive experience in academia and research, with active contributions to teaching, research, and student mentorship. Syibli research focuses on immuno-vaccinology, particularly the development and evaluation of vaccines and immune responses against infectious diseases using animal models, with a specific interest in zoonotic malaria.

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PCR-guided diagnosis and intrathecal salvage therapy for *Capnocytophaga* brain abscess with polymicrobial anaerobic ventriculitis in an immunocompetent host

Background: Brain abscess complicated by ventriculitis is a rare and life-threatening Central Nervous System (CNS) infection associated with high morbidity and mortality. While common pathogens include *Streptococci* and anaerobic oral flora, *Capnocytophaga* species are uncommon causes of CNS infection, particularly in immunocompetent hosts and in the absence of prior animal exposure. Diagnosis is frequently challenged by the fastidious growth characteristics of anaerobic organisms and prior antibiotic exposure, often resulting in persistently negative cultures. Molecular diagnostic techniques have emerged as valuable tools for pathogen identification in culture-negative infections; however, data guiding their use and subsequent management strategies remain limited.

Case Presentation: We report a 69-year-old immunocompetent woman with chronic periodontitis who presented with altered mental status and was found to have a left temporal lobe brain abscess with mass effect. Initial surgical drainage identified *Capnocytophaga* species, and she completed prolonged intravenous antimicrobial therapy. She was subsequently transferred to our institution with recurrent fevers, encephalopathy, and headaches. MRI demonstrated a recurrent temporal abscess with extensive ependymal enhancement and intraventricular purulence consistent with ventriculitis. Despite multiple neurosurgical interventions and persistently neutrophilic Cerebrospinal Fluid (CSF), cultures remained negative.

Broad-range bacterial PCR sequencing of CSF identified polymicrobial anaerobic pathogens, including *Prevotella* species, *Fusobacterium* species, *Streptococcus* mitis, and *Fannyhessea vaginae,* implicating an oral source. Vancomycin-resistant *Enterococcus faecium* was later

isolated and interpreted as a secondary pathogen. The patient was treated with intravenous meropenem and daptomycin, followed by intrathecal gentamicin, with consolidation to intravenous linezolid. After seven weeks of systemic therapy and two weeks of combined intrathecal treatment, CSF parameters normalized with simultaneous clinical improvement.

Conclusion: *Capnocytophaga* brain abscess can occur in immunocompetent hosts and may evade conventional microbiologic diagnostics. This case highlights the diagnostic and therapeutic challenges of culture-negative ventriculitis and underscores the value of molecular diagnostics in identifying oral-source polymicrobial anaerobic pathogens associated with complex *Capnocytophaga* brain abscess. In immunocompetent patients with coexisting periodontitis or recent dental procedures, early identification of *Capnocytophaga* may serve as a marker of a broader polymicrobial process and should prompt consideration of recurrent brain abscess and ventriculitis. Broad-range PCR sequencing represents a valuable adjunct in guiding targeted antimicrobial therapy when conventional diagnostics fail.

Biography

Dr. Alexis Torres-Rodriguez is an American Board-certified physician in Internal Medicine and an Infectious Diseases fellow at NewYork-Presbyterian Queens Hospital. He received his medical degree from Universidad Autónoma de Guadalajara in Mexico and completed his Internal Medicine residency at Universidad Central del Caribe in Puerto Rico. With over ten years of clinical experience across emergency, inpatient, ambulatory, correctional, and public health settings, Dr. Torres-Rodriguez has worked extensively with underserved and diverse populations. His research interests include CNS infections, infective endocarditis, and HIV, with a focus on diagnostic and management challenges in complex infectious diseases.

Amanda L. Fox*, Kerrie J. Espuga, Thomas C. Coates

Animal Research Initiative, Department of Agriculture, Seattle, United States

Discovery of reintroduction source and amplification vectors of Highly Pathogenic Avian Influenza (HPAI)

The spread of Highly Pathogenic Avian Influenza (HPAI) has recently expanded to unprecedented proportions. Its existence in livestock has been well documented with the primary animals of concern being chickens, ducks, turkeys, game birds, bovine, swine, sheep, mink, and foxes. With notable risk to wild bird populations and the added risk of pandemic potential in humans largely in part due to fever resistance, farming operations working with these animals merit a hyper cautious approach. This paper analyzes the existing evidence of disease spread in case studies and research papers and posits that fattened waterfowl operations are a particularly unnecessary farming practice that disproportionately contributes to the evolving problem. This specific practice has been linked to the spread of HPAI on numerous occasions with strong evidence indicating major outbreaks deriving from farms in France and Hungary. With the mobile nature of wild birds, implications of this are far reaching and amplify the HPAI numbers in distant regions. The vast majority of the European Union has banned artificially fattened waterfowl operations, and this paper offers that its remaining countries emulate this approach. In regions that lack these operations, pre-emptive prohibitions are recommended to assure a mitigation of spread before it can begin. Drawing from the established evidence, a global transition away from artificially fattened waterfowl farming in the interest of public health and ecological protection is recommended.

Biography

Amanda L. Fox was born in Cheverly, Maryland, on May 28, 1988. Previously studying at North Seattle College, Amanda is currently pursuing a Bachelor's degree in earth and environmental Sciences at Arizona State University in Tempe, Arizona. Amanda has spent the past decade working within the intersection of public health, animal welfare, and environmental science

and currently serves as the Senior Research Executive for Animal Research Initiative. Amanda research includes zoonotic disease prevention, invasive species, ecological resilience, and biodiversity preservation.

Dr. A. Mrudula Srinivasulu[1*], Dr. Afroze Sultana[2], P. Mahesh[3], S. Lakshmi Madhuri[3], Md. Amir Jaffer[3], G. Raju[3], G. Tirumala[3], G. Bhanu Prasad[3]

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Emerging burden of non-tuberculous mycobacteria in MGIT-based tuberculosis cultures: Insights from South India

Background: Non-Tuberculous Mycobacteria (NTM) are increasingly recognized as clinically significant pathogens that can mimic *Mycobacterium Tuberculosis* (MTB) in both clinical presentation and laboratory features. Because of intrinsic drug resistance and overlapping morphology, distinguishing them from MTB remains a challenge in diagnostic laboratories. This study aimed to determine the incidence and distribution of NTM among culture-positive mycobacterial samples processed at a tertiary-level diagnostic center in South India.

Methods: A retrospective cross-sectional analysis was conducted at Yoda Diagnostics, Hyderabad, covering the period from 16 May 2023 to 27 October 2025. A total of 932 clinical specimens received for mycobacterial culture were examined. Smear microscopy was performed using Ziehl-Neelsen staining, and cultures were processed in the BacT Alert MGIT 960 system. All culture-positive isolates were screened with the MPT-64 antigen rapid test to differentiate the MTB complex from NTM. Line Probe Assay (LPA) was used for NTM species identification, and drug-susceptibility testing was performed. De-identified data were compiled and analyzed descriptively.

Results: Of the 932 processed specimens, 143(15.3%) yielded culture-positive isolates. The highest culture yield was obtained from broncho-alveolar lavage (69/287, 24%), followed by pus (31/103, 30%) and sputum (23/58, 40%). Among these, 91(63.6%) were identified as MTB, 49(34.3%) as NTM, and 3(2.1%) showed mixed MTB+NTM growth. Pulmonary specimens-particularly BAL and sputum—accounted for nearly two-thirds of all NTM isolates (33/49, 67%),

indicating pulmonary predominance. Extra-pulmonary NTM were infrequent, found mainly in tissue (3 cases) and lymph-node aspirates (4 cases). The male-to-female ratio favored males (~1.5:1). A progressive increase in both MTB and NTM isolations was observed over the study period.

Conclusion: This study demonstrates a notable and rising incidence of NTM infections among culture- positive mycobacterial samples in southern India. Differentiating NTM from MTB is essential for accurate diagnosis and management. Integrating rapid antigen screening and molecular species identification into routine workflows enhances laboratory precision and patient care. Continued regional surveillance is warranted to monitor emerging NTM species and evolving resistance patterns.

Keywords: Non-*Tuberculous Mycobacteria* (NTM), *Mycobacterium Tuberculosis* (MTB), MPT- 64 Antigen Test, Line Probe Assay (LPA), MGIT Culture, Hyderabad.

Biography

Dr. A. Mrudula Srinivasulu is a Consultant Microbiologist specializing in Molecular Diagnostics in Infectious Diseases at Yoda Diagnostics, Hyderabad, India. She holds a PDCC in Transplant Virology from the Institute of Liver and Biliary Sciences (ILBS), New Delhi. Her areas of interest include mycobacterial disease diagnostics, antimicrobial resistance, and transplant virology. She has contributed to multiple research projects and scientific presentations in national and international forums, focusing on MGIT-based diagnostics and emerging NTM pathogens in high-burden regions.

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The impact of expanded adolescent vaccination against Omicron waves depends on the epidemic status: A mathematical modelling study

Background: Deployment of effective vaccination against the various SARS-CoV-2 variants was crucial for controlling the spread of COVID-19. These retrospective modelling analyses evaluated the impact of the expanded adolescent COVID-19 vaccination in England at two different epidemic points: In the autumn (August to November) 2021, in the presence of a large Omicron epidemic wave, and in the autumn 2022, when the subsequent Omicron epidemic was at an endemic stage.

Methods: We used the Covasim SARS-CoV-2 model for England to run two scenario analyses: a) Contrasting the strength of the BA.1 Omicron wave when vaccinating 18+ only versus additional 12+ vaccination from the autumn 2021, Contrasting varying adolescent vaccine uptake and vaccine implementation timing; and b) contrasting the strength of the BA.2/BA.4/BA.5/XBB Omicron waves, under the current immunisation strategy at the time versus additional 12+ vaccination from September 2022. We projected the number of new daily SARS-CoV-2 infections, hospitalisations and deaths related to SARS-CoV-2 during the periods 01/08/2021-28/02/2022 and 01/08/2022 - 28/02/2023 for the respective analyses.

Findings: In presence of the BA.1 Omicron wave in late 2021, the expanded adolescent vaccination averted around 3,000,000 cases across all-ages. 1,010,000 SARS-CoV-2 infections were averted during the period between 2 months to 6 months after vaccination began in the vaccinated 12-17-year old cohort. The impact declined six months after the onset of the vaccination, while earlier onset of the immunisation campaign had greater overall impact. During the later Omicron waves in 2022, additional adolescents vaccination did not lead to significant reduction in COVID-19 cases, hospitalisations or deaths in the entire population, nor within the vaccinated cohort.

Interpretation: Our findings highlight that adolescent vaccination impact depends on the timing/speed of implementation, other present intervention strategies, and the status of the epidemic at the time. Hence, it should not be considered as a stand-alone immunisation strategy, but alongside information on overall vaccine effectiveness, potential adverse events, the cost of roll out implementation and the operational constraints of its delivery.

Biography

Anna Fairweather is in the 1st year of her DPhil in Healthcare Data Science at the University of Oxford. She is specialising in improving calibration and wider application of agent-based models across infectious diseases. She is primarily focussing on pathogens which cause respiratory infectious diseases, in particular *Streptococcus Pneumoniae,* Coronavirus and Influenza. Prior to starting her DPhil, Anna.

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Validity of the pediatric age-adjusted shock index in the early assessment of shock among patients with sepsis: A five-year review

Introduction: Managing patients admitted to the PICU involves early detection and treatment of shock and hemodynamic stability. Various vascular and extravascular elements must constantly interact to maintain hemodynamic stability. These have been the basis of pediatric age-adjusted shock index parameters. This study aims to determine the validity of the pediatric age-adjusted shock index in predicting shock among pediatric patients with sepsis.

Methodology: This was a retrospective cross-sectional study that reviewed and analyzed the records of pediatric patients with sepsis and SIRS on admission from January 2018 to December 2022 in a tertiary hospital in Makati city, Philippines. Patient records were reviewed, and relevant data was obtained, including clinical-sociodemographic variables, vital signs, diagnoses, diagnostics done, the use of inotropes, the occurrence of shock, and mortality. The pediatric age-adjusted shock index's sensitivity, specificity, predictive values, and accuracy were computed.

Results: A total of 117 patients with systemic inflammatory response syndrome were included. No significant association was observed between the occurrence of septic shock and age-adjusted shock index classification at admission (p=0.522) and 4 hours (p=0.534). Also, no significant association was observed between mortality and age-adjusted shock index classification at admission (p=0.288) and 4 hours (p=0.509). In contrast, a significant association was observed between age-adjusted shock index classification at 6 hours and septic shock (p=0.029) and mortality (p=0.010). The prognostic accuracy in predicting septic shock is as follows: At admission=46.9% (sensitivity=66.7%, specificity=34.8%), at 4

hours=45.2% (sensitivity=71.1%, specificity=30.3%), and 6 hours=53.6% (sensitivity=80.6%, specificity=40.9%). The prognostic factors in predicting mortality are as follows: At admission, 48.3% (sensitivity=74.3%, specificity=37.0%); at 4 hours, 42.6% (sensitivity=71.9%, specificity=30.3%); and at 6 hours, 53.5% (sensitivity=85.7%, specificity=41.1%).

Conclusion: The pediatric age-adjusted shock index showed good sensitivity but poor specificity, indicating it can correctly identify most high-risk patients who will develop shock and mortality. It may also incorrectly identify low-risk patients as high-risk. While the pediatric age-adjusted shock index can screen high-risk patients, prioritizing limited hospital resources for low-risk patients incorrectly identified by the tool is inefficient. It is recommended to use this tool in conjunction with other factors, such as diagnostic tests, and to look for other tools that will yield better prognostic accuracy in predicting shock and mortality in septic children.

Biography

Beatricia Alyssandra L. Luceno MD is a graduate of the Human Biology Program at De La Salle University Manila. She obtained her medical license at the age of 23 and driven by her passion for caring for children, pursued residency training in Pediatrics with Ospital ng Makati. She is currently a fellow in Child Neurology at the Philippine General Hospital. Her clinical and academic interests include epilepsy, pediatric stroke, central nervous system infections, neurophysiology, and neuromuscular diseases. Dr. Luceno is committed to advancing patient-centered neurological care through continuous scholarship and clinical training.

Brahmchetna Bedi[1,2,3*] PHD, MBA; E. Britton Chahine[1,2,4] MD, MSCP; Tiffany Walker[1,2,5] MD, Jasmine Berry[1,3]; Jenny Han[1,2,6] MD, MSc

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Association of menopause and long COVID symptoms on vascular outcomes: AMLOV study

Introduction: Sex differences have been observed in both the incidence and symptom burden of Long COVID (LC), with women demonstrating a higher incidence than men (8.5% vs. 5.2%) and greater symptom burden (4.4% vs. 2.3%). Menopause is marked by declining estrogen levels, increased proinflammatory cytokines, and heightened immune activation. Estrogen deficiency can arise from menopause or LC and promotes systemic inflammation, which overlaps with inflammatory pathways implicated in LC. This suggests that LC may amplify or unmask menopause-related immune dysregulation. It is unclear whether viral persistence or sustained immune activation influences hormonal dynamics. Understanding this relationship is clinically important as both LC and menopause are independently associated with increased cardiovascular risk, including myocardial infarction, heart failure, arrhythmias, thrombotic events, and stroke, with menopause alone increasing cardiovascular risk factors by approximately 18%.

Significance: Despite strong mechanistic plausibility and population-level relevance, no studies have examined LC symptoms as a modifier of vascular events in menopausal-aged women.

Methods: We investigated the association of LC symptom burden in menopausal aged women with and without menopause and with and without LC and investigated the cardiovascular and stroke outcomes. Long Covid (LC) is defined as a Post-Acute Sequelae of SARS-CoV-2 (PASC) score of >11, a patient-reported outcome measure, indicating a high multi-symptom burden. Utilizing the Researching COVID to Enhance Recovery (RECOVER) adult cohort database. Odds Ratios (ORs) and 95% Confidence Intervals (CIs) were calculated with logistic regression to evaluate associations between long COVID and stroke and cardiovascular outcomes, stratified by menopausal status.

Results: We identified 2,345 biological female participants aged 40-56. 1,194 without menopause (age 40-56) with and without LC, and 1,151 with menopause (age 40-56) with and without LC. We found increased odds of cardiovascular events and strokes in women with Long COVID who were not in menopause.

	Menopause		No Menopause	
	Never Infected	Long Covid	Never Infected	Long Covid
Cardiovascular Disease Odds Ratio (95% CI)	0.71 (0.46 - 1.09)	**1.67 (1.16 - 2.41)***	0.19 (0.02-1.65)	**2.55 (1.70-3.82)***
	Never Infected	Long Covid	Never Infected	Long Covid
Stroke Odds Ratio (95% CI)	1.37 (0.19 - 9.79)	**9.24 (2.09 - 40.8)***	3.16 (0.65 - 15.33)	**7.45 (1.59 - 34.77)***

Conclusion: LC was associated with significantly increased odds of cardiovascular disease and stroke, regardless of menopausal status. No significant associations were observed among never-infected groups.

As next steps, we will investigate whether estrogen deficiency, specifically the distinction between acute and sustained deficiency, is the primary driver of inflammatory pathways that contribute to increased cardiovascular and stroke risk in women with LC.

Biography

Brahmchetna Bedi Ph.D., MBA is a senior scientist in the Division of Infectious Diseases at Emory University. She is a basic scientist trained in immunology and biomarker research, with over 20 years of experience in hypothesis-driven basic, translational, and clinical research. Dr. Bedi has an extensive publication record and has developed robust in vitro and in vivo disease models. She serves as the Laboratory Director of the Atlanta HUB for the NIH RECOVER study, a role she will continue in RECOVER 2.0.

Brooke Skinner*, Tanbir Najrana, Brajesh Singh, Aidan Biondi, Alan Ardito, Kanika Men, Lillianna Hammons, Jonathan Kurtis
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Novel antimalarial compound 2741-19 synergistically kills *P. falciparum* in vitro with artemisinin combination therapy partner drug, piperaquine

Plasmodium falciparum malaria infects 300-500 million individuals and accounts for over 600,00 deaths each year with the majority of deaths occurring in children under 5 years of age living in sub-Saharan Africa. In the past several years, morbidity and mortality due to *P. falciparum* have increased and the spread of parasites resistant to artemisinin, the mainstay of treatment, threatens to exacerbate this trend, underscoring the urgent need to identify novel antimalarial drugs. Previously, we identified a novel antimalarial small molecule drug, 2741-19, that binds with PfGARP, a malarial protein expressed on the exofacial surface of infected human erythrocytes. This drug kills malaria parasites with an IC_{50} of 50nM with no observable toxicity to mammalian cells. To forestall the development of resistance, *P. falciparum* infections are treated with artemisinin-based combination drug therapy. A key partner drug for artemisinin is the 4-aminoquinoline, piperaquine. To assess the potential for synergy in parasite killing between 2741-19 and piperaquine, we performed in vitro parasite growth assays using checkerboard dilution of these compounds. We quantified synergy using four mathematical models including, Loewe Additivity, Bliss Independence, Highest Single Agent (HSA), and Zero Interaction Potential (ZIP). In all models, 2741-19 demonstrated significant synergy with piperaquine in mediating parasite killing reflecting greater parasite killing than would be expected if the interaction were merely additive. This result suggests that 2741-19 has a mechanism of action that is distinct from piperaquine which kills parasites by inhibiting the detoxification of heme. These findings support further evaluation of 2741-19 in combination with artemisinin partner drugs as promising candidates for a next generation of antimalarial combination therapies.

Biography

Brooke is a recent graduate of Brown University's Biotechnology Master's program. Her research focuses on developing drug and vaccine candidates for blood-stage *P. falciparum.* Previously, she worked at Moderna in Portfolio Management and studied Computational Biology as an undergraduate at Brown University.

Camila Amormino Corsini[1*], Priscila Fernanda da Silva Martins[1], Priscilla Soares Filgueiras[1], Pedro Augusto Alves[1], Gabriel da Rocha Fernandes[1], Fernanda Castro Boulos[2], Caroline De Almeida Leitão Curimbaba[2], Maurício Lacerda Nogueira[3], Guilherme Rodrigues Fernandes Campos[3], Jaquelline Germano de Oliveira[1], Andrea Teixeira-Carvalho[1], Ana Carolina Campi Azevedo[1], Jordana Grazziela Alves Coelho dos Reis[4], Olindo Assis Martins Filho[1], Rafaella Fortini Queiroz e Grenfell[1,4,5]

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Immunogenicity and safety of inactivated SARS-CoV-2 vaccine (CoronaVac) using a two-dose primary protocol in children and adolescents (Immunita-002, Brazil): A phase IV one-year follow-up

The immune response induced by SARS-CoV-2 vaccination in children and adolescents is not yet well defined regarding the intensity and duration of protective immunity in the medium and long term, which may indicate the need for booster doses and support public health decisions. Given this context, the aim of this study was to evaluate the immunogenicity, effectiveness, and reactogenicity of the CoronaVac vaccine in children and adolescents aged 3 to 17 years over a one-year period after the second dose. Participants were recruited from public healthcare centers in Serrana (SP) and Belo Horizonte (MG), Brazil, and underwent physical examinations and clinical interviews (CAAE 55183322.6.0000.5091). Blood samples were collected before vaccination, one month after the first dose, and at 1, 3, 6, and 12 months after the second dose. Follow-up included a virtual platform for monitoring adverse events and COVID-19-related symptoms. Cases were confirmed by RT-qPCR and characterized

by Genomic Sequencing (NGS). The humoral immune response was assessed by ELISA for anti-S and anti-N IgG antibodies, and neutralizing antibodies against the B.1 lineage and Omicron variants (BA.1 and BA.5) were quantified by PRNT and VNT50. The cellular immune response was evaluated by flow cytometry, including the quantification of soluble mediators after in vitro antigenic stimulation. Follow-up of 640 participants demonstrated that CoronaVac significantly induced the production of total IgG antibodies against SARS-CoV-2 S and N proteins, as well as neutralizing antibodies against the B.1 lineage and Omicron subvariants BA.1 and BA.5 in both seronegative and seropositive individuals. In addition, a robust cellular immune response was observed, with a broad release of pro-inflammatory and regulatory soluble mediators in the early post-immunization period. Adverse events occurred in 30% of participants and were mostly mild and transient. During follow-up, 8.75% developed mild COVID-19, predominantly associated with BA.2 and BA.5 subvariants. These findings indicate that CoronaVac induces robust humoral and cellular immune responses against SARS-CoV-2 in children and adolescents over one year of follow-up, providing evidence supporting the safety and immunogenicity of this vaccine. Data from this study supported regulatory decisions by ANVISA to expand the use of CoronaVac in children, reinforcing its role as a pediatric immunization strategy against COVID-19. This publication was supported by the Fundação de Amparo à Pesquisa do Estado de Minas Gerais (Fapemig)-Grant APQ-04991-23 and the Instituto René Rachou/Fiocruz Minas.

Biography

Camila Amormino Corsini is a biologist, MSc, and PhD candidate in Health Sciences at Fiocruz Minas, with expertise in Cellular and Molecular Biology, Genetics, and Bioinformatics. Her research focuses on vaccine immunology, with emphasis on the design and conduct of clinical studies evaluating immunogenicity and vaccine effectiveness. She has strong experience in advanced immunological and molecular techniques, including ELISA, viral neutralization assays, flow cytometry, real-time PCR, and next-generation sequencing. She has undertaken research exchanges at the University of Georgia and has experience in national reference laboratories in Brazil, contributing to studies in parasitology, blood diagnostics, and laboratory quality control.

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Collaborative innovation in infection control: Redesigning clinical hand basin use through circles of influence in a multi-site hospital initiative

Traditionally, infection control has focused on direct person-to-person transmission of Carbapenemase-Producing Enterobacterales (CPE). However, emerging evidence highlights environmental reservoirs-particularly contaminated Clinical Hand Basins (CHBs) - as critical transmission sources. This infection control initiative, based in a regional New South Wales hospital, sought to reduce environmental contamination through clinical innovation, collaborative redesign, and reinterpretation of infrastructure guidelines.

Environmental sampling of existing in-patient units identified genetically linked CPE and multi-resistant Gram-negative organisms in CHBs and patient samples. Existing Health Facility Guidelines were critically analysed and reinterpreted to change CHB placement and density as well as PPE station placement in proximity to CHB to reduce contamination. A multi-disciplinary partnership was established between infection control practitioners, the health infrastructure, and capitol works teams.

Despite existing regulations, we made the deliberate and courageous decision to locate PPE stations outside of the splash zone, change CHB locations and guiding metrics in a new build. A considered and collaborative approach to reinterpreting guidelines and evidence has led to the development of safer, more clinically discerning environment. These changes are now shaping new guidelines-demonstrating the power of trusted partnerships and informed, practical innovation.

Effective infection control requires context-driven innovation and broad collaboration. This initiative demonstrates how clinical expertise, collaborative design, and flexible

reinterpretation of guidelines can shape safer hospital environments. It contributes to guiding principles for successful multi-site implementation strategies by leveraging local ownership and cross-disciplinary influence to achieve sustainable outcomes. This work demonstrated the power of advocacy and evidence-informed changes, directly influencing health infrastructure policy and improving infection control.

Biography

Carmel Couch is a Clinical Nurse Consultant from the NSW, Australia with over 15-years of experience in a variety of settings including Critical Care, Cardiology, Public Health, Respiratory, Medical, and Surgical nursing. Carmel works closely with Infrastructure teams, front-line Clinicians and Infectious Diseases Consultants to ensure informed and evidence-based approaches are paramount in building and renovating the hospitals of the future. She is an experienced IPC who is passionate about clinical innovation and education.

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Regulation of dikaryotic Arbuscular Mycorrhizal (AM) fungal infection in *Vigna angularis, Vigna radiata*, and *Allium tuberosum* by *Glomus mosseae*

The aim of this study is to investigate whether mycorrhizal fungi infect plant species such as *Vigna angularis, Vigna radiata,* and *Allium tuberosum* to promote growth, or whether they instead contribute to disease. Existing literature highlights the complexity of these interactions. For instance, root, hyphal, and spore propagules harbor distinct Arbuscular Mycorrhizal (AM) fungal communities when *Allium tuberosum* is cultivated in soils from contrasting sites (Arslan et al., 2025). Similarly, co-inoculation of AM fungi with *Bradyrhizobium* sp. substantially increases nodulation in mung beans, thereby boosting biological nitrogen fixation and overall plant performance compared to single inoculation or control (Gough et al., 2021). In this context, our study specifically examines how the dikaryotic AM fungus *Glomus mosseae* infects host roots and differentially influences the mycorrhizal responses of *Vigna angularis, Vigna radiata,* and *Allium tuberosum.* Fungal communities, or mycobiomes, are well known to colonize plant roots and surrounding soil, particularly within the rhizosphere, where they profoundly shape plant health and development. Beneficial fungi, including mycorrhizal and endophytic species, are capable of supporting plants directly or indirectly by enhancing resistance to environmental and biological stressors. By contrast, pathogenic fungi infect host tissues, disrupt metabolism, and ultimately hinder crop development, causing substantial yield losses and posing a major threat to agricultural productivity. To clarify these contrasting roles, we cultivated three environmentally tolerant plant species-*Vigna angularis, Vigna radiata*, and *A. tuberosum*-and inoculated them with *Glomus mosseae.* Plant growth and infection dynamics were monitored, recorded, and analyzed over a 93-day period. Cellular-level observations revealed that AM fungi replicate within root tissues and interact differently across species. The results indicate that

A. tuberosum initially benefits from *Glomus mosseae* infection, but plant health declines markedly after approximately half a month, leading to mortality. In contrast, *Vigna angularis* exhibits rapid mortality upon infection, though under certain conditions growth stimulation can persist. The results demonstrate that *Allium tuberosum* initially benefits from infection by *Glomus mosseae*, but plant health declines after approximately three and a half months, ultimately leading to death. In *Vigna angularis,* infection by mycorrhizal fungi induces a rapid decline and mortality, although in certain cases transient growth stimulation is observed. By contrast, *Vigna radiata* responds more gradually; while the benefits of infection emerge slowly, they persist over time, supporting continuous growth. Taken together, these findings highlight the species-specific outcomes of mycorrhizal infection, providing new molecular evidence that arbuscular mycorrhizal fungi manipulate innate immune signaling pathways to enable intracellular replication and sustain pathogen survival.

Biography

Lin Yucheng and Chihang Chang are dedicated to the study of fungal infection and plant-microbe interactions, with a particular focus on how arbuscular mycorrhizal fungi influence plant health and immunity. Their recent research explores the dual roles of *Glomus mosseae* in promoting growth or causing disease in species such as *Vigna angularis, Vigna radiata,* and *Allium tuberosum.* In 2025, they presented this work at the International Union of Immunological Societies (IUIS) Congress, highlighting new molecular evidence on how fungal infection manipulates innate immune signaling to enable intracellular replication and pathogen survival.

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Mathematical modeling of COVID-19 dynamics in a West African context

The novel Coronavirus Disease 2019 (COVID-19), which emerged in Wuhan, China is a highly infectious disease caused by (SARS-CoV-2) and has significantly affected public health and socio-economic well-being worldwide. Its transmission highlights the potentially important role of transmission heterogeneities, requiring better modeling approaches to determine their role in dynamics and control. This study aims to develop a method for detecting heterogeneities in susceptibility or connectivity in COVID-19 transmission by fitting a modified susceptible, infected, recovered model to incidence data. The parameters of the model are estimated using markov chain monte carlo techniques. The proposed method is tested on simulated data to ascertain its effectiveness before applying it to real-world incidence time-series from different Nigerian States supplied by their Centre for Disease Control. The best performing models including different sources of heterogeneity, is determined using the Watanabe-Akaike Information Criteria (WAIC) and Leave-One-Out-cross-validation (LOO) and used to make recommendations on possible interventions. By identifying and detecting heterogeneities that act to lower the Herd Immunity Threshold and the effective reproduction number, findings from this study will be useful in providing an improved understanding of disease spread, reducing the epidemic size and the burden of disease to make better-informed decisions for managing emerging and re-emerging infectious diseases like COVID-19.

Biography

Christabel Emaeyak James, a Doctoral Researcher in Infectious Diseases at the University of Glasgow. She holds a BSc and MSc in Statistics, with research experience in statistical, mathematical modelling and data analysis for health applications. She has worked extensively

on research projects, mostly related to health; carried out both quantitative and qualitative data collection using the Ordinary Data Kit and REDcap. Her Doctoral research focuses on applying advanced mathematical and statistical modelling to understand infectious disease transmission. Her broader interests include mathematical and statistical modelling, epidemiology, biostatistics, public health analytics and the use of quantitative methods to inform health decision-making.

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A comparison of current treatments for Clostridioides Difficile Infection (CDI) in adults and children

Background: Clostridioides Difficile Infection (CDI) is one of the most common and severe causes of healthcare-associated diarrhea and is associated with substantial morbidity and mortality. Although CDI has traditionally posed a major clinical challenge in adult healthcare settings, the number of pediatric cases has increased considerably in recent years. The aim of this study was to identify the most effective CDI treatments in adults and children and compare differences between the two groups.

Methods: We conducted a systematic review of studies published up to February 17, 2025, to compare therapies used for the treatment of CDI in pediatric and adult populations. The literature search covered the MEDLINE, EMBASE, and Cochrane Central databases.

Results: In the most recent meta-analysis in adults (27,959 patients; 49.2% women), Fecal Microbiota Transplantation (FMT) was the most effective among 28 interventions, both for overall recovery and relapse prevention. FMT proved to be the most effective therapy in recurrent cases, while fidaxomicin proved to be the most effective in non-recurrent cases. Probiotics were not effective in preventing CDI, with no significant difference between probiotics and placebo (even in old age). Among children, 84 studies out of nearly 12,000 publications identified on the subject met the inclusion criteria. Based on cure rates, we found no significant difference between metronidazole and vancomycin treatment, and combination therapies are no more

effective than monotherapies. Meta-analysis of proportions showed similar cure rates for each therapy.

Conclusion: Based on our systematic review of adult cases, FMT has been shown to be highly effective in the treatment of recurrent CDI, confirming the potential for wider clinical application of FMT. In non-recurrent cases, antibiotics, specifically fidaxomicin and vancomycin, appear to be the primary treatment of choice. Overall, therapies used in the treatment of pediatric CDI show high and comparable cure rates, with no clear therapeutic advantage identified. Due to its higher concentration in stool, vancomycin appears to be the first-line treatment, while fidaxomicin and fecal microbiota transplantation may be promising alternatives, especially in the treatment of recurrent cases.

Biography

Dániel Steve Bednárik is graduated in 2020 from University of Szeged as a medical doctor. In September of the same year, he started his residency at Heim Pál National Pediatric Institute, as a pediatrician, meanwhile he is also working on his PhD with a special interest in infectiology and gastroenterology. His main research field is related to Clostridioides difficile infection. He has presented his research at numerous domestic and international conferences. In 2025, he was awarded the University Research Scholarship Program (EKÖP) at Semmelweis University and that year he was selected for the Kerpel-Fronius Ödön Talent Development Program at Semmelweis University. His most recent publication on the effectiveness of different therapies for Clostridioides difficile infection in adults was published in The Lancet Regional Health–Europe.

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A rare co-occurrence of *Streptococcus pyogenes meningitis* and anti-N-methyl-D- aspartate receptor encephalitis: A case report

Streptococcus pyogenes meningitis is a rare entity, accounting for less than 1% of bacterial meningitis cases, with fewer than thirty cases reported in the past 25 years. It typically affects young children and older adults. In contrast, anti-N-Methyl-D-Aspartate Receptor (NMDAR) encephalitis is the most common autoimmune encephalitis, with an annual incidence of 1.5 per million, frequently associated with ovarian teratomas in women of reproductive age or occurring as a post-infectious complication, most often following herpes simplex virus infection. We describe the case of a 25-year-old female who presented with confusion and seizures, with rapid neurological decline requiring intubation. Cerebrospinal fluid analysis confirmed *Streptococcus pyogenes* infection by polymerase chain reaction and was positive for anti-NMDAR IgG antibodies. The patient showed marked improvement after initiation of immunosuppressive therapy. This report highlights the unprecedented coexistence of *Streptococcus pyogenes meningitis* and anti-NMDAR encephalitis, emphasizing the importance of maintaining a high index of suspicion for overlapping infectious and autoimmune etiologies in atypical neuropsychiatric presentations.

Keywords: Anti-NMDAR Encephalitis, Case Report, Bacterial Meningitis, *Streptococcus Pyogenes Meningitis*.

Biography

Dr. Dulce C. Gregorio-Talavera earned her Doctor of Medicine degree from Far Eastern University-NRMF. She completed her Internal Medicine residency at Quirino Memorial Medical Center and a fellow of Philippine College of Physicians. She is currently a fourth-year Neurology resident at East Avenue Medical Center and holds a Master's in Hospital Administration. Her research work includes studies on bacterial meningitis, autoimmune encephalitis, and delirium prevention. Dedicated to clinical excellence and academic growth, she remains actively involved in neuro- research and resident training.

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Legionella, scientific considerations on this pathogen threatening the civilized world. Why not Albania?

Introduction: Legionellosis is an infectious pathology caused by bacteria of the genus *Legionella*. *L.* Pneumophilia was recognized as the cause of the disease in 1976. Water reservoirs are its transmitting agents. There are risk factors and predisposing conditions. Travel is a serious risk factor. Albania is a well-known tourist destination with a high number of visitors accommodated in the numerous hotels of our main cities. Our country is located in the typical Mediterranean climate zone with considerable amounts of rainfall and solar radiation, all of which make *legionella* a real threat to our health.

Goal: To contribute to a better understanding of *Legionella* and its role in public health with a potential epidemic risk.

Method: The basis of the work was scientific findings on epidemiology, imaging or laboratory diagnostic methods, treatment and the role of *Legionella* in public health. We conducted a scientific narrative search in PubMed, Cochrane, Google Scholar, Scopus, Web of Science using keywords such as “legionnaires disease”, “risk factors”, “air conditioning”, “tourist” etc. We collected scientific sources published by the IHP, the Tourism Association, the Ministry of Culture. Our country has legislation and guidelines for the control of *Legionella.*

Results and Discussion: *Legionella* are found everywhere in the world, in environmental reservoirs such as cooling systems, drinking or domestic water systems, industrial chillers, hydromassage spas, Turkish baths, etc. *Legionella* spread far and wide through aerosols. There are risk factors and predisposing conditions such as cancerous diseases, autoimmune diseases, HIVAIDS, etc. Legionellosis occurs as Pontiac Fever and Legionnaires' Disease. The latter manifests itself with pulmonary (pneumonia, cavitary abscesses, etc.) and

extrapulmonary (neurological, renal, gastroenterological) involvement that results in respiratory, multiorgan failure, septic shock and death. The bacterium is known to cause sporadic, epidemic, hospital-acquired, atypical pneumonia. Diagnosis is based on clinical data, imaging and laboratory confirmation. Travel and tourism are risk factors. Albania is an attractive tourist destination as it was visited by 9 million tourists in the period January-August 2025 alone. This and the weather conditions create a breeding ground for *Legionella*. *Legionella* is a notifiable disease by the entire public and private healthcare system and the Institute of Public Health monitors this bacterium.

Conclusion: *Legionella* is a ubiquitous bacterium, so it constitutes a real threat to public health in the world and here of course. Legionnaires' disease is an under-reported infectious pathology also in Albania, so the professional construction of an epidemiological, diagnostic algorithm will help clinicians, including infectologists.

Keywords: *Legionella*, Risk Factors, Water Systems, Air Conditioning, Tourism, Public Health.

Biography

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

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Herpes zoster ophthalmicus following platelet-rich plasma therapy for androgenetic alopecia: A probable adverse reaction

Case: A man in his 60s presented with a 7-day history of progressive left periorbital oedema and pruritic vesicular following ipsilateral Platelet-Rich Plasma (PRP) injections for Androgenetic Alopecia (AA). Pain and swelling started on the day of injection. His past medical history included ischaemic cardiomyopathy, cerebrovascular infarction, atrial fibrillation, hypertension, asthma, benign prostatic hyperplasia, and gastro-oesophageal reflux disease. Initial assessments attributed the reaction to an allergy and later to bacterial cellulitis, for which he received oral corticosteroids and antibiotics. Despite this, symptoms worsened, prompting Emergency Department attendance where left periorbital oedema, vesicles, chemosis, and conjunctival hyperaemia were noted. Vision and ocular motility were preserved, and there were no other signs of ocular involvement.

CT imaging demonstrated preseptal cellulitis without orbital involvement. Lesional swabs were positive for Varicella Zoster Virus (VZV) on Polymerase Chain Reaction (PCR), and VZV IgG was detected serologically, confirming Herpes Zoster Ophthalmicus (HZO) with secondary preseptal cellulitis. Bacterial swabs and MRSA screening were negative. He was treated with intravenous aciclovir and ceftriaxone, with rapid clinical improvement. At follow-up, he had residual post-herpetic neuralgia and dermatomal pigmentation, managed with oral gabapentin.

Discussion: PRP is widely used for AA and is typically safe, with minimal reported side effects (Chen et al., 2018). However this represents the second reported case of HZO temporally associated with PRP administration, as Zeineddine et al. also described a case of HZO

activation within 24 hours of PRP therapy (Zeineddine et al., 2023). The temporal and anatomical association suggests a possible causal relationship, supported by a Naranjo Adverse Drug Reaction Causality Scale score of 5 ("probable") (Naranjo et al., 1981).

The platelet- rich concentrate in PRP extracted from centrifuged autologous blood has a high concentration of multiple growth factors and cytokines, which promote hair growth in AA (Alves et al., 2018). HZO occurs when VZV has been dormant in the trigeminal ganglion and reactivates in the ophthalmic branch of cranial nerve V (Shaikh et al., 2002). One hypothesis is that the growth factors and cytokines in PRP disrupt the local immune system equilibrium, providing latent VZV an opportunity to reactivate (Gershon et al., 2010). Alternatively, inadvertent infection could result from non-autologous sample injection, although VZV migrates to nerve root ganglions via T-lymphocytes and T-lymphocytes should be removed from PRP during centrifugation (Alves et al., 2018). Considering the negligible admission CRP, negative bacterial swabs and bacterial superinfection being a common severe complication of HZO, superimposed secondary cellulitis is more likely than primary cellulitis (Davies et al., 1996).

Conclusion: This case highlights the second reported instance of HZO following PRP therapy. While the exact mechanism remains unknown, the close temporal and anatomical association strongly suggests a causal relationship. Cross-contamination of PRP samples may explain this adverse event, whilst immunomodulatory effects may enable local latent VZV reactivation. Given the potential emerging side effects associated with PRP, strict standardised protocols must be developed. PRP should only be performed by trained medical professionals.

Biography

Dr. George Riding trained at Newcastle University, UK, where he completed his MBBS and a Master's in Research in Ageing and Health (Distinction). He undertook the UK Foundation Programme in the North London Deanery before relocating to Victoria, Australia, where he currently works in general medicine. George is actively involved in research: He has authored and presented peer-reviewed original research; he has contributed to national best-practice recommendations; and is a member and co-author within The Cochrane Collaboration.

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Genomic diversity of orthohantavirus Andesense (ANDV): Impact of non-synonymous SNVs on gene expression and immune system evasion

Introduction: The Andes Virus (ANDV), a rodent-borne Orthohantavirus, causes Hantavirus Cardiopulmonary Syndrome (HCPS) in Chile and Argentina. Its genome comprises three RNA segments: Large (L), Medium (M), and Small (S). The S segment encodes the Nucleocapsid (N) and the Non-Structural S (NSs) proteins. While the N protein is crucial in several stages of viral replication, including SmRNA translation, NSs act as an antagonist of the type-I Interferon (IFN-I) pathway, through interaction with MAVS, contributing to pathogenesis. This study examined the genetic diversity of the S segment and the functional impact of non-synonymous Single Nucleotide Variations (SNVs) within the N and NSs protein.

Methods: Complete S segments from 58 ANDV-genomes collected from human clinical samples were sequenced with Illumina. Phylogenetic analyses were performed with IQ-TREE. Structural predictions and stability analyses for NSs were conducted using Robetta, Quark, Swiss-Model, and FoldX. Selected non-synonymous SNVs were introduced by site-directed mutagenesis into plasmids expressing ANDV-His-N or ANDV-HA-NSs, confirmed by Sanger sequencing. Functional effects were assessed using a capped SmRNA viral-like reporter (for N) and an IFN-β promoter reporter assay (for NSs) in HEK293T cells.

Results: Phylogenetic analyses revealed two distinctive clades among Chilean isolates. Across both proteins (N and NSs), twenty-nine non-synonymous SNVs were identified, with 62% within the NSs. In N, the N46S mutation disrupted the ability to stimulate SmRNA translation. In NSs, structural modeling revealed a positively charged patch. Functional assays showed that the artificial double mutant R4L-Q5L abolished IFN-β inhibition. Among natural variants, the S32L mutation, detected only in a severe HCPS case, enhanced IFN-β inhibition, while I20V and N34S did not.

Discussion: These findings demonstrate that NSs is a hotspot for functional variability and that specific mutations in both N and NSs can modulate viral translation or immune evasion. Such insights may contribute to understanding disease outcomes and identifying potential therapeutic targets.

Biography

Hade Ramos Acevedo is a Biochemist from Pontificia Universidad Católica de Chile and currently a PhD candidate in Biological Sciences at the same institution. Her research focuses on the genetic diversity of Andes Hantavirus (ANDV), particularly how non-synonymous variations in the S segment influence viral protein function and immune evasion. She is passionate about teaching and science communication-She served as a teaching assistant in several undergraduate courses and as an instructor in programs for school students (such as Penta UC), as well as participating in multiple outreach activities to promote scientific understanding.

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When *Pneumococcal meningoencephalitis* masquerades as stroke: Recognizing the immune turning point

Background: In patients with *Pneumococcal meningoencephalitis*, neurological worsening is often reflexively labeled as ischemic stroke or failure of antimicrobial therapy. However, apparent clinical recovery can be deceptive. A hidden immune-mediated phase may emerge after infection control, where vascular inflammation-not active infection-drives brain injury. Failure to recognize this biological switch represents a dangerous diagnostic trap.

Objective: To demonstrate immune-mediated cerebral vasculitis as a critical and under-recognized cause of delayed neurological deterioration in *Pneumococcal meningoencephalitis* and to highlight the importance of identifying this therapeutic turning point.

Methods: We present two adults with microbiologically confirmed *Streptococcus pneumonia* meningoencephalitis who initially improved on appropriate antimicrobial therapy. In the first patient, early MRI suggested uncomplicated meningitis, followed by evolution of micro-abscesses and vasculitic infarcts without immediate clinical decline. Steroids were tapered as per routine practice, after which abrupt neurological deterioration occurred. Repeat MRI revealed progression of inflammatory lesions, prompting escalation of corticosteroid therapy with dramatic clinical recovery. Applying this insight, steroid tapering was deliberately deferred in the second patient with similar clinical and radiological features.

Results: Both patients exhibited a biphasic disease course, with delayed neurological deterioration characterized by infarct-like lesions mimicking stroke despite microbiological control. Serial MRI supported an immune-mediated vasculitic process. Targeted continuation or escalation of corticosteroids resulted in marked neurological improvement and radiological resolution in both cases.

Conclusion: Not every infarct in *Pneumococcal meningoencephalitis* is a stroke. Delayed deterioration may signal an immune-mediated turning point identifiable on evolving MRI. Recognizing this moment is crucial, as timely immunomodulation-rather than antibiotic escalation or antithrombotic therapy-can lead to neurological salvage.

Biography

Dr. Hariharan S. Naidu is a Radiology resident with keen interest in diagnostic radiology and committed about translating imaging findings into meaningful clinical insights. He is passionate about pattern recognition, disease pathophysiology and evidence based reporting with a focus on achieving imaging- pathology concordance.

Dr. Himanshu Gul Mirani[1*], Dr. Chinnu Prince[1], Dr. Lida Ahmad Jawid[1], Georgia Pratley[2], Georgia Swinnerton[2]

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Diastolic shock index as an early failure-to-normalize marker of persistent vasodilatory physiology in infection-related critical illness

Background: The Diastolic Shock Index (DSI), calculated as heart rate divided by diastolic blood pressure, has emerging utility as a marker of vasodilatory shock and progression to septic shock in the emergency department. While pre-hospital shock index thresholds are recognised as high risk, the role of DSI as a dynamic marker across the ED-intensive care pathway remains unclear, particularly when physiological abnormalities persist despite early resuscitation or are blunted by rate-limiting medications.

Objectives: To characterise pre-hospital and early ED DSI in adult patients admitted directly from the ED to ITU with an infectious cause, and to assess whether persistent elevation of DSI following initial resuscitation identifies patients with ongoing physiological risk who may benefit from earlier critical care involvement.

Method/Description: We conducted a retrospective review of adult patients (≥18 years) referred directly from the ED to ITU with an infectious cause at a single centre between 1 October 2024 and 30 September 2025 (n=144). Pre-hospital and ED physiological data were analysed, including the highest DSI recorded pre-hospital and within the first hour of ED arrival. Additional variables included use of rate-limiting or anti-arrhythmic medications, initiation of vasopressors in the ED, and time to ITU referral from ED arrival. Fluid volumes were not analysed because of inconsistent real-time documentation in high-acuity resuscitation scenarios; ED vasopressor initiation was therefore used as a reliable marker of haemodynamic failure. Descriptive statistical analysis and distributional assessment of DSI values were performed to examine patterns of physiological response following early ED resuscitation.

Results/Outcomes: Despite a reduction in DSI following ED resuscitation, a substantial proportion of patients demonstrated persistent haemodynamic abnormality. Among 144 patients admitted to ITU, 69.4% had an ED DSI ≥1.5 within the first hour and 23.6% remained ≥2.0, indicating ongoing vasodilatory physiology despite early management. Approximately one quarter of patients were receiving rate-limiting or anti-arrhythmic medications, yet elevated DSI remained common in this subgroup, suggesting that the signal reflects physiological stress rather than tachycardia alone. Vasopressors were initiated in the ED in 11.8% of patients, representing established or rapidly evolving circulatory failure. The median time to ITU referral was 198 minutes despite early physiological warning signs frequently being present. Persistent elevation of DSI following initial resuscitation was associated with vasopressor use, ITU referral, and a physiological pattern consistent with the δ clinical phenotype characterised by refractory vasodilatory physiology.

Conclusion: Elevated DSI is frequently present at first medical contact and often persists despite early ED resuscitation in patients requiring ITU admission. DSI ≥1.5 should therefore be considered a failure-to-normalise marker rather than solely a screening threshold. Pre-hospital DSI identifies haemodynamic risk at first contact, while persistent ED DSI elevation may prompt earlier critical care discussion in patients with advanced infection. Persistent elevated DSI after resuscitation predicts vasopressor requirement and ICU referral, aligning with the δ clinical phenotype and supporting its use as a physiology-based tool to guide earlier escalation and more personalised haemodynamic management.

Biography

Dr. Himanshu Gul Mirani is a Consultant in Emergency Medicine at Midland Metropolitan University Hospital, UK, where he serves as Quality Improvement and Sustainability Lead. He is a Fellow of the Royal College of Emergency Medicine, the European Board of Emergency Medicine & Fellow of the Higher Education Academy. His qualifications include MRCP, SCE in Acute Medicine, postgraduate diplomas in Critical-Care and Emergency & Resuscitation Medicine, Child Health, Geriatric Medicine, and Legal Medicine, alongside an MBA in Healthcare. Author of two books, Dr. Mirani is actively involved in teaching, international conference presentations, and advancing point-of-care-ultrasound and quality improvement in emergency care.

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A SIGNAL in early Canadian viral surveillance efforts for SARS-CoV-2

Sequencing technologies implemented across frontline and public healthcare settings were crucial in developing virus surveillance programs during the Coronavirus Disease 2019 (COVID-19) pandemic caused by the transmission of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2). Through these programs, we have observed several variants of SARS-CoV-2, such as B.1.1.529 (i.e., Omicron), which arose from mutations altering the virus's core genome. Continual surveillance of these mutations remains necessary as additional variants capable of vaccine or diagnostic escape can arise if repeated transmission remains uncontrolled. To aid in SARS-CoV-2 surveillance, we present the evolution of a standardized bioinformatics Snakemake workflow for Illumina short-read sequencing platforms called the SARS-CoV-2 Illumina GeNome Assembly Line (SIGNAL). With SIGNAL, we can characterize mutations from assembled consensus sequences relative to the first SARS-CoV-2 genome sequence (MN908947.3) and observe divergence affecting vaccine, PCR, and diagnostic primer targets. As variants emerged, we leveraged iVar and FreeBayes to produce a consensus genome sequence and identify critical mutations. We then coupled in-depth reports using the Phylogenetic Assignment of Named Global Outbreak LINeages (PANGOLIN) and NCoV-Tools to assign phylogenetic lineages and perform quality control of samples. SIGNAL is currently the main workflow used by Canada's National Microbiology Lab for processing Illumina SARS-CoV-2 sequencing data. Through McMaster's Sequencing Core and clinical/public health collaborations over the first year of the pandemic, SIGNAL processed about 50% of the Province of Ontario's data and about 20% of all Canadian SARS-CoV-2 data. SIGNAL has since contributed to routine surveillance of local communities, rapid outbreak responses, and academic studies on virus dynamics, including aerosol transmission. Tools like SIGNAL better equip us to handle future emergent viral threats through rapid, yet accurate, processing of large volumes of data.

Biography

Dr. Jalees Nasir is a postdoctoral fellow in the lab of Dr. Andrew McArthur at McMaster University. He completed his doctoral degree in the same lab, specializing in the bioinformatics surrounding respiratory virus surveillance and clinical epidemiology. He has contributed significantly to research on the Coronavirus Disease 2019 (COVID-19) pandemic by developing an Illumina-focused sequencing pipeline used by government, academic, and clinical facilities. His current work focuses on further developing tools for the Comprehensive Antibiotic Resistance Database (CARD) using novel data schema languages to bridge the gap between complex data structures.

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Application of machine-learning algorithms to identify the key determinants of risk for HIV, Hepatitis C and Hepatitis B in primary care settings

Background: Testing for Blood-Borne-Viruses (BBVs) such as the Human Immunodeficiency Virus (HIV), Hep-Atitis C Virus (HCV) and Hepatitis B Virus (HBV) is generally focused on specialist settings however people with undiagnosed infections are also present within the general populations. We explore whether using Machine-Learning algorithms (MLAs) can identify people at heightened risk of indi-vidual or multiple BBVs in primary care settings.

Methods: From de-identified electronic health records data from 165 general practices in North East Lon-don we extracted risk factors for HIV, HCV and HBV and used them to train (75% data) and test (25% data) three MLAs: Logistic Regression (LR), AdaBoost with Random Under Sampling (RUS-Boost) and Balanced Random Forest Classifier (BRFC). The ROC curves, ROC AUC, sensitivity and specificity values quantified the models' performance. Across the models the key features for individual and multiple BBVs positivity were identified.

Results: A total of 1,987,954 patients were included in the study, from whom 75 predictive features were selected for HIV, 24 for HCV, 37 for HBV and 88 for all three BBVs. Different models were optimal for individual BBVs positivity classification, depending on the

accuracy metric. As a single infection, HCV was predicted most accurately across models and accuracy metrics. When targeting multiple BBVs, LR was the model with highest AUC value, BRFC was the most sensitive model and RUSBoost was the most specific model. The key identified features were similar across models with age the key predictive feature for both individual and combined BBV positivity. A number of features were important for two of the BBV positive groups: Black African ethnicity (HIV and HBV), liver disease (HBV and HCV) and opiate and cocaine use (HBV and HCV). A number of individual features were important for individual BBVs positivity.

Conclusions: Our findings illustrate that combining digital technology with routinely available general practice data has promise in improving case-finding of targeted BBV testing. There are however challenges in identifying the optimal MLAs and the accuracy metrics for multiple HIV/HCV/HBV positivity. This underscores the importance of evaluating different models and applying a broad set of accuracy criteria when utilising digital technology for precision medicine.

Keywords: HIV, HCV, HBV, Machine-Learning Algorithms, Prediction of Blood-Borne Viruses Diagnosis.

Biography

Jasmina Panovska-Griffiths is an Associate Professor at the Pandemic Sciences Institute, a Lecturer in Probability and Statistics at The Queen's College and a co-director of the EPSRC Centre for Doctoral Training in Healthcare Data Science at the University of Oxford. Jasmina is also affiliated with the UK Health Security Agency (UKHSA). Jasmina's research combines mathematical and statistical methods with data analysis and numerical simulations to answer existing and emerging questions in infectious disease and public health. Jasmina is a Fellow of the Institute of Mathematics and its Applications, The Royal Statistical Society and The Royal Society for Public Health and is actively involved in promoting mathematics and statistics as well as other STEM subjects across schools in the UK.

Dr. Jay Bhargav

Musgrove Park Hospital NHS Foundation Trust, Taunton, United Kingdom

Optimising hepatitis B antiviral prescribing in a rural NHS population: A quality improvement study demonstrating £50k annual trust savings

Background: Optimising models of care for hepatitis B treatment delivery is an important component of global hepatitis elimination strategies. However, centralised dispensing may increase travel and financial burden for patients, particularly in rural populations.

Methods: A retrospective quality improvement audit was conducted of 95 patients receiving entecavir or tenofovir between 2020-2024 at a rural UK district general hospital. Prescribing route and patient travel distance were analysed. Trust medication costs were calculated using local pharmacy procurement prices and community prescribing tariffs. Patient burden was modelled using travel costs (£0.374/mile), average travel speed (35mph), parking costs (£2.50/hour assuming 2.5 hours per visit), and time costs (£15.50/hour). Environmental impact was estimated using UK government greenhouse gas conversion factors.

Results: Hospital dispensing produced substantial trust-level cost savings. If all patients received antiviral therapy through hospital pharmacy, the projected annual saving was £49,583.82. However, patients receiving hospital-dispensed medication incurred an estimated £118.74 per patient annually in travel, parking, and time costs. A targeted optimisation strategy identified 24 patients living within 15 miles currently receiving community prescriptions. Transitioning these patients to hospital dispensing could generate approximately £10,700 annual savings while minimising additional patient burden.

Conclusion: Implementation of a targeted prescribing pathway demonstrates that substantial system-level savings can be achieved while maintaining equitable patient access, supporting scalable models of care for hepatitis B elimination.

Biography

Dr. Jay Bhargav is a UK-based doctor with a clinical interest in gastroenterology and hepatology. His work focuses on healthcare quality improvement, service delivery optimisation, and improving access to treatment for patients with chronic liver disease. His current interests include hepatitis B management, healthcare sustainability, and innovative care models that balance system efficiency with equitable patient access.

Jenna Shoman
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Genomic surveillance-guided adaptive allocation significantly reduces projected malaria incidence under artemisinin resistance

Background: Emerging artemisinin resistance and escalating insecticide resistance threaten recent gains in malaria control across sub-Saharan Africa. Despite this growing heterogeneity in parasite genetics and transmission intensity, intervention strategies are frequently deployed using uniform national approaches. We hypothesized that integrating parasite genomic surveillance with spatially resolved transmission modeling could identify high-impact, region-specific allocation strategies that outperform standard uniform deployment.

Methods: Publicly available *Plasmodium falciparum* genomic datasets (n>12,000 isolates) were integrated with WHO malaria incidence estimates across 15 high-burden countries. Resistance-associated variants, including kelch13 and additional validated loci, were mapped using geospatial clustering and hotspot detection to identify regions of elevated resistance risk. These genomic risk surfaces were incorporated into a compartmental transmission model parameterized with vector dynamics, intervention coverage (ITNs, ACTs, IRS), treatment-seeking behavior, and health-system access. Standard national strategies were compared with genomic-guided adaptive allocation over a 10-year projection horizon. Probabilistic sensitivity analyses were conducted to evaluate robustness across plausible resistance growth and coverage scenarios.

Results: High-resistance clusters were associated with a modeled 18-27% reduction in ACT parasite clearance probability ($p<0.01$) and increased rebound risk under uniform allocation. Genomic-guided adaptive deployment reduced projected malaria incidence by 21.4%

(95% CI: 17.8–24.9%) compared with standard strategies and improved cost-effectiveness by 14% in DALYs averted per dollar spent. Benefits persisted across sensitivity analyses under realistic operational constraints.

Conclusions: Genomic surveillance-guided intervention allocation substantially improves projected malaria control outcomes relative to uniform national strategies. Integrating parasite genomics into malaria elimination programs provides a scalable precision-public-health framework capable of mitigating resistance-driven resurgence and accelerating durable elimination efforts.

Biography

Jenna Shoman is a sophomore at Harvard University concentrating in Human Evolutionary Biology with a secondary in Global Health and Health Policy. Her academic interests focus on molecular disease mechanisms and precision public health strategies to combat global infectious and noncommunicable diseases. She has prior faculty-mentored research experience in cancer progression and cellular plasticity, with strengths in quantitative data analysis. She is particularly interested in integrating genomic science with health systems implementation to address complex global health challenges such as infectious disease resistance.

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Decoy Therapeutics, Inc, USA

Pioneering D-MAVS: Designable multi-antivirals that transform how antivirals are created, developed, and used

Decoy therapeutics is a biotech company pioneering Designable Multi-Antivirals (D-MAVs™) to redefine how viral disease is treated and understood. By harnessing our proprietary IMP^{3}ACT platform, which integrates AI-enabled design with rapid synthesis, we develop adaptable peptide antivirals that target shared viral mechanisms rather than individual pathogens. Decoy is building toward a future where a single, affordable drug can protect many people against multiple viruses, moving faster into the clinic to address the persistent health and societal disruptions caused by viral infections. Our lead program offers a self-administered, intranasally delivered pan-coronavirus fusion inhibitor that exhibits broad, potent antiviral activity, both in the prophylactic and post-exposure dosing paradigms. Pharmacokinetic modelling demonstrates multiday protection, offering a strategic shift from reactive daily dosing to a more robust, durable multi-day antiviral intervention. Decoy's approach is applicable across multiple viral families and has the potential to redefine next-generation antiviral protection while expanding global access to broad, effective therapies.

Biography

Jodi Cooper is Director of Operations at Decoy Therapeutics and an accomplished pharmacologist with expertise in Oncology and Virology drug discovery across multiple therapeutic platforms. She has extensive experience advancing preclinical programs to IND-ready status through strategic study design, operational leadership, and execution across internal teams and global CRO partnerships. Jodi is recognized for building effective external collaborations, managing complex research operations, and driving cross-functional program execution. Her ability to align scientific strategy with operational excellence has contributed to the successful advancement of innovative therapeutic programs and strengthened translational research and development efforts across diverse drug discovery initiatives.

Jong-Hoon Kim

International Vaccine Institute, Seoul, Republic of Korea

Optimizing oral cholera vaccine allocation: Pre-emptive vs. Reactive strategies under uncertainty

Constrained global Oral Cholera Vaccine (OCV) supplies force difficult trade-offs between pre-emptive and reactive deployment in sub-Saharan Africa. To address this, we developed an analytical and simulation framework to optimize OCV allocation to minimize costs that account for costs associated with vaccination and those associated with disease outbreaks. We found that under scarce capacity, the optimal choice depends on comparing reactive effectiveness against pre-emptive effectiveness weighted by outbreak probability; abundant capacity favors pre-emptive allocation augmented by high illness costs. Furthermore, accurate risk targeting under heterogenous risk setting strongly shifts the advantage toward pre-emptive vaccination. Applying a prediction model trained on 2010-2023 surveillance data from sub-Saharan Africa to mixed-strategy simulations, we demonstrated that model-ranked targeting substantially outperforms random allocation. Depending on coverage capacity, the distribution of risks, costs of vaccination and outbreaks, the optimal pre-emptive vaccine fraction ranges widely, 0 to 1. These results provide actionable, data-driven guidance for customizing pre-emptive, reactive, or mixed OCV allocation strategies to specific regional contexts.

Biography

Jong-Hoon Kim Ph.D. is a theoretical epidemiologist who uses mathematical, statistical, and machine-learning models to study infectious disease epidemiology. His work involves developing theories about infectious disease transmission, making predictions, and designing optimal intervention strategies to improve public health. He works at the International Vaccine Institute, which is located in Seoul, South Korea. His current research primarily focuses on cholera and typhoid fever, and COVID-19.

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From gut dysbiosis to lung vulnerability: Influenza risk in diabetes

Respiratory viral infections, including influenza, remain a major global health concern and disproportionately affect individuals with diabetes, who are at increased risk of severe disease and complications. This heightened susceptibility has traditionally been attributed to the direct effects of hyperglycemia on lung epithelial integrity and immune cell function. Here, we identify a previously underappreciated gut-lung axis through which diabetes-associated gut microbiota alterations impair pulmonary innate immunity and antiviral defense. Using a streptozotocin-induced diabetic mouse model, we demonstrate that diabetes-driven changes in gut microbiota composition lead to increased systemic dissemination of Lipopolysaccharide (LPS), a key microbial-derived inflammatory mediator. Elevated circulating LPS reprograms mitochondrial metabolism in Alveolar Macrophages (AMs), resulting in excessive mitochondrial Reactive Oxygen Species (mitoROS) production and enhanced pro-inflammatory signaling. This metabolic reprogramming compromises AM phagocytic capacity and increases their susceptibility to infection-induced cell death, thereby weakening early antiviral responses to Influenza A Virus (IAV). Importantly, pharmacological inhibition of mitoROS restores AM function and improves host resistance to IAV infection in diabetic mice, highlighting a potential therapeutic target. Consistent with these experimental findings, analysis of colonic biopsies from diabetic patients revealed positive correlations between HbA1c levels, the abundance of mucosa-associated Gram-negative bacteria, and LPS concentrations, supporting the clinical relevance of this pathway. Furthermore, transfer of mucosal microbiota from diabetic patients into germ-free mice recapitulated AM dysfunction

and increased susceptibility to IAV infection in a Toll-Like Receptor 4 (TLR4)-dependent manner. Collectively, these findings establish a mechanistic link between diabetes-associated gut dysbiosis, mitochondrial dysfunction in AMs, and impaired antiviral immunity. Targeting microbiota-derived signals or mitochondrial stress pathways may represent promising strategies to reduce the burden of respiratory viral infections in individuals with diabetes.

Biography

Dr. Jun Zou has over a decade of experience investigating host-microbial interactions, with a focus on metabolic disease. At Georgia State University, his laboratory studies how diet-microbiota interactions regulate metabolic and immune homeostasis in obesity and diabetes. His work has demonstrated that dietary fiber reshapes the gut microbiota to improve metabolic outcomes through IL-22 and short-chain fatty acids, and that microbiota alterations can be vertically transmitted to influence disease risk. Building on this foundation, his current research focuses on how diabetes-associated gut dysbiosis impairs host defense against infections, including influenza A virus.

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Lenacapavir for HIV treatment and pre-exposure prophylaxis-evaluating efficacy and safety: A systematic review and meta-analysis

Background: Human Immunodeficiency Virus (HIV) remains a global health burden despite advances in Antiretroviral Therapy (ART). Challenges with daily adherence and Multidrug Resistance (MDR) necessitate novel approaches. Lenacapavir, a long-acting HIV-1 capsid inhibitor administered subcutaneously every six months, offers a promising alternative for both treatment and prevention. This systematic review and meta-analysis evaluated the efficacy and safety of lenacapavir for HIV management and Pre-Exposure Prophylaxis (PrEP).

Methods: A comprehensive search was conducted in PubMed, Web of Science, and Scopus up to 2025, including randomized controlled trials and cohort studies assessing lenacapavir in HIV-infected individuals and those at risk. Primary outcomes were HIV incidence, virologic suppression (HIV-1 RNA <50 copies/mL), CD4+ count changes, and adverse events. Data synthesis included qualitative analysis and meta-analyses using random-effects models.

Results: Six studies were included, encompassing treatment-naive individuals, MDR-HIV patients, and PrEP candidates. Meta-analysis of two large PrEP trials (n>4,000) revealed a significant reduction in HIV incidence with lenacapavir (pooled OR 0.058; 95% CI: 0.009-0.360; p=0.002). In MDR-HIV patients, 83% achieved virologic suppression at week 52 with lenacapavir plus optimized background therapy. Lenacapavir also showed comparable efficacy to standard ART in treatment-naive patients. While lenacapavir increased the odds of injection site reactions (pooled OR 3.055; p=0.001) and nausea (pooled OR 0.542; p<0.001), most adverse events were mild to moderate, with no significant difference in overall adverse event rates.

Conclusion: Lenacapavir offers highly effective, long-acting HIV prevention and treatment, particularly benefiting adherence-challenged and MDR-HIV populations. Despite some local and gastrointestinal side effects, its safety profile is favorable, representing a significant advance in HIV care.

Biography

Khaled Hemdan is a medical researcher and physician at October 6 University Hospital, Faculty of Medicine, Egypt, with a primary focus on infectious diseases, HIV therapeutics, and evidence-based medicine. He has authored several systematic reviews and meta-analyses examining antiviral agents and emerging treatment strategies. His research interests include long-acting HIV therapies, antimicrobial stewardship, and global health outcomes. He actively collaborate with multidisciplinary teams across the region and remain committed to advancing clinically impactful, data-driven approaches in infectious disease prevention and treatment.

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Non-albicans candidemia in intensive care units of a tertiary care hospital and the antifungal susceptibility pattern of the isolates along with biofilm formation

Background: *Candida* species are the commonest opportunistic fungal infections worldwide. In critically ill patients they may lead to fatal systemic infections. Candidemia is a fatal fungal infection with mortality ranging from 35% to 75%. Of all Blood Stream Infections (BSI), yeasts belonging to genus Candida are amongst the top 10 microorganisms. In ICU patients, the incidence varies from 0.24-34.3 patients per 1000 ICU admissions according to western literature. A wide variety of risk factors contribute to altering the epidemiology of *candidemia*. There has been a shift towards non-albicans species namely *Candida tropicalis, Candida parapsilosis, Candida krusei* especially in neutropenic patients and Candida glabrata in patients with solid tumour. Newer Candida species like *Candida auris*, Candida duobushaemulonii and Candida pelliculosa have a greater propensity for nosocomial infections and are increasingly being reported as multi drug resistant in ICUs. *Candida* species form biofilms that are architecturally very complex and associated with high degree of antimicrobial resistance thereby making the infections difficult to treat.

Materials & Methods: The study was undertaken in the microbiology department with collaboration of the ICU clinicians for a period of 2 years. Blood cultures obtained from ICU patients suspected of BSI were sent to the microbiology laboratory in BACTEC bottles. The automated culture bottles were incubated in the machine. Whenever a bottle "Flashed Positive", they were taken out and sub cultured on appropriate media for isolation of the pathogen. The pathogen was identified was MALDI-TOF. If the pathogen was a *Non-albicans* candida species, the clinical history of the patient was taken and antifungal susceptibility was performed by VITEK YST AFST cards. Biofilm formation was detected among the *Non-albicans* isolates by the Congo red agar method.

Results: A total of 1816 patients of suspected BSI were admitted in the ICUs during our study period. Blood culture specimens were sent for microbiological investigation from these patients. 63 of these samples were positive for growth of *Non-albicans Candida* species from suspected cases of BSI admitted in ICUs.

Surgical ICU had the highest candidemia rate. Commonest *non-albicans* species isolated were *C. tropicalis* (19) followed by *C. parapsilosis* (12). *Candida auris* was also found in 8 patients. Prolonged hospital stay of over 7 days, long term antibiotic therapy and surgery were found associated in a higher percentage among patients having *non-albicans* candidemia as compared to *albicans candidemia* with statistical significance.

Antifungal susceptibility of these *candida* isolates showed 100% susceptibility to Posaconazole and Flucytosine with lowest susceptibility for itraconazole and fluconazole. 9 isolates showed presence of biofilms.

Conclusion: Underlying comorbid conditions and risk factors of the ICU patients evaluated in the study will help the clinicians to suspect *Non-albicans* candidemia based on these conditions and start appropriate therapy as and when required. The present study will guide clinicians about the type of *candida* species and their antifungal susceptibilities prevalent in different ICUs of the present setup.

Biography

Dr. Kunalsen Jagatdeo works as Assistant Professor in the Microbiology Department since 2022. He is the member secretary of the Infection Prevention and Control Committee in the hospital. His fields of interest include Mycology, Molecular Diagnostics and Infectious Diseases. He has completed a certificate course in Antimicrobial Stewardship from CMC Vellore. He presented a poster in the recently concluded APCCMI 2025 held at Bangkok. He is actively involved in various multicentre studies with premier institutes of the country on Antimicrobial Resistance surveillance. He received Runner-up prize for his Oral presentation at CAHOTECH-2025.

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Bacterial resistance patterns and associated factors in pediatric urinary tract infections: A susceptibility profile analysis

Introduction: Pediatric Urinary Tract Infections (UTIs) represent an important reservoir of antimicrobial-resistant pathogens, predominantly *Escherichia coli,* with limited regional data on susceptibility patterns and factors associated with resistance. Antimicrobial resistance may be intrinsic or acquired; in this context, broad-spectrum β-lactamases (BLEA; classical β-lactamases conferring resistance to penicillins and early-generation cephalosporins) and Extended-Spectrum β-Lactamases (ESBL; enzymes hydrolyzing extended-spectrum cephalosporins) were the predominant resistance mechanisms, the latter contributing to Multidrug-Resistant (MDR), Extensively Drug-Resistant (XDR), and Pandrug-Resistant (PDR) phenotypes. Increasing global rates of ESBL-producing Enterobacterales have been reported, with pediatric prevalence reaching 14% worldwide and rising substantially over time. Resistance mechanisms, including ESBL, AmpC, and carbapenemases, compromise empirical therapy and limit oral treatment options. Regional variability and associations with prior antibiotic exposure and urinary tract abnormalities highlight the need for local susceptibility data to guide antimicrobial stewardship in pediatric UTIs.

Methods: An analytical multicenter cross-sectional study was conducted in three healthcare institutions in Colombia. Children aged 1 month to 12 years presenting to emergency departments or hospitalized pediatric services with urinary tract infection confirmed by urine culture were included. Significant bacteriuria was defined according to collection method and established colony count thresholds. Patients with contaminated samples, fungal isolates, oncologic disease, organ transplantation, pregnancy, or recurrent

UTIs were excluded. Non-probabilistic sampling was used. Antimicrobial susceptibility testing was performed using automated systems following Clinical and Laboratory Standards Institute (CLSI) guidelines. Selection and confounding biases were minimized through homogeneous inclusion criteria, standardized microbiological procedures, verification of covariate overlap, and adjusted statistical analyses to evaluate factors associated with antimicrobial resistance.

Results: 87 children with culture-confirmed UTI were included, with a mean age of 2.21 years; 69% were male. The overall prevalence of bacterial resistance was 82.75% (95% CI: 0.73–0.90). The most frequently isolated resistant pathogens were *Escherichia coli* (83.3%), *Proteus mirabilis* (6.9%), and *Pseudomonas aeruginosa* (1.38%). Resistance was significantly more frequent in *E. coli* infections compared with other pathogens (80.9% vs. 63.2%). The most frequent resistance mechanisms were broad-spectrum β-lactamases (BLEA/BSBL) (41.6%), penicillinase production (26.4%), Extended-Spectrum β-Lactamases (ESBL) (15.3%), AmpC (8.3%), and Inhibitor-Resistant TEM (IRT) (8.3%). Among *E. coli* isolates, BLEA predominated (48.3%), followed by penicillinase (23.3%) and BLEE (16.7%). After adjustment using Poisson regression with robust variance, the adjusted prevalence of bacterial resistance in *E. coli* isolates was 81.2% (95% CI: 0.72–0.89). Risk of malnutrition (p=0.023), urinary tract manipulation within the previous three months (p=0.042), hospitalization during the last six months (p=0.040), and patient age (p=0.0486) were significantly associated with bacterial resistance.

Conclusion: Antimicrobial resistance in pediatric UTI was highly prevalent across the evaluated centers, with widespread circulation of resistant pathogens. Malnutrition risk, recent urinary tract manipulation, hospitalization, and patient age significantly associated with resistance. Characterizing local etiological agents and susceptibility patterns provides essential, context- specific evidence to guide empirical antibiotic selection, optimize early clinical decision-making, and strengthen antimicrobial stewardship strategies. Tailoring therapeutic approaches to local resistance profiles is critical to improving the quality and safety of pediatric care and mitigating the further emergence of antimicrobial resistance.

Biography

Laura Camila Cáceres Delgado is a third-year pediatric resident in Colombia with clinical training in pediatric inpatient care and pediatric intensive care units. Her academic interests include pediatric infectious diseases and antimicrobial resistance. As part of her residency graduation requirements, she conducted an analytical multicenter study on antimicrobial resistance patterns and associated factors in pediatric urinary tract infections, which forms the basis of her current abstract. Her work focuses on generating locally relevant susceptibility data to support evidence-based empirical therapy and strengthen antimicrobial stewardship in pediatric clinical practice.

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Strengthening four communities of practice of the one health knowledge nexus: A community-driven platform for operationalizing one health

One Health (recognizes the interdependence of human, animal, plant, and environment health, yet its implementation continues to face context-specific challenges. To address these barriers, the one health knowledge nexus was established in 2023 in support of the quadripartite one health joint plan of action. The one health knowledge nexus connects over 2,700 stakeholders across eight Communities of Practice to strengthen countries' capacities to operationalize one health principles and practices.

Since 2024, a dedicated project has expanded the one health knowledge nexus activities in four communities of practice, using open, participatory mechanisms to promote collaborative guideline development, peer exchange through discussion boards and learning dialogues, and co-creation of context-appropriate technical resources. These activities aim to produce knowledge products that are directly relevant to country-specific needs and priorities.

Key outputs include 21 learning dialogues, 19 case studies, a conceptual framework on addressing the drivers of emerging animal and plant pests and diseases, training materials on one health return on investment, a one health policy database, one health governance monitoring and evaluation recommendations, and mapping of over 30 information and communication tools supporting one health intelligence, risk management, risk communication, and learning.

These outputs have informed policymakers in Malawi, Ghana, and Nigeria, strengthening multisectoral coordination, supporting evidence-based decision-making, and contributing to the development of costed one health national action plans. By fostering community-driven knowledge exchange and co-created resources, one health provides a scalable model for operationalizing the One Health approach to infectious disease prevention, detection, and response.

Biography

Lina Awada is a veterinary epidemiologist (DVM, MSc, PhD) with 15 years of experience in international organizations, specializing in animal disease surveillance, epidemic intelligence, data integration, and health information systems. Her work focuses on the One Health approach to understanding transboundary animal diseases and informing international surveillance and control policies across production animals, companion animals, wildlife, and trade. Lina currently works at FAO, where she coordinates a project under the One Health Knowledge Nexus, focusing on drivers of emerging pests and diseases, governance, digital technologies, and return on investment for One Health.

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Structural studies of the Hemagglutinin (HA)-membrane interaction

The viral fusion protein Hemagglutinin (HA) is the predominant influenza surface glycoprotein and mediates engagement with and entry into host cells. Influenza A virus HAs are categorised into two broad and immunologically distinct phylogenetic groups. Group 2 HA subtypes include H3, which is found in a large proportion of seasonal influenzas, and H7, which is present in some highly pathogenic avian influenzas.

HA is a single-pass, type I transmembrane protein and exists as a trimeric assembly on the surface of the influenza virus. Viral membrane fusion is induced through large, and relatively well characterised, conformational changes in the HA ectodomain. In contrast, very little is known about the architecture of HA's interaction with the phospholipid bilayer-a crucial element of the viral fusion machinery. To date, the only structural information about HA's transmembrane domain is derived from a group 1, H1 subtype in the pre-fusion conformation.

Through purification of group 2 HAs in lipid environments, followed by single particle analysis cryoEM, we have resolved the first structures of full-length post-fusion HA. These provide mechanistic insights into the architecture of the transmembrane domain of group 2 HAs, as well as the mode of interaction of HA's highly conserved fusion peptide with membrane.

Biography

Luke Perera studied Natural Sciences at Cambridge University before proceeding to carry out an MRes and PhD in the Cambridge Institute for Medical Research. Luke's PhD was conducted within the lab of David Ron, investigating the mechanism of post-translation Hsp70 chaperone regulation in endoplasmic reticulum protein folding homeostasis. Luke subsequently took up a postdoctoral fellow position in Steve Gamblin's lab at the Francis

Crick Institute, London. Here, Luke work focusses on the characterisation of viral membrane fusion pathways, in particular that of influenza A virus, through cryoEM-based studies of viral fusion proteins and their membrane interaction interfaces.

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Standardization of parasitic and molecular techniques for the detection and characterization of *Toxocara* spp. from feces and soil

Zoonotic parasites present in dogs and cats, such as *Toxocara canis* and *Toxocara cati*, pose a risk, especially in recreational areas where people live with their pets. These helminths are responsible for visceral larva migrans syndrome. The objective of this study was to standardize parasitological and molecular techniques for the detection and differentiation of *Toxocara* spp. species in fecal and soil samples. Diagnostic sensitivity was evaluated by inoculating parasite-free fecal (1g) and soil (10g) samples with *T. canis* and *T. cati* eggs at concentrations ranging from 1×10^4 to 1 egg obtained from a female *T. canis.* The parasitological method was performed by concentration and flotation with a saturated sugar solution [A/C]. DNA extraction was performed using the GENEJET kit, with prior mechanical lysis and quality verification by electrophoresis and A260/A280 spectrophotometry. A PCR assay specific to the genus *Toxocara*, targeting the IT1-IT2 intergenic region of the 5S ribosomal subunit, was standardized with different primer sets that produce 1000 and 500bp amplicons. Differentiation between species was achieved by RFLP analysis interpreted with Total1D software. The parasitological method recovered between 60 and 80% of the inoculated eggs and had a sensitivity of 1 egg for both the inoculum alone and with fecal and soil matrices inoculated with eggs. The 1000 and 500bp PCRs detected 10fg and 1 *Toxocara* egg (Te), and 10pg of DNA and 10Te, respectively. The sensitivity of PCR for detecting Te decreased to 0 eggs in fecal or soil matrices. The addition of 50µg of BSA improved amplification in inhibited samples, allowing the detection of between 1×10^2 Te in feces using the 500bp PCR. For both matrices, amplification was possible by combining parasitological and molecular methods, achieving a sensitivity of 1×10^0 Te. The polymorphism obtained from the 500bp amplicon allowed differentiation between *T. canis* and *T. cati*. These results support the use of [A/C] as the parasitological method for Te detection

and the 500bp PCR for the detection and molecular characterization of *Toxocara* spp. in fecal and soil matrices with high sensitivity, strengthening epidemiological studies in areas shared by humans and pets.

Biography

Maria Alejandra Vethencourt Ysea is a microbiologist who graduated from the University of the Andes in Venezuela (1991) and holds a Ph.D. in Science with a concentration in Immunology (2014) from the Venezuelan Institute for Scientific Research (IVIC), as well as a Master's degree in Molecular Biology from the European Center for Master's and Postgraduate Studies (2023). Maria has taught at the Central University of Venezuela (10 years), the University of Medical Sciences (Costa Rica) for 5 years, and currently, since 2025, at the Latin University of Costa Rica. Maria's current line of research is related to One Health, specifically the molecular detection of parasites and bacteria with zoonotic potential. Maria has more than 20 publications in this field.

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Role of serial serum Procalcitonin (PCT) levels in predicting severity and outcome in sepsis and its utility in antibiotic stewardship at a tertiary care hospital

Introduction: Sepsis is a life-threatening condition caused by a dysregulated host response to infection resulting in organ dysfunction. Early diagnosis and risk stratification are crucial to reduce morbidity and mortality. Procalcitonin (PCT), a biomarker of bacterial infection, has gained importance for early diagnosis and monitoring treatment response. This study evaluates the role of serial serum procalcitonin levels in determining disease severity and prognosis in patients with sepsis and assess role of procalcitonin in guiding patient antibiotic therapy.

Aims:

1. To evaluate the diagnostic and prognostic significance of serial PCT measurements (0hr, 24hr, 72hr) in patients with sepsis.
2. To assess role of procalcitonin in guiding antibiotic therapy in patients with sepsis.

Materials and Methods: This prospective observational study included adult patients (>18 years) diagnosed with sepsis as per Sepsis-3 criteria. Clinical and laboratory data including demographics, SOFA score, infection source, antibiotic regimen, and serial PCT values at admission, 24 hours, and 72 hours were recorded. Patient outcomes were categorized as recovered, saved, or died. PCT kinetics were analyzed to determine trends and their relationship to mortality and antibiotic adjustments.

Results: A total of 1152 patients with infection were screened for sepsis of whom a total of 97 patients with complete clinical, laboratory, and treatment-related data were confirmed to have sepsis and were included in the final analysis. The majority of patients belonged to the 40-65 years age group (51.5%), followed by >65 years (33.0%), 25-40 years (10.3%), and 18-25 years (5.2%). A male predominance was observed with 56 males (57.7%) and 41 females (42.3%). Mean PCT levels demonstrated a progressive decline from admission to 24 hours and 72 hours. Patients who recovered showed a significant reduction in PCT levels (≥50-70% by 72 hours), indicating better therapeutic response. In contrast, non survivors had persistently elevated or rising PCT levels despite treatment. Antibiotic de-escalation was feasible and safe in patients with consistently declining PCT values. Mortality was highest among patients with admission PCT levels >10ng/dL and those exhibiting minimal decrease over 72 hours, indicating poor prognosis. Regarding clinical outcomes, 79 patients (81.4%) recovered, while 18 patients (18.6%) succumbed to the illness. Mortality was predominantly observed in patients who had persistently elevated procalcitonin levels highlighting the prognostic value of procalcitonin in the assessment of septic patients.

Conclusion: Serial measurement of serum Procalcitonin (PCT) is a valuable biomarker for the early diagnosis and monitoring of sepsis. In the present study declining PCT levels over 72 hours were associated with clinical improvement and favourable outcomes, whereas persistently elevated or rising PCT levels were associated with increased disease severity and higher mortality. This dynamic kinetic profile makes procalcitonin a valuable biomarker not only for diagnosis but also for monitoring treatment response. PCT-guided antibiotic de-escalation enhances antimicrobial stewardship and helps to effectively control the rising problem of antimicrobial resistance.

Biography

Mariyah Yousuf M.Sc., Ph.D. Candidate, she is a medical microbiologist with expertise in bloodstream infections and sepsis research. Currently she is pursuing PhD at a 1200 bed tertiary care super specialty hospital. Her main focus is on Procalcitonin as a biomarker for sepsis diagnosis, its prognosis and antibiotic stewardship. She has over four years of clinical research experience and have many research article publications including one in a PubMed-indexed journal, contributing to advances in critical care microbiology.

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Sexually transmitted and blood-borne infections among People Living with HIV (PLHIV) in high-income countries: A systematic review and meta-analysis

Objective: People Living with HIV (PLHIV) have been disproportionately impacted by the burden of sexually transmitted and blood-borne infections. In this study, we examine the prevalence and incidence of eleven Sexually Transmitted and Bloodborne Infections (STBBIs) in PLHIVIV in high-income countries.

Methods: This systematic review and meta-analysis was performed using PRISMA guidelines and registered in PROSPERO. Eligible studies consisted of those published from 2018 to 2023 that reported incidence or prevalence data of Treponema pallidum, Neisseria gonorrhea, Chlamydia trachomatis, Mycoplasma genitalium, Hepatitis A, B, and C, Human Papillomavirus, Herpes Simplex Virus 1 and 2, or Trichomonas vaginalis. Two independent and blinded reviewers screened the titles and abstracts, and full-text papers. Extracted data included study characteristics, population demographics, risk factors, and co-infections.

Results: The prevalence of STBBIs in PLHIV varied between 1.6% to 96% depending on infection type. Sample sizes varied between 82 and 23,361 individuals, with mean/median ages in the 30's and 40's. Among 30 included articles, 8 studies were conducted among men who have sex with men, and only one among women living with HIV. Contributing factors to the significant prevalence rate include the high proportion of substance use, particularly injection drug use (15.6%; 52.7%). Differences can be explained by the STBBI infection, testing and samples used, study design and region.

Conclusion: PLHIV have a significant prevalence of STBBIs coinfections. PLHIV remain at a heightened risk for STBBIs due to the intersection of biological, structural, and behavioral factors. Females and women are underrepresented in STBBI research. Along with medical treatment for HIV care, it is essential to incorporate STBBI testing, treatment and prevention, before, at, and after HIV diagnosis for the person living with HIV and for their sexual partners, and wraparound interventions and multi-disciplinary teams addressing social determinants of health to reduce co-infection rates and improve health.

Biography

Maya Polevoi is third year medical student at the Max Rady College of Medicine in Winnipeg, Manitoba. Maya has a growing interest in the intersectionality of infectious diseases, mental health, and population health. Maya's research focuses on sexually transmitted and blood-borne infections among people living with HIV, with an emphasis on population-level trends and health outcomes. Maya is interested in exploring how social and behavioural factors influence health trajectories and in contributing to evidence-based approaches that improve patient care and public health interventions.

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Epstein–Barr virus-associated autonomic neuropathy presenting as isolated severe orthostatic hypotension

Background: Orthostatic hypotension is commonly attributed to volume depletion, medication effect, cardiac disease or endocrine dysfunction. However, persistent orthostatic hypotension after correction of reversible causes should prompt consideration of cardiovascular autonomic failure. Acute or subacute autonomic neuropathy is uncommon and is frequently idiopathic, although post-infectious and immune-mediated mechanisms are increasingly recognised. Epstein–Barr Virus (EBV)-associated autonomic neuropathy is rarely reported and usually presents with multi-domain dysautonomia.[1,2]

Clinical case: A gentleman in his early 60s with Rheumatoid Arthritis and Raynaud's phenomenon treated with Methotrexate and Amlodipine respectively, presented after an unwitnessed fall preceded by dizziness and light-headedness, sustaining a left clavicular fracture. He also reported a one-month history of progressive fatigue, dizziness, sore throat, night sweats and 5kg weight loss. Shortly before admission, he had been reviewed in Haematology clinic because of these constitutional symptoms with accompanying lymphocytosis, which persisted on his admission blood tests. This prompted investigations for infective and haematological causes; a Monospot test was positive with raised immunoglobulins. Clinical examination on admission was grossly unremarkable, bar an initial blood pressure assessment which demonstrated marked orthostatic hypotension, falling from 90/63mmHg to 70/52mmHg.

Amlodipine was discontinued and repeated intravenous fluid challenges were trialled without sustained improvement. Formal head-up tilt-table testing confirmed severe progressive orthostatic hypotension, with blood pressure falling from 108/69mmHg to 45/33mmHg within 8 minutes, reproducing symptoms of light-headedness and visual disturbance. Given the

positive Monospot test and persistent lymphocytosis, EBV PCR was performed and returned positive at 96,079.5 copies/mL, log 4.98, supporting recent or reactivated EBV infection. Extensive investigations did not identify an alternative cardiac, endocrine, autoimmune, paraneoplastic, malignant or large-fibre neurological cause. CT thorax demonstrated bilateral ground-glass change, small pulmonary nodules and mediastinal/hilar lymphadenopathy, considered inflammatory or reactive.

The patient was treated with fludrocortisone and midodrine, titrated to symptomatic response. Serial follow-up demonstrated falling EBV viral load in parallel with haemodynamic recovery, as shown on Table 1. EBV PCR decreased from log 4.98 during the index admission to log 3.4 by Month 5, by which point clinically significant orthostatic hypotension had resolved. Thoracic imaging abnormalities seen during admission also improved, with later resolution of pulmonary nodules and reduction in mediastinal lymphadenopathy.

Table 1. Serial EBV viral load and orthostatic blood pressure trend

Time point	EBV PCR	Orthostatic assessment
Month 0, during index admission	Log 4.98	Marked orthostatic hypotension: BP 93/61->62/38
Month 1	Log 4.33	No significant systolic fall: BP 92/58->85/50
Month 3	Log 3.61	BP 106/68, no significant fall
Month 5	Log 3.4	Sustained improvement

Conclusion: This case describes suspected EBV-associated autonomic neuropathy presenting predominantly as cardiovascular autonomic failure. The near-isolated orthostatic hypotension and serial EBV PCR correlation distinguish it from previously reported EBV-associated dysautonomia, where multi-domain autonomic involvement is more typical.

Biography

Muhammad Zakwan Zakariya is an Internal Medicine Trainee (IMT2) currently undertaking Neurology training at Royal Preston Hospital, United Kingdom. Zakariya has a strong passion for medical education and a keen interest in infectious diseases, particularly in advancing clinical knowledge and improving patient care. This abstract submission reflects his continued interest in contributing to the field of infectious diseases and engaging in academic and clinical discussions.

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Clinical outcomes and choice of antibiotics in AmpC β-lactamase hyperproducing enterobacterales bacteremia: A single-centre study

Background: AmpC β-Lactamase Hyperproducing Enterobacterales (ABLHE) are significant causes of bloodstream infections, often associated with multidrug resistance and high mortality. This study aimed to determine the 30-day all-cause mortality rate and its risk factors, to describe the epidemiology, clinical outcomes, and treatment of ABLHE bacteremia.

Methods: A retrospective single-centre study was conducted at Hospital Canselor Tuanku Muhriz (HCTM) from January 2015 to December 2022. This study primarily aimed to determine the 30-day all-cause mortality rate among patients with AmpC β-Lactamase-Hyperproducing Enterobacterales (ABLHE) bacteremia. Secondary objectives included describing empirical and definitive antimicrobial therapies, evaluating their association with length of hospitalization, and identifying risk factors for 30-day all-cause mortality. The sources of infection, patterns of community- versus nosocomial-acquired cases, and the prevalence of *Enterobacter cloacae, Klebsiella aerogenes*, and *Citrobacter freundii* were also analysed.

Results: A total of 196 patients with blood culture-confirmed ABLHE bacteremia (*Enterobacter cloacae, Klebsiella aerogenes*, and *Citrobacter freundii*) were included. The overall 30-day mortality rate was 32.7%. The commonest microorganism was *Enterobacter cloacae* at 71.4%. *Klebsiella aerogenes* and *Citrobacter freundii* accounted for 23.5% and 5.1% respectively. Nosocomial acquired bacteremia accounted for 40.3%. ABLHE bacteremia was mainly acquired via respiratory tract infection at 27.0% followed by catheter-related bloodstream

infection, at 23.5%. The commonest empirical antibiotic used in this study was piperacillin-tazobactam at 43.4% where else the commonest definitive antibiotic was cefepime accounting for 55.1%. Independent predictors of 30-day mortality included Pitt Bacteremia score (aHR: 6.533, 95% CI: 2.066-19.532, p=0.001), septic shock (aHR: 2.532, 95% CI: 1.448-4.428, p=0.001), mechanical ventilation (aHR: 3.381, 95% CI: 1.703-6.712, p<0.001) and inappropriate definitive antibiotic therapy (aHR: 2.435, 95% CI: 1.240-4.781, p=0.010). Cefepime had a shorter length of stay (aHR: 0.982, 95% CI: 0.968-0.995, p=0.007). There was no difference in the 30-day all-cause mortality in definitive cefepime and carbapenem treatment group (aHR: 0.908, 95% CI: 0.499-1.652, p=0.753).

Conclusion: ABLHE bacteremia was associated with high mortality, particularly among patients with severe illness and inappropriate definitive antibiotics therapy. The 30-day all-cause mortality between cefepime and carbapenem groups was comparable in ABLHE bacteremia. These findings emphasize the importance of appropriate intensive management in managing ABLHE bacteremia especially in this high risk group.

Keywords: AmpC β-Lactamase Hyperproducing Enterobacterales Bacteremia, 30-Day All-Cause Mortality, Cefepime, Carbapenem, Antibiotics Therapy.

Biography

Dr. Navanitha Chandrasekaran is a dedicated Internal Medicine doctor at Universiti Kebangsaan Malaysia (UKM), passionate about infectious diseases and antimicrobial resistance. She completed her Bachelor of Medicine and Bachelor of Surgery (MBBS) at AIMST University and Masters of Internal Medicine at UKM. Her research explores AmpC β-lactamase hyperproducing Enterobacterales bloodstream infections, focusing on antibiotic outcomes and predictors of mortality. Beyond her clinical and research work, she is deeply committed to advancing antibiotic stewardship and improving patient care through continuous learning and leadership in the medical community.

Naylya Djumaeva MD, PhD

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Electrodermal medicament testing and long COVID: Exploring functional patterns associated with persistent symptoms

Background: Long COVID is associated with persistent multisystem symptoms following SARS-CoV-2 infection, yet objective tools to assess ongoing regulatory dysfunction remain limited. Previous research has explored Electroacupuncture-According-To-Voll (EAV) diagnostics and Medicament Testing (MT) as bioelectrical techniques for evaluating altered electrodermal activity. Within this framework, MT may function both as an investigational diagnostic probe and as a functional, biofeedback-like tool for assessing individualized antiviral dose responsiveness.

Methods: Adult outpatients meeting clinical criteria for Long COVID underwent EAV assessment to identify Measurement Points (MPs) with reduced electrodermal activity. MT was subsequently conducted using chosen antiviral and immunomodulatory preparations to evaluate regulatory responsiveness. In a blinded, randomized, placebo-controlled study, MT was also applied to determine individualized ribavirin dosing based on electrodermal activity normalization at selected MPs. Patterns of MT reactivity and dose responsiveness were analyzed to explore reproducibility and potential functional associations.

Results: Decreased electrodermal activity was consistently observed at MPs associated with autonomic, immune, and circulatory regulatory pathways. In some patients, MT with selected agents normalized electrodermal activity at affected MPs. In the randomized controlled study, the MT-derived ribavirin dose varied across individuals. It showed an inverse association with the degree of baseline electrodermal reduction, suggesting that MT captures a functional dimension of regulatory disturbance relevant to antiviral dosing requirements.

Conclusions: These findings suggest that EAV-based MT may represent a non-invasive investigational diagnostic and functional assessment tool for Long COVID, capable of identifying altered electrodermal regulation and exploring individualized antiviral dose responsiveness within the same regulatory framework. As the approach relies on bioelectrical rather than virological confirmation, results should be interpreted as hypothesis-generating; nevertheless, the data support further interdisciplinary research into electrodermal diagnostics and personalized therapeutic strategies in post-viral disease.

Keywords: Long COVID, Electrodermal Activity, Electroacupuncture, Medicament Testing, Diagnostic Tools, Individualized Dosing, Post-Viral Syndromes, Public Health.

Biography

Naylya Djumaeva MD, PhD, is an independent clinician-researcher from Uzbekistan working in scientific collaboration with the Research Institute of Virology, Ministry of Health. She has over 30 years of medical experience and a long-standing research interest in chronic viral infections, post-viral syndromes, neuro-immune interactions, and regulatory diagnostics. Her recent work focuses on exploring Long COVID using electroacupuncture-based medicament testing as an investigational approach to study virus-associated regulatory involvement. She has presented her research nationally and internationally and continues to develop interdisciplinary perspectives on post-infectious disease mechanisms.

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Intravenous drug users and spondylodiscitis as an associated infection: A serious public health problem at the global level, including in Albania

Introduction: Intravenous Drug Use (IVDU) is a growing global health concern associated with severe infections and comorbidities. Among these, spondylodiscitis has been increasingly reported across Europe and is now observed in Albania. Data from the Institute of Public Health (IHP, 2022) show that 4.2% of adolescents aged 15-18 experimented with ecstasy, 1.2% with heroin and 3.2% with cocaine, highlighting a vulnerable subgroup and underscoring the clinical and socio-economic burden of IVDU-related infections.

Objective: To evaluate the association between Intravenous Drug Use (IVDU) and spondylodiscitis, emphasizing epidemiological trends, microbial etiology, and clinical outcomes, with a particular focus on Albania within the broader European context.

Methods: A systematic review of the English-language literature (Medline, Cochrane Library; was conducted using the search terms "intravenous drug use," "spondylodiscitis," "spinal infection," and "Albania." National epidemiological data from the Albanian Institute of Public Health (IHP, 2022) were integrated to contextualize local trends.

Results and Discussion: International literature shows that IVDU patients often present with bacteremia, abscesses, endocarditis, and musculoskeletal infections such as spondylodiscitis. The condition typically arises through hematogenous spread from peripheral foci, facilitated by the vascularity of intervertebral discs. Common pathogens include *Staphylococcus aureus, gram-negative bacteria, Cutibacterium acnes, Staphylococcus epidermidis* and fungi. In Europe incidence has increased significantly with Germany reporting a 104% rise between 2005 and 2021. IVDU patients are generally younger with fewer comorbidities but show

higher recurrence rates and poor adherence to long-term antibiotic therapy, complicating management and increasing socio-economic burden.

Conclusion: Intravenous drug use is closely associated with spondylodiscitis, a condition with rising incidence globally and in Albania. The microbial spectrum is diverse, and management is hindered by social instability and poor treatment compliance. Effective strategies require early diagnosis, tailored therapeutic approaches and close interdisciplinary collaboration among infectious disease specialists, neurosurgeons and public health authorities to mitigate the clinical and psychosocial impact of this dual challenge.

Biography

Dr. Neada Hoxha graduated in General Medicine from the University of Medicine in Tirana, Albania in 2013.In 2020, she received the title of Specialist in Infectious Diseases from the University of Medicine in Tirana. She is currently a PhD candidate with research focused on infectious spondylodiscitis. Her main scientific interests include infectious spondylodiscitis, brucellosis, infective endocarditis, HIV/AIDS and hepatitis B. Dr. Hoxha has co-authored several publications in international scientific journals and has presented as first author at national scientific conferences.

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TLR9-dependent modulation of adipocyte differentiation by *Brucella abortus* DNA induces an inflammatory response

Brucellosis, caused by *Brucella abortus* (Ba), remains a neglected zoonosis with significant human morbidity, often associated with chronic inflammatory manifestations. While traditionally regarded as passive reservoirs of energy, adipocytes are now recognized as immunometabolically active cells capable of shaping host responses during infection. However, how Ba impacts adipocyte biology and contributes to inflammation has not been fully elucidated.

In this work, we explored the effects of Ba on Mesenchymal Stem Cell (MSCs) differentiation into adipocytes, with particular emphasis on lipid remodeling, inflammatory mediators, and innate immune signaling. MSCs were infected with live or Heat-Killed Ba (HKBA), or exposed to purified bacterial DNA. Adipogenesis was assessed through confocal microscopy of Lipid Droplet (LD)-mitochondria dynamics, transcriptional profiling of adipogenic and metabolic genes (PPARγ, CEBPα, DGAT1/2, FASN, HSL, LPL, SREBP1/2, leptin, adiponectin), and quantification of triglycerides, cholesterol, and glycerol release. Inflammatory outputs were measured by ELISA. To dissect the underlying mechanism, functional assays with a TLR9 inhibitor were performed.

Ba infection profoundly reprogrammed adipocyte differentiation, enhancing LD size, elevating intracellular cholesterol, and impairing triglyceride turnover ($p<0.001$). These metabolic alterations were coupled with increased IL-6 secretion and a higher leptin/adiponectin ratio ($p<0.01$), hallmarks of a proinflammatory adipocyte phenotype. Strikingly, bacterial DNA alone was sufficient to replicate these effects, while pharmacological inhibition of TLR9 completely abrogated them, establishing this receptor as a central driver of Ba-induced adipocyte remodeling.

Together, our findings reveal a previously unrecognized role of Brucella abortus DNA in promoting a TLR9-dependent, immunometabolic reprogramming of adipocytes. This mechanism not only links altered lipid metabolism to inflammation but also positions adipocytes as active contributors to the immunopathogenesis of brucellosis, opening new perspectives for therapeutic intervention.

Biography

Nicole Freiberger is a PhD in Health Sciences from the University of Buenos Aires, Argentina, with a strong passion for infectious disease and immunology research. As an early-career female scientist, Nicole has secured multiple fellowships, authored several first-author publications, and presented Nicole work at international conferences. Nicole's research uncovers how pathogens modulate mesenchymal stem cell differentiation, integrating molecular, cellular, and immunological approaches. Nicole committed to building an independent research career, advancing rigorous and impactful science, and contributing to a diverse and collaborative global scientific community.

P. Christodoulou*, M. Mountzouri, M. Papadoulakis, A. Gkogkou, T. Kontopoulou

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Bacteremia from *E. cloacae, E. faecalis, C. tropicalis,* cardiac device related endocarditis and septic arthritis from *C. tropicalis*

A 71-year-old man was admitted to our department due to hematuria. From his medical history he reported multiple ischemic strokes in the setting of atrial fibrillation, a pacemaker due to complete atrioventricular block and diabetes mellitus on insulin.

From the clinical examination the patient was febrile with no other clinical finding, while from the laboratory testing we noticed mild leukocytosis and elevated CRP of 6mg/dl. From the urine test the total hemoglobin and red blood cells was elevated. He was empirically treated on IV piperacilline/tazobactam for Urinary tract infection.

Blood cultures yielded *C. tropicalis, E. faecium* and *E. cloacae,* while urine cultures yielded *E. cloacae* and *C. tropicalis*. Following the antibiogram his treatment was adjusted to IV ceftriaxone, IV vancomycin and IV micafungin. While receiving appropriate antibiotic treatment and having negative blood cultures, he presented with a new fever accompanied by pain, swelling and redness of the right knee joint, with simultaneous recurrence of mycetemia as well as isolation of *C. tropicalis* from the synovial fluid culture.

Transthoracic and transoesophageal echocardiography showed vegetations of the pacemaker leads. The pacemaker was removed, an epicardial pacemaker was placed, and the leads were sent for culture and molecular testing for fungi and common microbes, from which *C. tropicalis* was eventually cultured, while the molecular testing was negative for other pathogens.

He completed six weeks of treatment for fungal pacemaker lead related endocarditis and Septic Arthritis with micafungin. The joint was surgically cleaned and serially punctured due to persistent symptoms, with *C. tropicalis* recurrently isolated. Based on cases in the international literature, it was decided to perform an intra-articular injection of amphotericin B, an intervention that ultimately helped sterilize the joint. Septic arthritis from *C. tropicalis* is a rare clinical manifestation, with few cases in the international literature, mainly involving immunosuppressed patients with hematological malignancy. To our knowledge this is the first case with *C. tropicalis* endocarditis having as immunosuppression the uncontrolled insulin dependent Diabetes Mellitus.

Biography

Panayiota Christodoulou is a medical doctor from Cyprus and a third-year Internal Medicine resident at the General Hospital of Athens Evangelismos. She obtained her medical degree in General Medicine from Pavol Jozef Šafárik University in Slovakia. She also holds a Master's Degree in Business Administration from the European University of Cyprus. She is currently pursuing a Master's Degree in Diabetes Mellitus and Obesity at the National and Kapodistrian University of Athens. Her academic and clinical interests include internal medicine, metabolic diseases, and infectious diseases, with a focus on improving patient care and clinical outcomes.

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Evaluating the effectiveness of antimicrobial stewardship on *Escherichia coli* resistance in patients with urinary tract infection: A systematic review and meta-analysis

Objectives: Although several studies have shown that the application of Antimicrobial Stewardship (AMS) has a positive impact on reduction of antimicrobial resistance and therefore the clinical outcomes of patients, most of the studies were conducted some years ago, and there have been no recent reviews that specifically measures the impact of AMS on urinary tract infections caused by *Escherichia coli.* The purpose of this study is to evaluate the effectiveness of AMS on adult patients with urinary tract infections caused by *E. coli* using studies that have been published in the last 15 years.

Methods: This systematic review and meta-analysis followed the Preferred Reporting for Systematic Review and Meta-Analysis (PRISMA) guidelines. Three electronic databases were searched: EMBASE, PubMed, and Medline for studies published from 2007 to 2022.

Results: Ten studies reported data in antimicrobial resistance following AMS intervention between 2007 and 2022. A total of 398,957 participants were included in all the studies. A meta-analysis of all the included studies demonstrated a reduction in the antimicrobial resistance rate after AMS intervention (pooled percentage change=3.65, P<0.05). Studies that stopped certain antibiotics or switched them to another agent without any other forms of intervention achieved the highest antimicrobial resistance reduction of 9.43% (P=0.02).

Conclusion: Our findings suggested that the introduction of antimicrobial stewardship programme could reduce *E. coli* resistance seen in adult patients, both in the hospital and in the community, with urinary tract infections.

Biography

Dr. Paulo Bautista Arroyo is a Foundation Year 1 Doctor at George Eliot Hospital in the West Midlands, United Kingdom. He graduated with an MBChB in Medicine from University of Warwick in 2025, having previously completed a BSc in Biology at Queen Mary, University of London in 2016. This conference marks his first international conference for an oral presentation, representing an important milestone early in his medical career.

Percival C. Dilla MD
Region II Trauma and Medical Center, Philippines

Association between cardiometabolic 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 cardiometabolic 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 cardiometabolic 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 27.3times (OR: 27.3, p<0.001), Atrial Fibrillation 5.8times (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 Cardiometabolic Risk Factors on COVID-19 mortality and clinical severity.

Biography

Dr. Percival Dilla obtained his Doctor of Medicine degree from the Virgen Milagrosa University Foundation in the Philippines and underwent his Residency Training Program as an Internist at the Region II Trauma and Medical Center in 2024. He is presently working as Medical Officer IV at Conner District Hospital. His research is centered on the molecular epidemiology and genomic characterization of zoonotic viruses, including the Corona Virus, along with zoonotic bacteria such as Streptococcus acidominimus. In this presentation, he highlights the relationship between cardiometabolic risk factors and the progression of severe COVID-19 in patients at a rural tertiary hospital. Additionally, although S. acidominimus is mainly recognized as a veterinary pathogen, it has the capacity to cause severe infections in humans, especially in those with pre-existing health issues. Proper identification and prompt treatment are vital for effectively managing these infections.

Percival C. Dilla MD
Region II Trauma and Medical Center, 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.

Introduction: *Streptococcus acidominimus,* a gram-positive, spherical, short chained, catalase-negative, and weak facultative anaerobic cocci, is classified within the viridans *streptococci* group and is typically regarded as a bacterial pathogen in the realm of veterinary medicine. It is predominantly recognized as a veterinary pathogen, particularly linked to metritis in cattle. Although it is infrequently pathogenic in humans, it has been associated with a range of invasive infections, including pneumonia, pericarditis, meningitis, brain abscesses, and infective endocarditis. Infections in humans caused by this pathogen are uncommon, and when they do occur, they often manifest with permanent deafness and endocarditis as sequelae of meningitis. In this report, we present a case of septicemia and meningitis attributed to *Streptococcus acidominimus* in a 37-year-old man who had a history of contact with live pigs in Caglayan, Conner, Apayao, where the pathogen was identified in both the blood and CSF cultures of the patient. We meticulously examined the patient's medical history, the microbiological diagnostic process, drug sensitivity testing, and the treatment regimen, while also reviewing and discussing the pertinent literature.

Conclusion: In conclusion, although *S. acidominimus i*s mainly recognized as a veterinary pathogen, it has the potential to lead to severe infections in humans, especially among those with pre-existing health issues. Proper identification and timely treatment are essential for effectively managing these infections.

Keywords: *Streptococcus Acidominimus,* Meningitis, Septicemia.

Biography

Dr. Percival Dilla obtained his Doctor of Medicine degree from the Virgen Milagrosa University Foundation in the Philippines and underwent his Residency Training Program as an Internist at the Region II Trauma and Medical Center in 2024. He is presently working as Medical Officer IV at Conner District Hospital. His research is centered on the molecular epidemiology and genomic characterization of zoonotic viruses, including the Corona Virus, along with zoonotic bacteria such as *Streptococcus acidominimus*. In this presentation, he highlights the relationship between cardiometabolic risk factors and the progression of severe COVID-19 in patients at a rural tertiary hospital. Additionally, although *S. acidominimus* is mainly recognized as a veterinary pathogen, it has the capacity to cause severe infections in humans, especially in those with pre-existing health issues. Proper identification and prompt treatment are vital for effectively managing these infections.

Qian Wang

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Archaeological and genetic evidence of earliest records of plague endemic (5,100-5,600 years bp) and its especial relevance to zoonotic pathogen ecology, human resilience, public awareness, and health policy

Deadly infectious diseases such as the medieval Black Death (plague) and 20th-century Ebola have caused catastrophic loss of human life and generated great fear in the past and in contemporary human populations. Infectious disease epidemics persist as a threat and certainly will continue to do so in the future. A complete understanding of the history of human infectious diseases is beneficial as it can aid in disease prediction, prevention, and control in living populations. Therefore, there is a critical need to characterize their existence and behavior, and geographic and temporal variation thereof, based on evidence from past outbreaks. However, in the absence of relevant historic records, deadly infectious diseases, which caused rapid mortality and thus did not leave diagnostic bony lesions, are undetectable in skeletal assemblages using conventional macroscopic paleopathological approaches. This leaves us with a significant knowledge gap about infectious disease in the prehistoric era. A recently discovered Neolithic Hamin settlement dated to 5,100-5,600 years ago was abandoned as a result of the rapid death of a mass number of village dwellers. While circumstantial human skeletal morphology and mortality patterns and archaeological evidence suggest the manner of death not a result of interpersonal conflict but more likely a deadly infectious disease, new genetic evidence confirms the presence of Yersinia pestis, a bacterium of zoonotic origin that is responsible for plague. By integrating pathogen screening within the context of environmental and sociocultural shifts, our NSF-funded multidisciplinary study provides an unprecedented look at human history and beginnings of civilizations as a story of interspecies entanglements and human resilience across millennia. Moreover, it has an important impact on public awareness and policy making regarding deadly infectious diseases for contemporary populations with different economic-social status, ranging from

pre-agriculture to modernization. By revealing what happened leading to the demise of the Hamin Settlement in its ecological and microbiological contexts, findings of this study will not only inform future epidemics with firsthand health status and diseases patterns of an evolutionary sense, but also expand existing databases for global and local health agency authorities to motivate action in the face of crises today, such as policy-making encouraging disease research, and efforts to reduce socioeconomic disparities that affect vulnerability and mortality during crises.

This project is supported by NSF grant BCS#2040388 to Q. Wang and S. DeWitte.

Biography

Dr. Qian Wang is a Professor at Texas A&M University College of Dentistry. Wang has Bachelor's and Master's degrees in paleontology from Nanjing University, China and a Ph.D. degree in biological anthropology from Chinese Academy of Sciences, Beijing, China. Wang also had training in paleoanthropology and human biology in France and South Africa. Wang's NSF funded research is focused on the history of diseases and bone biology. Wang initiated an international collaborative project within the Global History of Health Project to systematically document and synthesize health/disease status of human skeletal remains of the past 10,000 years in Asia.

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Single step immunoblot tests with recombinant protein antigens for detecting IgG and IgM antibodies in lyme disease

Detection of specific antibodies is important for diagnosing Lyme Disease (LD). Until recently, this required two separate tests termed the Standard Two-Tier Tests (STTTs). The development of one-step Immunoblot (IB) tests for detecting IgG and IgM antibodies in patient sera, termed iDartTM IgG and IgM IB tests, are described here. Recombinant proteins from several US and European *Borrelia* species and strains causing LD were applied as antigens in separate lines on nitrocellulose strips for the IB tests. IgG and IgM antibodies in patient sera reacting with protein antigens on the strips were then detected with specific anti-human IgG and anti-human IgM secondary antibodies, respectively. Specificity of the IB tests was established with sera from healthy persons living in LD-endemic and non-endemic areas, and persons with potentially confounding medical conditions and infections. Sensitivity of the tests was determined with LD patient sera from a US CDC test panel and a different collection of sera from US patients with acute-phase LD. The diagnostic performance of the iDart IgG and IgM IB tests was comparable to a US FDA-cleared STTT and better overall for detecting antibodies in early-stage LD. The iDart IgG IB test and a modified version of the iDart IgM described here have been approved by the US FDA for diagnostic use.

Biography

Ranjan Ramasamy obtained a BA and PhD from the University of Cambridge, UK. He has held academic appointments in the UK and abroad including Australia, Sri Lanka and the USA. He was the Chairman of the National Science Foundation of Sri Lanka, and held Professorial appointments in Biochemistry, Immunology and Life Sciences. He was a member of the Board of Governors of the International Centre for Genetic Engineering and Biotechnology

(ICGEB), and a member of Committee for Scientific Planning and Review (CSPR) of the International Council for Science (ICSU) for several years. He has 300 publications pertaining to Biochemistry, Immunology and Infectious Diseases.

Ranjan Ramasamy

IDFISH Technology, CA, USA

Hypothesis linking the major predisposing factors for multiple sclerosis including Epstein-Barr virus infection to its etiology

Epstein–Barr virus infection and Human Leukocyte Antigen Class II allele DRB1*1501 increase the risk of developing multiple sclerosis, an autoimmune disease of the central nervous system. Human endogenous retroviral envelope proteins, molecular mimicry and neuroinflammation have been linked to multiple sclerosis. While the pathology of multiple sclerosis has been well-studied, the molecular and cellular mechanisms underlying interactions between the different predisposing factors in its etiology are not clear and are now presented in a new overarching hypothesis. Besides advancing understanding of multiple sclerosis etiology and promoting further research, this hypothesis can generate new approaches for treating multiple sclerosis.

Biography

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

Ray John M. Salud RND, MD
Rizal Medical Center, Philippines

Neuroschistosomiasis in an adolescent presenting with seizure and headache: A case report

Background: Schistosomiasis, a neglected tropical disease, remains endemic in certain regions of the Philippines. This case highlights the importance of considering *Neuroschistosomiasis* in the differential diagnosis of pediatric patients presenting with unexplained neurological symptoms, particularly those with relevant exposure history.

Clinical Case: A 16-year-old Filipino male from Northern Samar, residing in Pasig City, presented with a 6-month history of seizures and headaches. His initial seizure was generalized tonic-clonic, with upward rolling of the eyeballs and stiffening of extremities. Concurrent with seizure onset, he developed occasional, frontal headaches, which progressed in frequency, severity, and duration over time. He had notable exposure history: Regular swimming in a river and consumption of snails, both risk factors for schistosomiasis.

Initial management focused on symptomatic treatment and other causes of seizure was entertained and ruled out. However, due to the patient's persistent symptoms and exposure history, *Neuroschistosomiasis* was strongly suspected. Further workup, including Circumoval Precipitin Test (COPT) and Kato Katz Test were facilitated. Cranial MRI revealed findings suggestive of *Neuroschistosomiasis,* and further confirmed by positive COPT. Dexamethasone was continued and started on Praziquantel Therapy for 5 days. No further seizure recurrence, headache, or vomiting was noted during the succeeding hospital days. The patient was discharged and advised for a repeat Cranial MRI after 2 weeks.

Conclusion: A high index of suspicion for *Neuroschistosomiasis* should be considered in patients with relevant exposure to freshwater and snails. Early recognition and appropriate management can prevent long-term neurological sequelae associated with this parasitic infection.

Biography

Dr. Ray John M. Salud was born on April 5, 1994 and resides in Angono, Rizal, Philippines. His educational background includes a Doctor of Medicine degree from the University of the East Ramon Magsaysay Memorial Medical Center, Inc. (2016-2020) and Bachelor of Science in Nutrition and Dietetics from the University of Santo Tomas (2011-2015). He is a licensed professional, having passed the Nutrition and Dietetics Licensure Examination in August 2015 and the Physician Licensure Examination in March 2022. Dr. Salud is currently the Chief Resident in the Department of Pediatrics at Rizal Medical Center.

Caroline Vieira Gonçalves, Maria Poliana Leite Galantini, Igor Pereira Ribeiro Muniz, Paulo Henrique Bispo Lima, Israel Souza Ribeiro, Maria Eduarda Santos de Oliveira, Caio Oliveira Lopes de Magalhães, Maria Elisa Santos Flores, Samara Lopes de Oliveira, Catarina Silva Guimarães, Paulinne Moreira Lima, Luísa Carregosa Santos, Daiana Silva Lopes, Juliano Geraldo Amaral, Robson Amaro Augusto da Silva*

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Illuminating new frontiers: Exploring the photosensitizing potential of passiflora species in combatting Methicillin-Resistant *Staphylococcus Aureus* (MRSA) and their infection in senescent mice

Antimicrobial Photodynamic Therapy (aPDT) has become a potential alternative for treating multidrug-resistant bacterial skin infections like those caused by Methicillin-Resistant *Staphylococcus Aureus* (MRSA), who are at high risk in older people. One of the main components of aPDT is the chemical agent called Photosensitizer (PS). This work evaluated the photosensitizing activity of *Passiflora edulis, Passiflora alata,* and *Passiflora cincinnata* extracts. *P. cincinnata* was used to evaluate its activity in antimicrobial photodynamic therapy against an intradermal infection caused by MRSA in a murine senescence model of the C57BL/6 lineage. Tests in vitro were performed to determine the lowest dose of extracts that exert activity photosensitizer and to evaluate the cytotoxicity of the extracts and singlet oxygen production. For in vivo tests, all animals were infected with MRSA and divided into three groups: 1-Animals without treatment (Vehicle), 2-Animals infected and treated with *P. cincinnata* (*P. cincinnata)* and 3- Animals treated with *P. cincinnata* photoactivated (aPDT). We evaluated the production of cytokines in the draining lymph nodes, and the ears were collected to determine the bacterial load and characterize the inflammation in the tissue. The animals treated with *P. cincinnata* had better bacterial load control, less leukocyte infiltration, and lower weight loss throughout the MRSA infectious process. Moreover, the interactions between IL-10 with

TNF-α and IL-12 with IL-17 became more prominent in an aPDT group. In this way, our results are promising because little is known about how aPDT acts in senescent animals and brings to light *P. cincinnata* as a photosensitizer.

Biography

Professor Robson Amaro Augusto da Silva has a Master's and PhD in Human Pathology. He is currently a Full Professor at the Federal University of Bahia in Brazil (UFBA). He was local Vice-Coordinator of the Multicenter Postgraduate Program in Physiological Sciences (2018-2020) and he was coordinator of the Health Technology Center at UFBA from 2008 to 2013. In recent years, he has been developing research projects associated with the areas of development of biotechnological products and processes, as well as Pathology, with an emphasis on Immunopathology, antimicrobial resistance and development of new photosensitizers for photodynamic therapy for infection control.

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

Targeting vitamins B1, B3 and B5 metabolism reduces *Streptococcus Pneumoniae* virulence in a murine influenza co-infection model

Co-infection studies indicate that primary influenza infection promotes pneumococcal virulence by causing capillary leakage of nutrients into the lower respiratory tract. This study investigates whether limiting the availability or uptake of auxotrophic B-vitamins can mitigate this nutrient-driven advantage and serve as a potential antimicrobial strategy. Specifically, a two-pronged in vivo approach was studied that combines inhibition of pneumococcal vitamin transporters with short-term dietary restriction of the corresponding host B-vitamins. The well-characterised serotype 4 strain, D39, was used both in vitro, and in a murine co-infection model over an 8-day infection period. A chemically defined minimal media supporting robust growth of *S. pneumoniae* D39 was first formulated de novo. Then, auxotrophic requirements for individual B-vitamins were determined using growth curve assays in which single vitamins were omitted, and vitamins B1, B3 and B5 were identified as auxotrophic requirements for pneumococcus. Putative vitamin transporter genes were selected and deleted, with mutants confirmed by PCR. Dose-response growth assays across a range of vitamin concentrations were then performed to estimate half-maximal Effective Concentration (EC_{50}). SPD2025, SPD0625to27 (gene cluster of SPD0625, SPD0626, SPD0627), panT and niaX were genes implicated as putative transporters, as deletion, confirmed by PCR, led to increased EC_{50} for its respective vitamin in these assays. Based on EC_{50} results, B1 and B5 mutants were prioritised for in vivo testing. C57BL/6J mice (n=10 per group) were infected intranasally with 30 PFU of influenza A virus, followed 7 days later by intratracheal infection with ~10^4 CFU of pneumococci; any specific diets were administered from days 0 to 7. Lungs and blood were collected 24h after bacterial infection on day 8, and CFU counts were enumerated on day 9. Bacterial burdens were log_{10}-transformed after substituting zero counts with the limit of detection minus one, and groups were compared using unpaired, two-tailed parametric t-tests assuming Gaussian

distribution. B1 and B5 transporter deletion mutants exhibited varying levels of reduced virulence in vivo, and short-term depletion of vitamins B1, B3 and B5 from the host diet similarly attenuated wild-type pneumococcal virulence. In summary, genetic disruption of vitamin B1, B3, or B5 transporters increased the requirement for exogenous vitamin supplementation in vitro and significantly attenuated pneumococcal virulence in vivo. Furthermore, dietary depletion of vitamins B1, B3, and B5 in the host also reduced wild-type pneumococcal virulence in vivo. Ultimately, these findings highlight pneumococcal vitamin transporters and short-term vitamin dietary modulation as complementary strategies that could inform the development of novel therapeutic and prophylactic approaches against pneumococcal infection.

Biography

Sai Yan Pyay Aung is Originally from Myanmar, is a fourth-year PhD candidate at the Lee Kong Chian School of Medicine in Nanyang Technological University (NTU), Singapore. He obtained his Bachelor of Science in Biological Sciences from NTU as a graduate of the CN Yang Scholar's Program. He has co-authored a 2021 publication on integrating real-time data analysis into automatic tracking of social insects and has now turned his research focus to infectious diseases microbiology. He recently received second runner-up at the NTU Three Minute Thesis Competition, and the People's Choice Award at the Singapore 3MT Meet 2025, reflecting strong skills in scientific communication and public speaking.

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Disseminated cryptococcosis with concurrent pneumocystis jirovecii pneumonia in newly diagnosed advanced HIV complicated by refractory raised intracranial pressure requiring external ventricular drainage

Background: Disseminated cryptococcosis remains a major opportunistic infection in advanced HIV and is associated with significant morbidity and mortality.

Case Presentation: A 27-year-old man with newly diagnosed HIV infection (CD4 count 9 cells/μL; viral load 920,000 copies/mL) presented with constitutional symptoms, headache and respiratory complaints. CT thorax demonstrated bilateral diffuse ground-glass opacities consistent with Pneumocystis jirovecii pneumonia. Blood cultures and CSF analysis confirmed disseminated Cryptococcus neoformans infection with cryptococcal meningitis and an opening pressure of 40 cm H_2O. Despite serial lumbar punctures, he developed refractory intracranial hypertension requiring intensive care admission, mechanical ventilation and external ventricular drain insertion. Following antifungal therapy and delayed antiretroviral initiation, he developed cryptococcal IRIS which responded to corticosteroids.

Conclusion: This case highlights the challenges of managing concurrent opportunistic infections in advanced HIV and emphasises the importance of aggressive intracranial pressure management, multidisciplinary care and careful timing of antiretroviral therapy.

Biography

Dr Salman Ali Syed is a Trust Grade Registrar in Acute Medicine at University Hospitals of North Midlands NHS Trust, United Kingdom. He holds MRCP (UK) and FCPS (Medicine) qualifications and has interests in HIV medicine, opportunistic infections, acute care and medical education.

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Creutzfeldt-Jakob Disease (CJD) in the Philippines: Diagnostic challenges, clinical features and insights from the first multicenter registry and descriptive analysis

Background: Creutzfeldt-Jakob Disease (CJD) is an exceedingly rare, fatal, and rapidly progressive neurodegenerative disorder caused by misfolded prion proteins. In the Philippines, CJD is underrecognized and underreported due to limited access to diagnostic modalities and the absence of a national registry.

Objectives: This multicenter case registry aimed to characterize the clinical, demographic, and diagnostic features of Filipino patients with CJD, determine subtype distribution, describe presenting symptoms and disease progression, assess diagnostic modalities, estimate diagnostic delays and survival time, and identify unique regional features.

Methods: A retrospective multicenter case series was conducted involving patients from the Philippines diagnosed as probable or suspected CJD from January 2000 to June 2025. Data were collated from hospitals and neurology clinics, and included demographics, clinical presentation, neuroimaging, EEG, CSF biomarkers, PRNP gene analysis, management, and outcomes. Descriptive statistics and Kaplan-Meier survival analysis were used.

Results: Eight CJD cases were identified (mean age: 68 years, 5 males), with distribution across Luzon, Visayas, and Mindanao. Myoclonus (75%) and rapidly progressive dementia (50%) were the most frequent symptoms. Diagnostic workup commonly included MRI (cortical ribboning, caudate-putamen hyperintensity), EEG (periodic sharp wave complexes), and limited CSF biomarker testing (RT-QuIC, 14-3-3, tau). Seven cases were classified as probable CJD; average survival was 5.5 months. Stroke and other neurological disorders were common initial misdiagnoses.

Conclusion: This registry is the first of its kind in the Philippines and highlights the rarity, varied presentation, and diagnostic challenges of CJD in a resource-limited setting. It underscores the urgent need for systematic surveillance, clinician education, and improved access to definitive diagnostic testing.

Keywords: Creutzfeldt-Jakob Disease, CJD, Prion Disease, Neurodegenerative Disorders, Philippines.

Biography

Dr. Samuel T. Ayo MD, is a dedicated physician and a first-year Internal Medicine resident currently training at Chong Hua Hospital–Fuente. A graduate of the Cebu Institute of Medicine (Batch 2023), he completed his post-graduate internship at Cebu Velez General Hospital (CVGH). Dr. Ayo maintains a strong, active interest in Infectious Diseases and is actively involved in Chong Hua Hospital's Clinician Research Educator Advancement and Training Excellence (CREATE) program. This case report exemplifies his commitment to advancing patient-centered care and contributing to academic discourse within the global Infectious Diseases community.

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The transformation of Personalized and Precision Medicine (PPM) model towards infectious diseases monitoring & management: From mass vaccination to personalized vaccinomics

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

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

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

PPM and systems vaccinology are becoming a valuable tool in the vaccine development whilst prompting application of systems vaccinology for investigating complex pathogens or oncogenes to get the vaccines of the next-step generation made. These promising changes call for the inclusion of systems vaccinology as early as possible in the vaccine development chain to better understand why some vaccines work and others do not. This will enable efficiency of vaccine development proportionally in the design phase and will lead to improved vaccine evaluation in early phases, thereby reducing time and costs.

Meanwhile, a lack of medical guidelines has been identified by responders as the predominant barrier for PPM adoption, indicating a need for the development of best practices and guidelines to support the implementation of PPM! This is the reason for developing global scientific, clinical, social, and educational projects in the area of PPM to elicit the content of the new branch.

Biography

Sergey Suchkov was born in the City of Astrakhan, Russia, in a family of dynasty medical doctors. In 1980, graduated from Astrakhan State Medical University and was awarded with MD. In 1985, Suchkov maintained his PhD as a PhD student of the I.M. Sechenov Moscow Medical Academy and Institute of Medical Enzymology. In 2001, Suchkov maintained his Doctor Degree at the National Institute of Immunology, Russia. From 1989 through 1995, Dr. Suchkov was being a Head of the Lab of Clinical Immunology, Helmholtz Eye Research Institute in Moscow. From 1995 through 2004-a Chair of the Dept for Clinical Immunology, Moscow Clinical Research Institute (MONIKI). In 1993-1996, Dr. Suchkov was a Secretary-in-Chief of the Editorial Board, Biomedical Science, an international journal published jointly by the USSR Academy of Sciences and the Royal Society of Chemistry, UK. At present, Dr. Sergey Suchkov MD, PhD, is: Professor and 1R&D Director, Centro de Estudios de la Fotosintesis Hu-

mana, Aguascalientes, Mexico. Member, The Russian Academy of Natural Sciences (RANS), Russia. Member, New York Academy of Sciences, USA. Secretary General, United Cultural Convention (UCC), Cambridge, UK. Dr. Suchkov is a member of the: American Chemical Society (ACS), USA; American Heart Association (AHA), USA; European Association for Medical Education (AMEE), Dundee, UK; EPMA (European Association for Predictive, Preventive and Personalized Medicine), Brussels, EU; ARVO (American Association for Research in Vision and Ophthalmology); ISER (International Society for Eye Research); Personalized Medicine Coalition (PMC), Washington, DC, USA.

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Strengthening immunization systems in a decentralized health system: Availability and readiness of primary healthcare services in the Federation of Bosnia and Herzegovina

Suboptimal immunization coverage remains a major public health concern in middle-income countries, particularly in decentralized health systems. Recent measles outbreaks in the Federation of Bosnia and Herzegovina (FBiH) highlight critical gaps in service delivery and continuity of vaccination. Generating operational evidence on system performance is essential to support effective disease prevention and control strategies.

A cross-sectional assessment was conducted in 2025 across all 77 primary healthcare centers (87 immunization services) in FBiH. Data were collected using a WHO SARA-based tool, combining structured interviews and direct observation. Indicators included service availability, workforce capacity, cold chain management, data systems, and immunization coverage.

Immunization services were widely available, with 77% of facilities providing daily vaccination. However, significant system constraints were identified. Nearly one in five services (17.2%) operated without a permanently employed physician, and 31% relied on external staff. While basic cold chain equipment was universally available, only 62.1% of facilities had standard operating procedures, and 73.6% had backup power supply. Electronic immunization registries were implemented in only 40.2% of facilities, with marked regional disparities. Vaccine availability was generally high, but intermittent shortages were reported, particularly for measles-containing vaccines.

Coverage Analysis Revealed Critical Drop-Offs: ≥90% coverage was achieved in 54.8% of facilities for the first pentavalent dose, declining to 32.9% for the third dose and 38.4% for MMR, indicating gaps in follow-up and completion of vaccination schedules.

Despite good structural access to immunization services, system readiness and continuity remain insufficient to ensure optimal coverage. Strengthening workforce capacity, cold chain resilience, digital immunization registries, and active follow-up mechanisms is essential to prevent outbreaks and improve vaccination outcomes. These findings provide actionable evidence for strengthening immunization systems in decentralized settings and are directly relevant to global infectious disease control efforts.

Biography

Siniša Skočibušić MD, PhD, is a specialist in infectious diseases and Director of the Institute for Public Health of the Federation of Bosnia and Herzegovina. He is actively involved in national and international public health initiatives, particularly in immunization programs, infectious disease control, and health system strengthening. His work focuses on improving vaccination coverage, digitalization of immunization systems, and evidence-based public health policy development.

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When acute EBV mimics HIV: A case of false positive p24 antigen and low-level HIV antibody reactivity

False positive HIV screening results, while uncommon, carry significant clinical and psychological consequences due to the anxiety and diagnostic uncertainty they generate. One recognised but rare cause is acute Epstein-Barr Virus (EBV) infection, which may cross-react with fourth-generation HIV assays, particularly the p24 antigen and low-level HIV antibody reactivity.

We describe the case of a 57-year-old man with a background of hypothyroidism and atrial fibrillation who presented with sore throat, diffuse rash, dark urine, fatigue, and tender cervical and occipital lymphadenopathy. Laboratory findings showed lymphocytosis and markedly elevated liver enzymes. Fourth-generation HIV tests were repeatedly reactive, demonstrating p24 antigen and low-level HIV-1/2 antibody reactivity. However, HIV-1 and HIV-2 RNA viral loads were consistently undetectable. EBV serology confirmed acute infection, with VCA IgM positivity and transient EBV DNA detection. Other viral and syphilis serologies were negative, and an initial weakly positive monkeypox PCR was not reproducible. The patient's wife, who was pregnant, tested negative for HIV. Clinical recovery was achieved with supportive management, liver function normalised, and subsequent HIV serology remained negative, confirming a false positive HIV result due to acute EBV infection.

This Case Highlights an Important Diagnostic Pitfall: EBV infection can mimic acute HIV seroconversion. The consequences of a false HIV diagnosis are significant, extending beyond clinical mismanagement to serious psychosocial implications, particularly in the context of a pregnant partner. The discrepancy between reactive screening tests and undetectable HIV RNA levels underscores the necessity of confirmatory testing and careful clinical correlation.

Clinicians should remain vigilant for this rare phenomenon, as recognising EBV-associated false positives can prevent misdiagnosis, alleviate unnecessary psychological distress, and reinforce the importance of cautious interpretation of discordant HIV results.

Biography

Dr. Smriti Chaudhary is a medical graduate from Maharani Laxmi Bai Medical College, India, and currently registered with the GMC. She is undertaking a clinical observership at St. Mary's Hospital, Imperial College Healthcare NHS Trust, London, after completing her Foundation Year 1 training with diverse rotations across medicine and surgery. She has experience in audits, teaching, and research training, with a particular interest in general medicine. Outside medicine, she enjoys playing guitar, singing, and sketching.

Dr. Su Latt Paing*, Dr. Margaret Ugbo*, Dr. Christopher Baker
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Unilateral ptosis, proptosis and limb weakness-unusual signs of a rare complication; Lemierre's syndrome-A case report

Lemierre's syndrome, thrombophlebitis of the Internal Jugular Vein (IJV) with secondary sepsis and infective metastatic lesions, is a rare complication typically of anaerobic bacterial infection of the oropharynx, occurring predominately in the younger adult population. About half the reported cases, termed variants, do not fit the classical definition and can pose diagnostic difficulties.

This case report is of a 63-year-old man who presented to the Emergency Department with a 24-hour history of worsening confusion and a fever. His only significant medical history was of an iron deficiency anaemia currently under investigation and a recent blood transfusion. Initial management focused on resuscitation for a sepsis secondary to a pneumonia confirmed on imaging. Approximately 10 hours later, when clinically stable and with the delirium settled, a history of headaches, left neck pain, recent left ptosis, diplopia and mild left sided weakness, confirmed on examination, was established. Also evident was a new left proptosis with worsening chemosis and conjunctival injection. The possibilities of a right MCA territory stroke, carotid artery dissection and orbital cellulitis were raised. Blood cultures taken on admission grew a *Streptococcus sp.* in both bottles.

A CT head showed no established infarct. An urgent ophthalmology review confirmed a partial 3rd nerve palsy and raised the possibility of Orbital Apex Syndrome while an urgent MRI head showed Superior Ophthalmic Vein thrombosis bilaterally-worse on the left-and probable transverse and sigmoid sinus thrombosis.

Subsequent targeted imaging confirmed extensive sinus thrombosis extending to the left IJV, a large organized non-occlusive thrombus in the left IJV and left cervical paravertebral collections, all leading to a definitive diagnosis. The organism cultured was of the *Streptococcus milleri* group.

Diagnosis here passed through various stages on account of several factors: The condition's atypical presentation, its evolution during admission, and the patient's age demographic. Further imaging showed no other organ involvement and no underlying malignancy. The symptoms of diplopia and weakness resolved with treatment.

Biography

Dr. Su Latt Paing is a Resident Doctor (Senior House Officer) in General Medicine at Torbay Hospital. She is a medical graduate of University of Medicine (1), Yangon, Myanmar and completed her Foundation training in the UK. She was awarded FY2 Doctor of the Year in 2025. She has a strong commitment to education and is working towards a career in General Practice with a special interest in Diabetology.

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The hidden burden of human parvovirus B19 infection among patients with suspected dengue fever

Acute febrile illnesses in tropical countries are commonly attributed to dengue infection; however, other viral pathogens such as Human Parvovirus B19 (B19V) may present with similar clinical and hematological manifestations, leading to diagnostic challenges and possible misclassification. This study aimed to determine the prevalence of Human Parvovirus B19 infection and its co-infection with dengue among patients clinically suspected of dengue fever and to evaluate its association with clinical and laboratory features. A cross-sectional study was conducted from November to December 2025 at Sri Ramachandra Medical College & Research Institute (SRMC&RI), Chennai (IEC: CSP/25/OCT/169/544). A total of 105 anonymized residual serum samples from patients suspected of dengue fever were included. After routine dengue testing, post-diagnostic sera were stored at -20°C and tested for Human Parvovirus B19 IgM and IgG antibodies using commercial ELISA kits (NovaLisa®, Novatec, Germany) according to the manufacturer's instructions. Optical density values were converted to NovaTec Units (NTU) using the formula NTU=(sample absorbance/cut-off absorbance)×10, with NTU>11 considered positive and <9 negative. Among the 105 patients (age range: 10 months–86 years), B19V IgM and IgG antibodies were detected in 27.6% (n=29) and 28.6% (n=30), respectively, with overall seropositivity observed in 43.8% (n=46). Based on serology and clinical correlation, 27.6% of patients were classified as having active B19V infection, while 6.7% had dengue-B19V co-infection. Fever was the most common clinical symptom (72.4%), followed by chills and vomiting, while anemia (37.9%) and thrombocytopenia (17.2%) were frequently observed hematological abnormalities. Co-infected patients demonstrated higher rates of hematological abnormalities, suggesting increased clinical severity. These findings highlight the under-recognition of Human Parvovirus B19 in patients presenting with dengue-

like illness and support its consideration in the diagnostic evaluation of acute febrile illnesses to improve accurate diagnosis and patient management.

Biography

Dr. Swati Kumari is an Assistant Professor in the Department of Microbiology at Sri Ramachandra Medical College and Research Institute (SRMC&RI), Chennai. She completed her MBBS and MD in Microbiology from Rajiv Gandhi University and is currently pursuing her PhD at SRMC&RI. With over 10 years of experience in medical microbiology, her research interests focus on clinical virology, particularly the molecular characterization and seroepidemiology of viral infections such as Human Parvovirus B19 and adenovirus in vulnerable populations. Dr. Kumari has authored several peer-reviewed publications in reputed journals including Scientific Reports, and Heliyon, and has presented her work at national and international conferences such as Microcon, the Clinical Virology Summit, and the World Congress on Infectious Diseases. Her research on Parvovirus B19 in blood donors has gained public attention and was featured in the Times of India. She has also contributed to book editing and academic publications in medical sciences and holds patents related to biomedical peptides and diagnostic assays. Dr. Kumari is a lifetime member of the Indian Association of Medical Microbiologists and the Infectious Diseases Society of India.

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Rare cause of septic arthritis: Knee infection by *Streptococcus sanguinis* post intra-articular injection

Objectives: Septic arthritis is a potentially devastating complication of intra-articular injections, typically caused by *Staphylococcus aureus* or β-*hemolytic Streptococci*. Infections due to viridans *streptococci* are exceedingly rare. Among them, *Streptococcus sanguinis,* an oral commensal frequently associated with endocarditis, has only rarely been described as a pathogen in septic arthritis. We present such a case to raise awareness of this rare cause of septic arthritis.

Methods: A 68-year-old female developed acute knee septic arthritis 10 days after an intra-articular injection (hyaluronic acid to treat chronic knee arthritis). On admission (18/07/2025), she presented with fever, severe pain, joint swelling and restricted range of motion. Arthroscopic lavage was performed, and empiric therapy with vancomycin, clindamycin, and ciprofloxacin was initiated. Synovial fluid cultures yielded *Streptococcus sanguinis*. No oral or dental pathology was identified as a possible source of bacteremia. Based on susceptibility testing, treatment was switched to tigecycline and benzylpenicillin. The patient showed progressive clinical improvement and was discharged on 30/07/2025 with oral amoxicillin/clavulanate and minocycline for two more weeks. The patient was regularly reevaluated through clinical examinations and laboratory tests.

Results: On the last follow-up examination, her knee showed no effusion, maintained good joint function and CRP levels were within the normal range. She reported occasional pain and difficulty in walking, attributed to her underlying knee osteoarthritis. *Streptococcus sanguinis* septic arthritis is very uncommon, with only sporadic cases described in the literature. The temporal association with intra-articular injection suggests either direct inoculation or hematogenous spread from an unrecognized oral source. This case underscores the

importance of prompt surgical intervention, broad empiric coverage, and subsequent adjustment according to culture results.

Conclusion: *Streptococcus sanguinis* has only exceptionally been described as a pathogen in septic arthritis. Its occurrence after intra-articular injection highlights the need for strict aseptic technique. Clinicians should consider unusual organisms such as *S. sanguinis* in post-procedural septic arthritis. Early microbiological confirmation and targeted therapy are critical for favorable outcomes.

Biography

Thomas K. Repantis MD, PhD is a Consultant Orthopaedic Surgeon at the General Hospital of Patras "Agios Andreas." He holds a PhD from the University of Patras Medical School and has completed fellowships at Northern General Hospital, UK (AO Spine Foundation), and Martin Luther University, Halle-Wittenberg, Germany (EFORT Foundation). His clinical and research interests focus on spinal disorders, sports injuries, and knee and hip pathology, and he has authored and presented numerous scientific works in these fields.

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Severe pharyngo-cervical infection and persistent oropharyngeal-cervical fistula following needle aspiration in a previously irradiated clival chordoma: A case report

Objectives: Deep neck infections in previously irradiated tissues are rare but potentially devastating complications. Impaired vascularity, radiation-induced necrosis, and mucosal fragility predispose these patients to severe infections even after minor mucosal interventions. We present a case of a pharyngo-cervical infection with formation of a persistent oropharyngeal-cervical fistula following needle aspiration in a patient with a history of high-dose local radiotherapy for clival chordoma.

Methods: A 40-year-old woman, previously treated for clival chordoma with subtotal resection and proton beam radiotherapy (2008), and for C1-C2 recurrence with CyberKnife radiotherapy (2015), underwent needle aspiration of the upper oropharyngeal mucosa in December 2021. Soon after, she developed severe cervical infection involving the oropharynx, parapharyngeal, and upper cervical spaces. Imaging revealed a pathological fracture of the anterior arch of C1 and the formation of a fistulous tract between the oropharyngeal cavity and the C1-C2 vertebral region, consistent with osteoradionecrosis complicated by deep infection. In April 2022, an occipitocervical fusion was performed to stabilize the pathological fracture. Intraoperative cultures yielded Serratia odorifera and Klebsiella pneumoniae as the causative pathogens. The patient was treated successfully with targeted intravenous antibiotics-Meropenem (Meronem) and Daptomycin (Cubicin)-achieving control of systemic infection and normalization of inflammatory markers. Despite infection control, the oropharyngeal–cervical fistula persisted.

Results: At the latest follow-up in October 2025, the patient remained neurologically intact and functionally independent. A CT scan demonstrated a large communication between the oropharyngeal cavity and the pre- and paraspinal spaces on the left, extending beyond the midline at the C2 level, with an enlarged communication channel compared to imaging two years earlier. A multidisciplinary team (Infectious Diseases, Plastic Surgery, and Neurosurgery) proposed surgical closure of the defect using a vascularized free flap. However, the patient declined due to concerns about surgical morbidity. She continues under close clinical and laboratory surveillance with intermittent antibiotic therapy. PET-CT showed no evidence of tumor recurrence.

Conclusion: This case highlights the profound vulnerability of irradiated cervical tissues to infection after minor iatrogenic injury. The combination of mucosal breach, osteoradionecrosis, and deep contamination can lead to persistent fistula formation between the oropharynx and the cervical spine. Management is complicated by poor tissue vascularity and proximity to critical neurovascular structures. Targeted antimicrobial therapy and multidisciplinary coordination are essential to achieve infection control and prevent catastrophic sequelae.

Biography

Thomas K. Repantis, MD, PhD is a Consultant Orthopaedic Surgeon at the General Hospital of Patras "Agios Andreas." He holds a PhD from the University of Patras Medical School and has completed fellowships at Northern General Hospital, UK (AO Spine Foundation), and Martin Luther University, Halle-Wittenberg, Germany (EFORT Foundation). His clinical and research interests focus on spinal disorders, sports injuries, and knee and hip pathology, and he has authored and presented numerous scientific works in these fields.

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E2 ubiquitin-conjugating enzymes regulates dengue virus-2 replication in *Aedes albopictus*

Aedes albopictus (Ae. albopictus), an important vector of Dengue Virus (DENV), is distributed worldwide. Identifying host proteins involved in flavivirus replication in *Ae. albopictus* and determining their natural antiviral mechanisms are critical to control virus transmission. Revealing the key proteins related to virus replication and exploring the host-pathogen interaction are of great significance in finding new pathways of the natural immune response in *Ae. albopictus*. Isobaric Tags for Relative and Absolute Quantification (iTRAQ) was used to perform a comparative proteomic analysis between the midgut of *Ae. albopictus* infected with DENV and the control. 3,419 proteins were detected, of which 162 were ≥1.2-fold differentially upregulated or ≤0.8-fold differentially downregulated ($p<0.05$) during DENV infections. This study explores the interaction between E2 ubiquitin-conjugating enzymes (Ubc9) and DENV-2 proteins (NS1, NS5, and E) using cell culture and mosquito models. The replication of DENV-2 and the knockdown efficiency of the Ubc9 gene were assessed through reverse transcription-quantitative polymerase chain reaction. The DENV-2-related protein expression was evaluated via Western blot analysis. The interaction between Ubc9 and DENV E and NS5 proteins was investigated through confocal immunofluorescence and co-immunoprecipitation. RNA interference technology was employed to silence Ubc9 expression in C6/36 cells and in A. albopictus mosquitoes. The expression level of Ubc9 in the DENV-2-infected group was 3.5-fold higher than that in the control group. The Ubc9 gene expression in the midgut tissue of the mosquito was significantly upregulated. Transfection of C6/36 and BHK-21 cells with the pAc5.1b-EGFP-Ubc9-HA vector led to the overexpression of Ubc9, which decreased the transcription levels of DENV E and NS1, NS5 proteins. The difference was statistically significant ($F=24.27$, $p<0.01$). The expression levels of DENV NS5 and E proteins significantly decreased after infection with DENV-2, suggesting that the depletion of Ubc9 may limit the replication of DENV-2. Ubc9 regulates DENV-2 replication through SUMOylation in the cells

and *A. albopictus,* potentially affecting vector competence and DENV transmission. This is the first study to demonstrate that the Ubc9 of *A. albopictus* plays a significant role in regulating the replication of DENV in both mosquito cells and the mosquito itself. The study results may prove useful in designing appropriate therapeutic approaches for dengue and associated complications.

Biography

Zheng Xueli Professor, Southern Medical University, doctoral supervisor. In 2016, it won the key project of the Life Science Department of the National Natural Science Foundation of China, and in 2018, it won the key project of Guangzhou. He has published more than 180 academic papers at home and abroad. It has won 3 invention patents. Chief editor of 1 textbook. As the deputy editor in chief, he participated in the compilation of Modern Tropical Medicine, a large-scale reference book, and five books. In 2018, the key science and technology for the prevention and control of important vector mosquitoes won the first prize of the Science and Technology Progress Award of the People's Government of Guangdong Province.

Yongfeng Yang*, Jie Yu, Ping Liang
Chinese PLA General Hospital, 100853, Beijing, China

Ultrasound diagnosis of hepatic *Echinococcosis* using a deep convolutional neural network model in China: A large-scale, multicentre, diagnostic accuracy study

Background: Ultrasonography is the most widely used technique to diagnose *Echinococcosis*; however, challenges in using this technique and the demand on medical resources, especially in low-income or remote areas, can delay diagnosis. We aimed to develop a Deep Convolutional Neural Network (DCNN) model based on ultrasonography to identify *Echinococcosis* and its types, especially alveolar *Echinococcosis.*

Methods: This retrospective, large-scale, multicentre study used ultrasound images from patients assessed at 84 hospitals in China, obtained between Jan 1, 2002, and Dec 31, 2021. Patients with a diagnosis of cystic *Echinococcosis*, alveolar *Echinococcosis,* or seven other types of focal liver lesions were included. We tested ResNet-50, ResNext-50, and VGG-16 as the backbone network architecture for a classification DCNN model and input the perinodular information from the ultrasound images. We trained and validated the DCNN model to diagnose and classify *Echinococcosis* using still greyscale ultrasound images of focal liver lesions in four stages: Differentiating between *Echinococcosis* and other focal liver lesions (stage one); differentiating cystic *Echinococcosis*, alveolar *Echinococcosis,* and other focal liver lesions (stage two); differentiating cystic Echinococcosis, alveolar *Echinococcosis,* benign other focal liver lesions, and malignant focal liver lesions (stage three); and differentiating between active and transitional cystic *Echinococcosis* and inactive cystic *Echinococcosis* (stage four). We then tested the algorithm on internal, external, and prospective test datasets. The performance of DCNN was also compared with that of 12 radiologists recruited between Jan 15, 2022, and Jan 28, 2022, from Qinghai, Xinjiang, Anhui, Henan, Xizang, and Beijing, China, with different levels of diagnostic experience for *Echinococcosis* and other focal liver lesions in a subset of ultrasound data that were randomly chosen from the prospective test dataset.

Findings: The study took place between Jan 1, 2002, and Dec 31, 2021. In total, to train and test the DCNN model, we used 9631 liver ultrasound images from 6784 patients (2819 [41.7%] female patients and 3943 [58.3%] male patients) from 87 Chinese hospitals. The DCNN model was trained with 6328 images, internally validated with 984 images, and tested with 2319 images. The ResNet-50 network architecture outperformed VGG-16 and ResNext-50 and was generalisable, with areas under the receiver operating characteristic curve (AUCs) of 0·982 (95% CI 0·960-0·994), 0·984 (0·972-0·992), and 0·913 (0·886-0·935) in distinguishing Echinococcosis from other focal liver lesions; 0·986 (0·966-0·996), 0·962 (0·946-0·975), and 0·900 (0·872-0·924) in distinguishing alveolar *Echinococcosis* from cystic *Echinococcosis* and other focal liver lesions; and 0·974 (0·818-1·000), 0·956 (0·875-0·991), and 0·944 (0·844-0·988) in distinguishing active and transitional cystic Echinococcosis from inactive *Echinococcosis* in the three test datasets. In identifying *Echinococcosis*, the model showed significantly better performance compared with senior radiologists from a high-endemicity area (AUC 0.942 [0.904-0.967] vs 0.844 [0.820-0.866]; p=0.027) and improved the diagnostic ability of junior, attending, and senior radiologists before and after assistance with AI with comparison of AUCs of 0·743 (0·714-0·770) versus 0·850 (0·826-0·871); p<0·0001, 0·808 (0·782-0·832) versus 0·886 (0·864-0·905); p<0·0001, and 0·844 (0·820-0·866) versus 0·870 (0·847-0·890); p=0·092, respectively.

Interpretation The DCNN model was shown to be accurate and robust, and could improve the ultrasound diagnostic ability of radiologists for *Echinococcosis* and its types for highly endemic and remote regions.

Biography

Yongfeng Yang presided over 1 National Natural Youth Project, Published 7 papers, including lancet digital health (top journal, IF 30.8), etc. By the World Health Organization authoritative review, the cumulative IF48.73; World Federation of Ultrasound Medicine Best Abstract Award (International Academic Award, the only one in the world); First Prize of Science and Technology Award of China anti-Cancer Association (2025-9); Beijing Youth Excellent Scientific Paper Award.

Zeynep Burcin Yilmaz
Inonu University, Turkey

A case of silent chronic hepatitis B following uncontrolled treatment discontinuation: Can antiviral treatment be discontinued in chronic hepatitis B?

Chronic Hepatitis B (CHB) is a significant public health problem affecting approximately 254 million people worldwide and causing 1.1 million deaths annually. Currently, functional cure—defined as HBsAg loss — is achieved at limited rates with existing antiviral treatments; even with ten-year Nucleos(T)Ide Analogue (NA) regimens, this rate remains between 1% and 4%. This reality confronts clinicians with the question of whether to continue or discontinue treatment in patients who have achieved long-term viral suppression.

Studies show that discontinuing treatment under controlled conditions can significantly increase the chance of functional cure, particularly in patients with low HBsAg levels. Large-scale studies such as retract-B reported a 13% HBsAg loss rate at 48 months after NA discontinuation; in the finite study, this rate reached 14% in the treatment discontinuation arm. However, the risk of virological relapse remains high, with HBV DNA rebounding in the vast majority of patients, particularly within the first three to six months. The strongest predictor of sustained response following treatment discontinuation has been shown to be HBsAg quantification at the end of treatment; levels below 100–200 IU/mL significantly increase the likelihood of functional cure. In clinical practice, it is well established that in cirrhotic- and especially decompensted-patients, treatment should not be discontinued until HBsAg negativity is achieved, as this group carries substantial risks of severe exacerbation and mortality.

In conclusion, treatment discontinuation in appropriately selected CHB patients who have achieved long-term virological suppression under NA therapy offers a valuable opportunity for functional cure. However, this decision must be individualized, taking into account the presence of cirrhosis, HBsAg levels, and emerging biomarkers such as HBcrAg. Patients should be closely monitored following treatment discontinuation, and antiviral therapy should be promptly reinitiated if exacerbation criteria are met. Here, we present a case of silent chronic hepatitis B from our clinic in which the patient discontinued treatment on their own initiative.

Zoya Malik*, Sadia Faisal, Urooj Saeed*

The Dudley Group NHS Foundation Trust, United Kingdom

Solitary neurocysticercosis mimicking a parietal brain tumour in a young woman: A diagnostic challenge

A 24-year-old previously healthy woman presented with a one-week history of severe, sharp right occipital headache (pain score 9-10/10). There were no visual, auditory, or focal neurological symptoms, and no history of trauma or systemic illness. Neurological and systemic examinations were unremarkable, with full motor strength and intact cranial nerves.

Initial CT imaging revealed a right parietal lesion with surrounding oedema. Subsequent MRI demonstrated a solitary 11x13mm rim-enhancing lesion in the right parietal lobe with vasogenic oedema. Further investigations excluded arteriovenous malformation and neoplastic processes. The case was reviewed by a multidisciplinary team, and corticosteroid therapy was initiated to reduce oedema, resulting in marked symptomatic improvement.

Follow-up imaging described the lesion as non-inflammatory, with features suggestive of either a cavernoma or Neurocysticercosis (NCC). The patient was referred to a tertiary centre for further evaluation, where serological testing confirmed Taenia solium infection. Targeted antiparasitic therapy was commenced, leading to clinical improvement.

This case underscores the diagnostic challenge posed by solitary enhancing brain lesions and highlights the importance of considering neurocysticercosis in the differential diagnosis, even in patients without an endemic exposure history.

Biography

Zoya Malik grew up in a small town in Pakistan, and from early on she always dreamed of training internationally. She completed her MBBS in Hyderabad, Pakistan, and over time developed a real interest in Infectious Disease. Along the way, Zoya has published a case report, completed two QIPs, and carried out two cycles of an audit. Submitting this abstract is crucial to her because it's not just another requirement, it's a chance to show her genuine commitment to this specialty and the path she hope to follow.

Dr Urooj Khalida Saeed is a Simulation Clinical Fellow in Intensive Care at Russells Hall Hospital, Dudley Group NHS Foundation Trust. She completed her foundation training in Pakistan and gained valuable intensive care experience before transitioning to the NHS, where she has gained experience across acute and critical care specialties. She has successfully passed MRCP Part 1 and Part 2 and is currently preparing for MRCP PACES. Her professional interests include critical care, medical simulation, clinical education, and patient safety. Dr Saeed is committed to advancing evidence-based practice and contributing to high-quality medical training within the NHS.

10TH EDITION OF

WORLD CONGRESS ON INFECTIOUS DISEASES

HYBRID EVENT

25-27 JUNE 2026

POSTER PRESENTATIONS

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Profile of children with candidemia: A 10-year experience from a tertiary care centre in India

Background: Systemic fungal infections cause significant morbidity and mortality in children. Antifungal resistance is a matter of concern, as choice of antifungal therapy for empirical and therapeutic purposes, is guided by existing sensitivity patterns among *Candida* isolates.

Rationale of the Study: Data on *Candida* bloodstream infections in pediatric patients from India remain limited. Hence this study was aimed at addressing these concerns.

Objectives: The primary objective of the study was to describe the clinical profile of paediatric patients developing candidemia, and to examine the microbiological profile of *candida* strains isolated in children. The secondary objective was to compare the clinical factors associated with developing *Candida tropicalis vs. non-tropicalis spp.* blood stream infection, to study the available antifungal sensitivity of various species, and to identify factors associated with poor outcome.

Methodology: This was a retrospective study in children less than 16 years with blood stream Candida infection in a tertiary health care centre in India. Data was collected from medical and laboratory records over a 10-year period between 1 January, 2013 and 31 December, 2022. Data was tabulated and analysed using SPSS software 21.0.

Results: There were 243 children identified in the 10-year study period. Median age at diagnosis was 1 year. Common clinical manifestations were fever (47.5%) and shock (60%). Major co-morbid conditions included-hemato-oncological diseases, cardiovascular disease and inborn errors of immunity. Most common *Candida* species isolated was *C. tropicalis* (43%), followed by *C. albicans* (14.8%). For the *C. tropicalis* isolates that were tested, fluconazole sensitivity was 87%, amphotericin sensitivity was 92%, voriconazole sensitivity was 33%, and caspofungin sensitivity was 88%. For C. albicans, Fluconazole was sensitive in 77%, amphotericin sensitive in 100%, voriconazole sensitive in 33% and caspofungin was 100% sensitive. Disseminated candidiasis was seen in 10%, with hepato-splenic being the most common involvement. Mortality was noted in 35% of the study cohort. Significant overall predictors of mortality included malnutrition, shock requiring inotropic support and thrombocytopenia.

Conclusions: Majority of the candidemia was caused by *C. tropicalis* species. Candidemia in children resulted in high mortality. Overall antifungal susceptibility was highest for amphotericin and echinocandins, moderate for fluconazole, and low for voriconazole across *Candida* species. Malnutrition and thrombocytopenia were significant predictors of poor outcomes.

Biography

Abhipsha Anuranjana is a Senior Resident in Paediatrics with over four years of experience in the care of children across tertiary healthcare settings in India. She has recently completed her pediatric residency and have a keen academic and clinical interest in pediatric infectious diseases, particularly invasive fungal infections and antimicrobial resistance. Her research work includes a retrospective analysis of pediatric candidemia over a 10-year period (2013–2022), involving a cohort of 243 children, which is her original work and has not been published yet.

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Antimicrobial resistance of *listeria monocytogenes* in meat-based ready-to-eat products from Romania: Implications for public health

Listeria monocytogenes remains a major concern for food safety, particularly in meat-based Ready-to-Eat (RTE) products that are consumed without further heat treatment. This study focused on the occurrence, virulence characteristics, and antimicrobial resistance of *L. monocytogenes* isolated specifically from meat-derived RTE foods in northwestern Romania between 2019 and 2022.

Out of 8,151 RTE samples analyzed, contamination was predominantly associated with pork and fish products, indicating meat as the primary source of *L. monocytogenes* isolation. A total of 26 strains were identified, with a marked increase in detection during 2022. Serotyping revealed that the majority of isolates belonged to serotype 1/2a, followed by 1/2b and 1/2c—serotypes commonly linked to human listeriosis.

All isolates carried essential virulence genes, including *hlyA* and *prfA*, confirming their pathogenic potential. Notably, strains isolated in 2022 exhibited a broader virulence profile, testing positive for all investigated virulence determinants, suggesting a possible increase in pathogenicity over time within meat-associated strains.

Antimicrobial susceptibility testing revealed significant resistance to trimethoprim-sulfamethoxazole (26.92%) and oxacillin (23.07%). Additionally, a concerning proportion

of isolates (23.07%) displayed multidrug resistance, most frequently involving resistance to oxacillin, penicillin, and tetracycline. Despite this, all strains remained susceptible to fluoroquinolones such as ciprofloxacin, levofloxacin, and moxifloxacin. Molecular analysis identified a high prevalence of tetracycline resistance genes (*tet(C), tet(M), tet(K)*) as well as *ampC* and *dfrD*, indicating the presence of multiple resistance mechanisms in meat-derived isolates.

These findings emphasize that meat-based RTE products, particularly pork, represent a significant reservoir for virulent and antimicrobial-resistant *L. monocytogenes* in Romania. Strengthened monitoring and targeted control strategies in meat processing environments are essential to reduce contamination risks and protect public health.

Biography

Experienced Researcher: Associate Professor PhD Alexandra Tăbăran, 41 years old, U-1700-039E-2520. She is an accomplished researcher with extensive expertise in Food Safety and microbiological methods for bacterial detection, including both classical and molecular characterization techniques. Her academic achievements include 26 ISI-indexed publications, 4 academic books, 194 citations (excluding self-citations), and an h-index of 7 according to Web of Science. Alexandra has received 6 UEFISCDI awards and has supervised 20 undergraduate theses. She has coordinated one national research project and participated as a member in 6 national and 4 international research projects.

Bárbara Alves Rhomberg*, Júlia de Souza Capuano, Adriana Pina, Carlos Alberto Fonte de Souza, Orival Silva Silveira, Monique Marques da Silva Sant'ana, Beatriz Medeiros Correa

UNOESTE University, Brazil

Fulminant hepatic failure associated with hepatitis A virus in a previously healthy patient: Case report

The Hepatitis A virus usually causes a self-limiting disease, with fulminant hepatic failure occurring in less than 1% of cases. A 40-year-old white male patient, self-employed, with a personal history of cholecystectomy 11 months prior, with no other comorbidities or ongoing medication use, was admitted to an emergency care unit with myalgia, fever, and nausea that had been present for four days. Laboratory tests showed elevated liver enzymes and bilirubin at the expense of the direct fraction. Total abdominal tomography revealed signs suggestive of diffuse hepatic steatosis and mild splenomegaly. After five days of hospitalization, he developed clinical deterioration and progression to hepatic encephalopathy and was transferred to an infectious disease hospital due to suspected acute viral hepatitis. Upon admission to the intensive care unit, he presented with ascites and severe hepatic encephalopathy. Laboratory tests showed prolonged prothrombin time (increased international normalized ratio), elevated direct bilirubin, falling liver enzymes, and hypoalbuminemia. Child-Pugh score of 14 points (classification C) and Model for End-Stage Liver Disease score of 3.0 with 28 points. Serology for human immunodeficiency virus, hepatitis B, and hepatitis C were nonreactive, while serology for hepatitis A was positive (IgM antibody). Supportive measures for severe liver failure were initiated, with sparing intravenous hydration and use of lactulose due to the absence of signs of intracranial hypertension. He showed significant clinical and laboratory improvement, with discharge from the intensive care unit after four days and hospital discharge after seven days of hospitalization.

Biography

Doctor Barbara Alves Rhomberg is affiliated with UNOESTE University. She has a degree in Medicine, a specialization in General Surgery, and a postgraduate degree in Intensive Care Medicine. She is currently pursuing a postgraduate degree in Palliative Care and Pain Therapy and an Interdisciplinary Master's Degree in Health Sciences. She coordinates the Intensive Care Unit and serves as Vice President of the Palliative Care Commission at a hospital specializing in infectious diseases. She also teaches Clinical Medicine at a medical school.

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UNOESTE University, Brazil

Rare complication of dengue fever: Severe acute liver failure-Case report

Elevated liver enzymes occur in up to 50 to 90% of patients with dengue, usually with a slight elevation and no clinical significance. In severe cases, the elevation can reach up to ten times the normal value, associated with severe liver inflammation and liver failure in about 0.35% of cases. A 31-year-old female patient, brown-skinned, with no comorbidities, was admitted to the emergency room with myalgia, abdominal pain, nausea, vomiting, and diarrhea that had been present for three days. Laboratory tests showed leukopenia, thrombocytopenia, elevated liver enzymes, and hyperbilirubinemia, and she was referred to an infectious disease hospital for suspected dengue fever. Chest and abdominal CT scans showed pleural and pericardial effusions and ascites, as well as signs of pulmonary inflammation, pulmonary congestion, splenomegaly, and acalculous cholecystitis. She had severe thrombocytopenia (13,000/mm^3), coagulation disorders with prothrombin activity of 50.6% and INR 1.55, hyperbilirubinemia at the expense of the direct fraction (total bilirubin: 2.7mg/dL and direct: 1.8mg/dL), elevated inflammatory tests (lactic dehydrogenase: 4855.1 U/L, C-reactive protein: 74.2mg/L, and ferritin: 2000ng/mL), and significantly elevated liver enzymes (oxaloacetic transaminase: 7442 U/L and pyruvic transaminase: 2901.7 U/L). Serology tests for human immunodeficiency virus and hepatitis A, B, and C were negative. Rapid testing for dengue NS1 and serology tests for IgG and IgM were reactive, confirming recent infection with the dengue virus via the ELISA method. The patient progressed favorably with resolution of symptoms and organ dysfunction and was discharged after eight days of hospitalization.

Biography

Doctor Barbara Alves Rhomberg is affiliated with UNOESTE University. She has a degree in Medicine, a specialization in General Surgery, and a postgraduate degree in Intensive Care Medicine. She is currently pursuing a postgraduate degree in Palliative Care and Pain Therapy and an Interdisciplinary Master's Degree in Health Sciences. She coordinates the Intensive Care Unit and serves as Vice President of the Palliative Care Commission at a hospital specializing in infectious diseases. She also teaches Clinical Medicine at a medical school.

Bruna Barros da Fonseca*, Adriana Pina, Orival Silva Silveira, Flávio Rossi de Almeida, Monique Marques da Silva Sant'ana, Marizia do Amaral Toma, Beatriz Medeiros Correa, Bárbara Alves Rhomberg

UNOESTE University, Brazil

Acquired immunodeficiency syndrome with multiple opportunistic coinfections: Tuberculosis, cytomegalovirus, *Pneumocystis pneumonia*, and malaria-report of a rare and challenging case

This case illustrates a rare and challenging clinical presentation of AIDS with multiple simultaneous opportunistic coinfections, including viral, bacterial, fungal, and parasitic etiologies. We report the case of a 30-year-old male patient admitted to the intensive care unit of a referral hospital for infectious diseases, with a recent diagnosis of HIV infection and severe immunosuppression (CD4 count: 4cells/mm^3). He presented with a prolonged clinical course including persistent fever, weight loss, diarrhea, dry cough, and genital lesions. He had been on antiretroviral therapy (Tenofovir, Lamivudine, and Dolutegravir) for 13 days. On physical examination, he was in fair general condition, pale, dehydrated, febrile, and exhibited ulcerated lesions on the glans penis, with purulent base and erythematous borders. Upon admission, due to the severe immunodeficiency, expanded infectious screening was requested.

Results Revealed: Positive PCR for cytomegalovirus (4,426copies/mL), positive urinary TB-LAM antigen, and PCR for Pneumocystis jirovecii in bronchoalveolar lavage (642,000copies/mL). Culture of the lavage fluid isolated multidrug-resistant Pseudomonas aeruginosa, sensitive only to carbapenems. CT scans showed extensive pulmonary consolidations, cavitations, ground-glass opacities, pericardial effusion, and mediastinal and abdominal lymphadenopathy. During hospitalization, the patient persisted with daily afternoon fever, raising the suspicion of malaria based on epidemiological context. Thick blood smear tested positive for Plasmodium vivax, and treatment with chloroquine and primaquine was initiated. He showed progressive clinical improvement, was discharged from the ICU after nine days, and from the hospital after 21 days. It highlights the importance of broad diagnostic

investigation in febrile immunosuppressed patients and the potential for recovery with appropriate multidisciplinary management.

Biography

Bruna Barros da Fonseca is a student and teaching assistant of infectology at a medical school.

Bruna Barros da Fonseca*, Adriana Pina, Orival Silva Silveira, Elisabeth Dotti Consolo, Monique Marques da Silva Sant'ana, Bárbara Alves Rhomberg

UNOESTE University, Brazil

Takotsubo syndrome as a rare complication in a young patient with pulmonary tuberculosis: Case report

Takotsubo syndrome, also known as broken heart syndrome, is characterized by transient left ventricular dysfunction. Previous clinical conditions, such as Mycobacterium tuberculosis infection, can act as precipitating factors. It is a rare condition, more common in white women with a mean age of 60 years, with only 3% of cases occurring in women under 50 years of age. A 24-year-old female patient, brown-skinned, was admitted to an infectious disease hospital with a diagnosis of pulmonary tuberculosis undergoing irregular treatment, presenting with anemia, chest pain, dyspnea, pallor, hypotension, and tachycardia. On the second day of hospitalization, she developed acute respiratory failure and septic shock of pulmonary origin. On the fourth day, she experienced cardiac arrest in ventricular fibrillation, with return to spontaneous circulation after two cycles of cardiopulmonary resuscitation and defibrillation. Transthoracic echocardiogram showed akinesia of the entire apical region of the left ventricle, diffuse hypokinesia of the other walls, moderate global contractile dysfunction, hypokinesia of the right ventricular septal wall, moderate mitral regurgitation, and ejection fraction of 43.21% (reference value ≥55%), changes suggestive of Takotsubo cardiomyopathy. Subsequent tests showed improvement in ventricular function. Despite recovery from ventricular dysfunction, she had an unfavorable clinical course, with progressive therapeutic failure, and palliative care was instituted. She died after 73 days of hospitalization. Although Takotsubo syndrome has gained prominence in cardiological investigations, its pathophysiology, management, and clinical outcome are still poorly understood.

Biography

Bruna Barros da Fonseca is a student and teaching assistant of infectology at a medical school.

Bruna dos Santos Costa*, Adriana Gibotti, Geraldo Alécio de Oliveira, Elisabeth Dotti Consolo, Daniela Martins da Silva, Marizia do Amaral Toma, Bárbara Alves Rhomberg

UNOESTE University, Brazil

Severe acute respiratory distress syndrome secondary to viral pneumonia caused by varicella zoster: Case report

Viral pneumonia caused by the Varicella Zoster virus is a rare but serious complication with a high mortality rate. A 17-year-old male patient, previously healthy, was admitted to an infectious disease hospital with confluent, polymorphic, centripetal papulovesicular rashes that began seven days earlier, associated with abdominal pain, low back pain, productive cough with purulent sputum, and respiratory distress. Chest X-ray showed diffuse bilateral interstitial infiltrate, consistent with primary viral pneumonia. Laboratory tests showed leukopenia, thrombocytopenia, coagulation disorders, elevated liver enzymes, elevated inflammatory markers, renal dysfunction, and increased canalicular and cardiac enzymes. Abdominal ultrasound revealed active acalculous cholecystopathy. Echocardiogram showed septal wall hypokinesia, global systolic dysfunction, hypokinesia of the septal and anterior walls of the right ventricle, and pulmonary hypertension with right ventricular systolic pressure of 40 mmHg. After five hours of hospitalization, he developed hypoxemic respiratory failure and septic shock, likely of pulmonary origin. Ceftriaxone, acyclovir, and corticosteroid therapy were initiated. The patient developed multiple organ dysfunction: Acute renal failure, acute liver failure, myositis, myocarditis, coagulation disorder, loss of lung function with refractory hypoxemia, and irreversible septic shock. He died on the fourth day of hospitalization. Varicella zoster infection was confirmed by real-time Polymerase Chain Reaction (PCR), a method based on Fluorescence Resonance Energy Transfer (FRET).

Biography

Bruna dos Santos Costa is a student and teaching assistant of infectology at a medical school.

Alver Cruz-Cacais, Sergio Ricaurte-Ruiz, Vanesa Vázquez-Godoy, Milena Maya-Hoyos, Carlos Y. Soto-Ospina*

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A double mutant of *Mycobacterium Tuberculosis* targeting membrane transporters CtpF and MmpL7 as a promising live-attenuated vaccine candidate

Tuberculosis (TB) remains the leading cause of death from a bacterial pathogen worldwide, and the limited efficacy of the century-old *Mycobacterium bovis* Bacillus Calmette–Guérin (BCG) vaccine underscores the urgent need for novel, rationally designed vaccines capable of inducing durable protection. Previous studies have identified the P-type ATPase CtpF as a validated attenuation target in *Mycobacterium tuberculosis* (Mtb), given its essential role in calcium transport, oxidative stress response, and intracellular survival. Mutants lacking ctpF display significant attenuation in both cellular and animal models, confirming its role in virulence.

Building upon this evidence, single deletion mutants, MtbH37RvΔctpF and MtbH37RvΔmmpL7, were constructed (ΔmmpL7) and characterized to assess their phenotypic and molecular features. Both mutant strains displayed phenotypic traits commonly associated with attenuation in Mtb, including changes in colony morphology, reduced surface hydrophobicity, and alterations in the composition of cell envelope lipids-particularly in PDIMs, TDMs, and PIMs, the first two being well-recognized virulence factors.

These findings guided the rational construction of a double mutant, MtbH37RvΔctpFΔmmpL7, devoid of antibiotic resistance markers and preserving the secretion of ESAT-6 and CFP-10, two major immunomodulatory antigens essential for host immune recognition. The combination of reduced virulence, cell envelope remodelling, and maintenance of major immunomodulatory antigens highlights the MtbH37RvΔctpFΔmmpL7 strain as a promising candidate for next-generation live-attenuated vaccine against TB.

Biography

Carlos-Yesid Soto is a Full Professor at the National University of Colombia, where he leads the research group Biochemistry and Molecular Biology of Mycobacteria. He holds an M.Sc. in Microbiology and a Ph.D. in Biological Sciences from the Universitat Autònoma de Barcelona, with postdoctoral training at the University of Zaragoza. His research focuses on biomarkers of mycobacterial virulence and latency, P-type ATPases as targets for attenuation and vaccine design, and novel antitubercular compounds. Professor Soto served as President of the Latin American Society of Tuberculosis and Other Mycobacteriosis - SLAMTB (2020-2023).

Carolyn Cross
Ondine Biomedical Inc., Vancouver, Canada

Breaking the mupirocin paradox: Light activated nasal decolonization achieves 66% SSI reduction and sustained cost savings without resistance signals in spine surgery over 8 years

Background: Nasal decolonization is central to SSI prevention, with mupirocin long regarded as the topical "gold standard" for eliminating *Staphylococcus aureus* carriage. However, real world implementation exposes a mupirocin paradox: Programmes that successfully reduce SSIs also accelerate mupirocin resistant strains, require complex screening and adherence workflows, and risk eroding future prevention efficacy. Emerging evidence from the Carriage Study 2025 further suggests that repeated intranasal antibiotics targeting Gram positive organisms may disrupt the commensal nasal microbiome, potentially impairing host defence and fostering ecological conditions favourable to resistant or opportunistic pathogens. As AMR pressure intensifies, guidelines increasingly highlight the need for non antibiotic, resistance proof decolonization technologies that preserve both microbiome integrity and antimicrobial utility.

Aim: To contrast the mupirocin paradox and its microbiome implications with long term clinical and economic outcomes from a universal, non antibiotic nasal photodisinfection protocol in spine surgery, highlighting its potential as a durable, resistance proof alternative for SSI prevention and health system sustainability.

Methods: A large tertiary centre implemented a universal pre surgical decolonization bundle combining intranasal photodisinfection and Chlorhexidine Gluconate (CHG) body wipes for major spine procedures. Over an 8-14year period, more than 13,000 spine surgery patients were followed under routine clinical conditions and infection prevention surveillance. We examined changes in SSI rates, estimated cost impact per surgical patient, and evaluated

any emergence of resistance related performance loss or safety concerns. Findings were contextualized against the known constraints, microbiome disruption risk, and resistance liabilities of mupirocin based decolonization described in contemporary literature, including the Carriage Study (2025).

Results: Introduction of the universal nasal photodisinfection plus CHG protocol was associated with a 66-67% relative reduction in spine SSI rates (from 7.98% to 2.67%, $p<0.001$). Hospital economic analysis estimated net institutional savings of approximately $19.9 million over 8 years, corresponding to about $2.49-$2.58 million per year, or roughly $2,458-$2,578 saved per surgical patient. Across the entire study period, there were no reported protocol related serious adverse events and no evidence of diminished efficacy suggesting emergence of photodisinfection resistance. In contrast to mupirocin based programmes, this universal, procedure embedded approach eliminated the need for pre operative screening logistics and multi day home regimens, avoided selective pressure focused on Gram positive flora, and did not add to the antibiotic resistance reservoir.

Conclusion: The experience with universal nasal photodisinfection demonstrates that a non antibiotic decolonization bundle can deliver large, durable SSI reductions and substantial per patient cost savings without detectable resistance signals or antibiotic driven microbiome damage. This directly addresses the Mupirocin Paradox by decoupling SSI prevention from selective antibiotic pressure, microbiome disruption, and long term resistance risk. For health systems facing AMR, surgical backlogs, and budget constraints, resistance proof, microbiome sparing decolonization strategies offer a compelling path to protect patients, preserve antibiotic utility, and unlock recurring capacity and financial gains.

Biography

Carolyn Cross M.S.C., CFA, MBA is Founder and Chief Executive Officer of Ondine Biomedical Inc., a global leader in photodisinfection technologies for infection prevention and antimicrobial resistance. With more than two decades of experience advancing non antibiotic medical innovations, she has led translational research collaborations across leading academic and clinical institutions worldwide. Ms. Cross has served on Canada's National Research Council and the Board of the Canadian Foundation for Innovation, shaping national strategies in biomanufacturing and research excellence.

Carolyn Cross
Ondine Biomedical Inc., Vancouver, Canada

The double whammy of cardiac SSI under-reporting: Correcting incidence and inflation to unlock capacity and eradicate AMR debt

Surgical Site Infection (SSI) surveillance in cardiac surgery is distorted by a double whammy: Systematic under-reporting of true infection rates and reliance on outdated, non inflation adjusted cost data. Enhanced recovery protocols have shortened inpatient stays, but national registries still track mainly in-hospital infections. This creates an in patient illusion where official SSI incidence appears to be only 1-2%, while WHO aligned surveillance capturing post discharge infections consistently finds rates nearer 5-6%. This gap falsely positions SSI prevention as a marginal priority undermining investment.

To quantify the impact of this distortion, a health economic model was developed for 1,000 UK cardiac surgeries. Two scenarios were evaluated: A Registry Scenario using the reported 1.5% incidence and historical costs (£10,000 per SSI), and a corrected reality scenario applying a 5.0% incidence, inflation adjusted costs (£17,150 per SSI), and an additional 12 day excess length of stay per infection. The model incorporated lost Opportunity Revenue from the crowding out effect, whereby SSI related bed occupancy displaces new elective admissions.

Registry based assumptions identify only 15 SSIs, implying modest clinical and financial risk. Corrected modelling reveals 50 SSIs, consuming 600 excess bed days and £857,500 in direct costs, effectively an "infection tax" of £857.50 per surgery. Each infection also represents a biological debt of avoidable antibiotic exposure, directly undermining Antimicrobial Stewardship (AMS) goals. A resistance proof, non antibiotic prevention strategy achieving a 50% SSI reduction would prevent 25 infections, save £428,750 in direct costs, free capacity for 50 additional elective cases, and generate £750,000 in opportunity revenue (at £15,000 revenue per new surgery). The combined net economic value exceeds £1.17 million per 1,000,

alongside reduced antibiotic use and AMR risk. This is a gain of £1,179 per surgical patient, or 7.9% of the average cost per surgery.

These findings demonstrate that current reporting practices suppress the apparent value of prevention and entrench a false economy that delays investment in innovative AMS solutions. Accurate post discharge SSI surveillance and inflation adjusted costing are prerequisites for robust business cases that align clinical governance, capacity planning, and AMS. In cardiac surgery and other high risk specialties, correcting the SSI double whammy can unlock capacity, eliminate hidden AMR debt, and reposition non antibiotic, resistance proof interventions as strategic assets for both patient safety and hospital performance.

Biography

Carolyn Cross M.S.C., CFA, MBA is Founder and Chief Executive Officer of Ondine Biomedical Inc., a global leader in photodisinfection technologies for infection prevention and antimicrobial resistance. With more than two decades of experience advancing non antibiotic medical innovations, she has led translational research collaborations across leading academic and clinical institutions worldwide. Ms. Cross has served on Canada's National Research Council and the Board of the Canadian Foundation for Innovation, shaping national strategies in biomanufacturing and research excellence.

Chiguer Chaimae*, El Mostadi Abderrahmane, Erragh Anas, Nsiri Afak, Al Harrar Rachid

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Prognostic role of fever in severe brain trauma

Introduction: Severe Traumatic Brain Injury (TBI) is defined as a high-risk global condition with a Glasgow Coma Scale score ≤8 that continues to challenge global public health, particularly among young adults. Despite the recent advances in the critical care arena, mortality and morbidity are still elevated and mostly associated with secondary brain injury and infectious complications acquired in the Intensive Care Unit (ICU).

Methods: We carried out a retrospective, descriptive, and analytical analysis over two years with 62 patients hospitalized in the ICU for severe TBI. Epidemiological, clinical, paraclinical, infectious, and outcome data were collected and analyzed. Patients were divided into two groups according to the duration of their febrile plateau (<48h vs. ≥48h).

Results: The mean age of patients was 33.7 years, with 73% under 40 years and a strong male predominance (87%). Road traffic accidents were the most common cause (83 percent), with assaults coming after (16.1 percent). Mechanical ventilation was needed in all patients (mean 13.8 days). Infectious complications were common, with Ventilator-Associated Pneumonia (VAP) being the most frequent site. Both groups included predominance of gram-negative bacilli. Patients with severe fever (≥48h) exhibited a greater spread of infection and greater mortality (52%), due predominantly to an acute neurologic decompensation (90%).

Conclusion: Young male patients with severe TBI suffer from increased rates of infectious complications, especially with VAP. Mortality is still strongly associated with secondary brain injury and nosocomial infections. Optimized prehospital care, enhanced infection prevention, and prescription of specific antibiotics are among the essential measures to improve the outcomes of such a vulnerable group.

Biography

Dr. Chaimae obtained her MD degree in 2020 and completed her specialty training in Anesthesiology and Intensive Care in 2025 at the Faculty of Medicine and Pharmacy of Casablanca. She successfully passed the competitive examination for assistant professor in June 2025 at the same institution. She is currently an Assistant Professor in the Surgical Emergency Intensive Care Unit at Ibn Rochd University Hospital, Casablanca, Morocco. Her main interests include infectiology and hematology. She is currently enrolled in a DIU in Hematology at Université Paris Cité and conducts research on nutrition and muscle status in traumatic brain injury patients. She has published more then five articles and regularly participates in national and international conferences.

Chun-Hsiang Chiu*, Ying-Chuan Wang
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Critical risk factors for COVID-19-associated pulmonary aspergillosis identified in hospitalised patients

Background: The long-term impact of coronavirus (COVID)-19 and the possibility of secondary infections have not yet been defined. Because COVID-19 has become a common community infection, patients are often hospitalised with COVID-19 accompanied by unrelated comorbidities (overlooked and secondary infections). This retrospective study investigated the risk factors and prevalence of COVID-19-Associated Pulmonary Aspergillosis (CAPA) among hospitalised patients.

Methods: We analysed data from 912 patients hospitalised with COVID-19 in Taiwan between 1 April and 1 July 2022 to identify risk factors and CAPA prevalence.

Results: Among these patients, 36(3.9%) were diagnosed with CAPA 23 d (median onset) after testing positive for COVID-19. Risk factors included age >60 years, male sex, body weight <40kg, Body Mass Index (BMI) <17.5kg/m^2, Charlson Comorbidity Index (CCI)>5, and severe COVID-19. Patients with CAPA had leukopenia, lymphopenia, thrombocytopenia, renal dysfunction, hypoalbuminemia, and elevated inflammatory markers (C-Reactive Protein [CRP], D-dimer, ferritin, Lactate Dehydrogenase [LDH], and Erythrocyte Sedimentation [ES]). Systemic corticosteroids (particularly doses ≥480mg hydrocortisone-equivalent within 90d before/after infection) significantly increased CAPA risk. Remdesivir was associated with CAPA because it was administered to severely ill patients instead of direct causation. Antibiotic therapy increased fungal susceptibility and CAPA was linked to increased mortality rates (10.7% vs. 2.4%), prolonged quarantine (>13d), and delayed diagnosis, particularly among patients with milder initial symptoms.

Conclusions: Increased mortality and diagnostic delays are associated with multifactorial CAPA. Vigilance is required in ICUs and other settings regarding the customisation of treatment and prophylactic strategies.

Biography

Chun-Hsiang Chiu is the Director of the Medical Department at Tri-Service General Hospital, Keelung Branch, Taiwan, and an Associate Professor at the National Defense Medical University. His research interests include COVID-19, antimicrobial resistance, hospital-acquired infections, and clinical outcomes of bloodstream infections. His work integrates clinical epidemiology and translational research to improve the management of emerging and drug-resistant pathogens.

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Vegetable-associated *Escherichia coli* ST446 carrying $bla_{CTX-M-1}$ and *mcr-1* raises concerns regarding difficult-to-treat foodborne infections

Antimicrobial resistance is a pressing global issue with significant implications for human health. The presence of human bacterial pathogens resistant to last-line treatments in ready-to-eat vegetables is particularly concerning, as it compromises food safety and poses a serious threat to public health. In this study, an *Escherichia coli* strain (P13) isolated from a cabbage leaf obtained from a cultivation area in Serrana, São Paulo, Brazil, was characterized phenotypically, molecularly, and genomically. Cabbage leaves were processed in saline solutions by shaking to obtain epiphytic bacteria. Selective isolation was performed on MacConkey agar plates supplemented with 4mg/L of ceftriaxone, and genomic DNA was extracted using a silica column-based purification procedure. Molecular identification was performed by 16S rRNA sequencing. Antimicrobial susceptibility was determined using disk diffusion and broth microdilution methods following the Brazilian Committee on Antimicrobial Susceptibility Testing/European Committee on Antimicrobial Susceptibility Testing (BrCAST-EUCAST, v.10.0, 2024) guidelines. Whole-genome sequencing was performed using Oxford Nanopore Technologies, and de novo genome assembly was conducted using Flye v.2.9.1. Genomic characterization, including Antimicrobial Resistance Genes (ARGs), virulence determinants, multilocus sequence typing, serotyping, phylogroup, and plasmid detection, was performed using tools available from the center for genomic epidemiology. The P13 strain exhibited resistance to ampicillin, amoxicillin-clavulanic acid, ampicillin-sulbactam, cefazolin, ceftriaxone, cefotaxime, ceftazidime, cefepime, aztreonam, nalidixic acid, norfloxacin, streptomycin, tetracycline, doxycycline, minocycline, trimethoprim-sulfamethoxazole, and fosfomycin. Notably, this strain showed a minimum inhibitory concentration of 4mg/L for colistin, demonstrating resistance to this antimicrobial. Accordingly, the P13 strain harbored

the following ARGs: *bla*$_{CTX-M-1}$ (β-lactam resistance, including third-generation cephalosporins), mcr-1 (polymyxin resistance), aadA (aminoglycoside resistance), sul2 (sulfonamide resistance), and tetA and tetB (tetracycline resistance). Additionally, this strain presented a mutation in GyrA (S83L) related to fluoroquinolone resistance. Strain P13 belonged to the Sequence Type (ST) 446, serotype O54:H32, phylogroup A, and harbored two plasmid replicons, IncI1 and IncX4. Moreover, this strain carried several virulence determinants, highlighting those related to adhesion and biofilm formation (fimH, csgA), bacteriocin production (cea, cib), cytotoxicity (hlyE), immune evasion (ompT), and stress tolerance (gad, terC). These results highlight the presence of a potentially virulent *E. coli* ST446, a One Health clone linked to human infections, harboring ARGs associated with resistance to last-line antimicrobials at the food-health interface. Therefore, these findings underscore the importance of surveillance and control measures along the vegetable production chain to ensure food safety and protect human health.

Biography

Eliana Guedes Stehling is an Associate Professor at the School of Pharmaceutical Sciences of Ribeirão Preto, University of São Paulo, Brazil, and advises master's and doctoral students in the Biosciences and Biotechnology Graduate Program. She represented South America in 2018 JPIAMR (Joint Programming Initiative on Antimicrobial Resistance) Network Call on Surveillance, served as Guest Editor for Frontiers in Microbiology and Frontiers in Veterinary Science, and has published more than 100 research articles in peer-reviewed journals. Her research focuses on the genomic characterization of bacterial strains of critical WHO importance isolated from the soil-food-water interface, with emphasis on extra-hospital reservoirs and their impact to public health.

Em Brenner
University of Strathclyde, UK

Institutional gaps and healthcare inequalities: Blood-borne virus healthcare from prison to the community

People in prison and prison leavers experience disproportionately poorer health outcomes compared to the general population, including a relatively higher prevalence of blood-borne viruses. This is often reported as due to a higher likelihood of risk factors such as sexual practice, sexual assault, and intravenous drug use. Existing research points to compounding stigma associated with prison leaver and blood borne virus diagnosis status contributing to barriers to health maintenance after release. Yet, limited research explores the role of the state and prison system contributing to the health outcomes of this specific population and how this, often intertwined with stigma, contributes to health inequality in Scotland. Isolated approaches to both healthcare and re-entry ignore the reality of how these facets interact with each other, and the overall impact on life after release. Building off of a pilot study, this presentation addresses systemic concerns across the National Health Service (NHS) and Scottish Prison Service (SPS) on initiating, maintaining, and bridging blood borne virus healthcare through custodial sentences and release. As part of the CSO Health-Justice Nexus project, this PhD research addresses shortcomings of Scottish health-justice policy, the impact on health inequality, and target areas for improving blood borne virus healthcare for those particularly vulnerable. Critiquing the lauded 'Equivalence of Care' model adopted by the NHS within UK prisons, this presentation argues that efforts to improve blood borne virus healthcare within prisons to match the efforts and quality of care found in the community is not sufficient in addressing these health outcomes. Instead, an 'Equity of Care' model is more appropriate, to address the additional needs required by this population to maintain blood borne virus healthcare amongst competing priorities and challenges after release.

Biography

Em Brenner is currently a 2nd year PhD candidate in the Department of Social Work and Social Policy at the University of Strathclyde. Brenner's PhD research on blood borne virus healthcare accessibility from prison through release sits within the NHS CSO Scottish Health-Justice Nexus project, addressing areas for healthcare improvement for those navigating Scotland's justice system. Brenner holds an MRes with distinction in Criminology from the University of Glasgow, with research interests in prisons and public health.

Gustavo Gomedi*, Ivana Teixeira de Aguiar, Erica Nishida Hasimoto

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Epidemiological profile, diagnosis, and treatment of pleural empyema in adult population treated at a tertiary hospital in Brazil

Introduction: The Complicated Parapneumonic Pleural Effusion (CPPE), or empyema, stands for an important pneumonia's complication, being associated to higher morbimortality, hospitalization and the frequent need to surgical approach. This article's goal was to describe the epidemiology, diagnosis, treatment and outcome in CPPE in adults admitted in a public tertiary hospital in Brazil, during 2022 to 2024.

Methodology: A cross-sectional, retrospective study analyzing medical records of patients over 15 years old diagnosed with CPPE and followed by the thoracic surgery service from January 2022 to December 2024. Demographic data, diagnostic tests performed, treatment modalities used, average length of hospital stay, and mortality rates were collected. A descriptive analysis was performed.

Results: A total of 66 adults with CPPE (19 in 2022, 22 in 2023, and 25 in 2024) were identified during the study period. Regardless of the year analyzed, the majority of patients were male (75.8%). Regarding age group, in 2022 and 2023, the group over 45 years old predominated (63.2% and 77.3%, respectively). In 2024, the incidence was practically equivalent between the groups, with 13 patients under 45 years old and 12 over 45 years old. There was seasonality, with a higher number of cases in the winter months, averaging 15 diagnoses from May to August for each year analyzed. Chest X-ray was the primary diagnostic test used (40 patients, 16 in 2022, 12 in 2023, and 12 in 2024), followed by computed tomography (23 patients, 3 in 2022, 10 in 2023, and 10 in 2024), and pulmonary ultrasound, which was used in only 3 patients in 2024. All patients underwent some intervention in addition to antibiotic therapy, and in all years evaluated, the number of patients undergoing pleural drainage was higher than those

undergoing any surgical procedure: 94.7% in 2022, 72.7% in 2023, and 68% in 2024. In 2022, the average length of hospital stay was 23 days and the mortality rate was 36.8% (7 cases); in 2023, the average length of hospital stay was 18 days and 5 patients died (mortality rate of 22.72%). In 2024, there were 3 deaths (mortality rate of 12%), and patients were hospitalized for an average of 15 days.

Conclusion: CPPE in adults is a serious condition with a high mortality rate. However, there has been a trend toward improved outcomes over the years, particularly in terms of mortality rates and length of hospital stay. This progress may be related to the adoption of more effective treatments, as evidenced by the increased use of pulmonary decortication and, above all, the growing use of less invasive approaches, such as Video-Assisted Thoracoscopic Surgery (VATS).

Biography

Gustavo Gomedi is a Brazilian physician graduated with academic award in Cesumar University (Unicesumar), Maringá, Parana, Brazil. Gustavo is Currently specializing in general surgery in São Paulo State University (UNESP), Botucatu, São Paulo, Brazil, master's student also in this university, with a research project focused in the complicated parapneumonic effusion's treatment.

Gustavo Gomedi*, Ivana Teixeira de Aguiar, Erica Nishida Hasimoto

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Epidemiological profile, diagnosis, and treatment of pleural empyema in pediatric population treated at a tertiary hospital in Brazil

Introduction: The Complicated Parapneumonic Pleural Effusion (CPPE), or empyema, stands for an important pneumonia's complication in pediatric population, being associated to higher hospitalization and the need to surgical approach. Current medical literature describes higher incidence in younger patients, especially between 1 and 9 years old, most occurring in winter months. This article's goal was to describe the epidemiology, diagnosis, treatment and outcome in CPPE in children admitted in a public tertiary hospital in Brazil, during 2022 to 2024.

Methodology: A cross-sectional, retrospective study analyzing medical records of children aged 0 to 15 years diagnosed with CPPE and followed by the thoracic surgery service from January 2022 to December 2024. Demographic data, diagnostic tests performed, treatment modalities used, average length of hospital stay, and mortality rates were collected. A descriptive analysis was performed.

Results: A total of 110 children with CPPE (31 in 2022, 29 in 2023, and 50 in 2024) were identified during the study period. A similar distribution by sex was observed across the three years studied. The most affected pediatric age group was 1 to 5 years old in all years analyzed. Seasonality was observed, with a higher number of cases in the winter months, averaging 15 diagnoses from May to August in each year analyzed. Chest X-ray was the primary diagnostic test (95 children), followed by computed tomography (4 children) and pulmonary ultrasound, the last showing a progressive increase in use over the years, rising from 3 cases in 2022 to 6 in 2024. All patients underwent some kind of intervention in addition to antibiotic therapy. In 2022 and 2023, the primary treatment modality was Video-Assisted Thoracoscopic (VATS)

(51.6% and 55.1%, respectively), followed by chest tube drainage. In 2024, however, the most common treatment was closed pleural drainage (56%), followed by VATS (42%). In the year 2023 occurred the highest number of surgeries (VATS and thoracotomy), with 63% of children undergoing some form of intervention, and it was also the period during which no deaths were observed. A progressive reduction in the average length of hospital stay was observed, from 22 days in 2022 to 15 days in 2024. Mortality was low, ranging from 0% to 6%.

Conclusion: It is observed that the seasonality of empyema tends to follow a bimodal pattern, with one peak during the winter months and another during the transition from spring to summer. Furthermore, it is noted that advances in diagnostic methods and surgical approaches have contributed to a reduction in morbidity, particularly through the use of less invasive methods. These data are important for justifying the importance of investing in new technologies and in the training of professionals, especially surgeons, to enable appropriate diagnosis and treatment.

Biography

Gustavo Gomedi is a Brazilian physician graduated with academic award in Cesumar University (Unicesumar), Maringá, Parana, Brazil. Gustavo is Currently specializing in general surgery in São Paulo State University (UNESP), Botucatu, São Paulo, Brazil, master's student also in this university, with a research project focused in the complicated parapneumonic effusion's treatment.

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Atypical presentation of disseminated herpes zoster in an immunocompetent adult

Disseminated Herpes Zoster (DHZ) is typically seen in immunocompromised patients and is rare in immunocompetent individuals, posing a significant diagnostic challenge when it presents atypically. We report a case of a 47-year-old immunocompetent female with no identifiable risk factors, such as corticosteroid use or HIV history, who developed disseminated herpes zoster. She initially presented with a one-week history of left lower extremity and knee pain without skin findings. Deep Vein Thrombosis (DVT) was ruled out, and a CT scan of the left knee showed no abnormalities. She was sent home with pain medication, but one week later, she returned with an itchy, painful rash localized to the L3 dermatome on her left lower extremity, which later spread to the upper leg, back, and chest. Physical examination revealed erythematous papules and vesicles across non-contiguous dermatomes, raising suspicion of disseminated herpes zoster. Varicella-Zoster Virus (VZV) PCR from lesion swabs confirmed the diagnosis. Ocular involvement was ruled out. She was treated with intravenous Acyclovir and Gabapentin, with marked improvement. Upon discharge, she was transitioned to oral antivirals, with subsequent improvement and outpatient follow-up. This case illustrates the rare occurrence in immunocompetent patients, emphasizing the importance of diagnostic vigilance regardless of the patient's immune status. Despite lacking typical risk factors, this patient developed disseminated zoster. Therefore, this highlights the importance of early recognition and prompt treatment, which is crucial in reducing morbidity, preventing complications, and optimizing outcomes.

Biography

Dr. Hana Raza is a PGY-2 Internal Medicine resident at McLaren Oakland in Pontiac, Michigan, USA, committed to providing high-quality, patient-centered care and expanding her clinical expertise. Her training spans a broad spectrum of internal medicine, with hands-on experience in complex inpatient and outpatient care. She is passionate about learning through real-world cases and collaborative practice, emphasizing evidence-based decision-making and holistic patient management. Outside of her clinical duties, she engages with the medical community through social media, sharing glimpses of life in residency and reflections on work-life balance. Her goal is to grow as a skilled, compassionate, and well-rounded physician.

Hannah Bray[1*], Katarzyna Purzycka[2], Megan Rose[2], Gordana Simeunovic[1]

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Quadruple-valve endocarditis due to *Candida parapsilosis*: A previously unreported presentation

Introduction: Four-valve endocarditis is exceedingly rare, typically bacterial in origin, and associated with high morbidity and mortality. To our knowledge, we report the first case of quadruple-valve endocarditis caused by *Candida parapsilosis*.

Case Presentation: A 38-year-old female with a history of Intravenous Drug Use (IVDU), prior Staphylococcus aureus tricuspid valve endocarditis, and end-stage renal disease on Hemodialysis (HD) via right jugular permcath presented with fluid overload after missing HD for months. On arrival, she was afebrile, tachycardic, with renal failure. Due to non-functioning HD catheter, a femoral line was placed for emergent HD, Blood cultures (Bcxs) and permcath culture were obtained, and vancomycin and ceftriaxone were initiated. On hospital day two, Bcxs grew *Streptococcus mitis* and antibiotics were narrowed. The permcath was removed on hospital day two with purulence noted. Bcxs were repeated. Transthoracic Echocardiogram (TTE) demonstrated vegetations on all four valves. On hospital day five, Bcxs from day two grew *Candida parapsilosis*, prompting initiation of fluconazole. Permcath culture remained negative. Transesophageal Echocardiogram (TEE) confirmed involvement of the aortic, mitral and tricuspid valve, with severe dysfunction; pulmonic involvement was not visualized. Her hospital course was complicated by septic emboli to the lungs, kidney, left thigh, brain and retina.

Persistent candidemia, despite multiple line holidays, prompted addition of micafungin on day 13. On day 17, she underwent aortic valve replacement, repair of aortic root abscesses, and mitral and tricuspid valve repair. Intraoperative aortic valve tissue culture confirmed *Candida parapsilosis*. Bcxs cleared postoperatively. Micafungin was discontinued on day 23. She completed a six-week course of ceftriaxone and high dose fluconazole from day of surgery and was discharged on day 69 on fluconazole with plans for suppression.

Conclusion: This case describes previously unreported quadruple-valve endocarditis due to *Candida parapsilosis*. It highlights the aggressive nature of fungal endocarditis, particularly in patients with indwelling vascular access and IVDU. Diagnosis may require multimodal imaging, as valvular involvement can evolve or embolize-in our patient pulmonic valve involvement was suggested on TTE but not confirmed on TEE, with embolization remaining a possible explanation. Management necessitates prolonged antifungal therapy and complex surgical intervention. Early recognition and multidisciplinary care are critical to improving outcomes.

Biography

Hannah Bray is a current first year Infectious Disease Fellow at Corewell Health West/Michigan State University where she also completed her Internal Medicine Residency and Chief Resident year. Hannah completed her medical school training at Michigan State University College of Human Medicine. Hannah is eager to complete her final year of training and to further explore her interests in infectious disease, medical education, and research.

Yasmin Santos[1], Angélica Nunes[1], Raquel Sanfelice[1], Virgínia Concato[2], Taylon Silva[2], Fernanda Tomiotto-Pellisier[3], Mariana Detoni[1], Danielle Lazarin-Bidoia[1], Sara Suzuki[1], Luiz Barros[4], João Garcia[4], Ivete Conchon-Costa[1], Wander Pavanelli[1], Renata Kobayashi[5], Izadora Rossi[1], Bellisa Barbosa[6], Eloisa Ferro[6], Idessania Costa[1*]

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Anti-proliferative and metabolic activity of the compounds caffeic acid and oregano essential oil in human trophoblast cells infected with the RH strain of *Toxoplasma gondii*

Introduction: Toxoplasmosis, an infection caused by the protozoan *Toxoplasma gondii,* becomes serious in immunocompromised individuals, ocular toxoplasmosis, and, especially, in cases of congenital infection. Treatment of toxoplasmosis is hampered by the toxicity of conventional medications, sulfadiazine, and pyrimethamine. Therefore, other compounds have been evaluated as alternative treatments for this infection, such as Caffeic Acid (CA), a phenolic compound found abundantly in many plants and foods, with proven antimicrobial, antioxidant, anti-leishmanial, and anti-trypanosomal effects. Oregano (*Origanum vulgare*) Essential Oil (OEO) presents a promising alternative due to its antibacterial, antifungal, and antiparasitic potential. The objective of this study was to analyze the antiproliferative capacity and the direct mechanisms of action of OEO and CA on *T. gondii* tachyzoites (RH strain).

Materials and Methods: To evaluate the cytotoxicity of the compound, HTR8/SVneo and BeWo cells were cultured in 96-well plates for 24 hours in an incubator at 37°C and 5% CO_2. Subsequently, the cells were treated, respectively, with AC at concentrations of 10-10000µg/mL and OEO at concentrations of 0.7 to 150µg/mL for 24 hours. To investigate the direct effect of the compound on the free forms of *T. gondii* tachyzoites, a viability test was performed using the trypan blue exclusion method. Tachyzoites (5x105) were treated with AC (1-200µg/mL) and OEO (0.7-150µg/mL) for 1 hour, stained and counted under an optical microscope. Finally, to verify the effect of the compound on *T. gondii* infection, HTR8/SVneo cells were maintained in 24-well plates containing 13-mm round coverslips for 24 hours and then infected with 5x105 tachyzoites of the RH strain of T. gondii. After 3 hours of infection, the cells were washed and treated with AC at concentrations of 5, 10, 25, and 50µg/mL and OEO at concentrations of 6.2, 12.5, 25, and 50µg/mL for 24 hours. Subsequently, the coverslips were stained and mounted for analysis under a light microscope (E100, Nikon-LED, 100X objective). Subsequently, to determine the mechanisms leading to parasite death, mitochondrial membrane potential and lipid droplets were evaluated, as well as autophagy by monodansylcadaverine. Finally, scanning and transmission electron microscopy analyses were performed.

Results: After treatment, the results showed that both compounds exhibited low cytotoxicity in cells and reduced tachyzoite viability. There was a reduction in infection and intracellular proliferation of 55% and 84% at concentrations of 25 and 50µg/mL of OEO, respectively, and 76.5% and 80.5% at concentrations of 25µg/mL and 50µg/mL of AC. In free tachyzoites, both treatments caused mitochondrial membrane depolarization and lipid droplet formation, as well as mitochondrial swelling, observed by TEM. These changes are linked to the induction of autophagy and plasma membrane permeabilization, with leakage of cytoplasmic contents and nuclear alterations, confirmed by TEM and SEM, culminating in parasite death.

Conclusion: Treatments with OEO and AC demonstrated anti-*T. gondii* activity, directing the death of the parasite through metabolic alterations without causing toxicity to cells, and can be considered promising compounds in the treatment of congenital toxoplasmosis in the future.

Biography

Idessania Nazareth Costa is a CNPq productivity fellow since 2018. Biologist with a postdoctoral degree (2018), PhD (2009) and Master's degree (2002) in Applied Immunology and Parasitology from the Federal University of Uberlândia, Brazil. She has been teaching in the Master's and PhD programs in the Postgraduate Program in Experimental Pathology at the State University of Londrina-PR, Brazil (CCB-UEL) since 2012. She works as a professor and coordinator of the Parasitology area at the same institution where she coordinates Research and Extension projects. She has experience in parasitic diseases, focusing on the immunoparasitological and molecular diagnosis of human strongyloidiasis and the alternative treatment of toxoplasmosis.

Jalees A. Nasir[1,2*], Andrew G. McArthur[1,2]

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CARD-LinkML: Connecting the dots to develop frameworks for multicomponent antibiotic resistance

Antibiotic resistance is a complex problem with many interwoven concepts, spanning from individual drug-to-gene interactions to entire gene clusters working in tandem to evade antibiotics. The Comprehensive Antibiotic Resistance Database (CARD) represents individual Antimicrobial Resistance (AMR) genes using bioinformatic models, each storing the necessary sequence information and uses ontologies to characterize the overall resistance profile. These models are used alongside the Resistance Gene Identifier (RGI) software to report observed Antibiotic Resistance Genes (ARGs) for given sequencing or assembly data. However, some AMR gene families comprise multiple components, whose combined impact leads to phenotypic resistance. Such gene families include glycopeptide resistance gene clusters, such as VanA in *Enterococcus faecium*, and eflux pump complexes, such as Mex in *Pseudomonas aeruginosa*. Currently, RGI can only detect individual components of AMR and cannot assess further functional relevance without properly connecting them back to their respective gene clusters or eflux pumps.

To resolve the gap, we began developing CARD-LinkML, leveraging the Linked Data Modelling Language (LinkML) to standardize the data structure for multicomponent systems for resistance. A schema written in LinkML uses classes representing overarching categories. Each class contains parameters that specify data and accepted data types, such as strings or identifiers. The developing CARD-LinkML module can perform two overarching functions. The first converts the existing CARD reference data into a schema where LinkML classes represent multicomponent gene clusters or eflux pumps. Parameters for each class include the necessary reference accession identifiers or values that characterize the resistance profile of each AMR gene. Further, we can connect the required components that make up a gene cluster or eflux pump by leveraging the underlying CARD ontology, each represented by

separate LinkML classes. The second component takes RGI results into a LinkML-compatible YAML format where observed AMR genes are clustered into their respective multicomponent gene clusters or eflux pumps. Values from RGI are cross-referenced to classes in the reference schema, enabling functional assessment of the observed cluster or eflux pump based on observed AMR components.

By leveraging the LinkML schema as a tether connecting observed ARGs to their likely functional relevance, we hope to expand the RGI suite and then develop tools to aid in interpreting RGI results for more nuanced biology as observed in multicomponent systems.

Biography

Dr. Jalees Nasir is a postdoctoral fellow in the lab of Dr. Andrew McArthur at McMaster University. He completed his doctoral degree in the same lab, specializing in the bioinformatics surrounding respiratory virus surveillance and clinical epidemiology. He has contributed significantly to research on the Coronavirus Disease 2019 (COVID-19) pandemic by developing an Illumina-focused sequencing pipeline used by government, academic, and clinical facilities. His current work focuses on further developing tools for the Comprehensive Antibiotic Resistance Database (CARD) using novel data schema languages to bridge the gap between complex data structures.

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Chong Hua Hospital, Cebu city, Philippines

Infected pseudoaneurysm from septic embolism of the left common iliac artery in a seventy-five-year-old man

Introduction: Infected pseudoaneurysms, though rare, are serious complications arising from septic emboli and pose significant diagnostic and management challenges. The common iliac artery is an unusual site for such aneurysms, accounting for only 2-6% of documented cases. This report details a 75-year-old hypertensive and diabetic male who developed an infected pseudoaneurysm of the left common iliac artery, successfully treated with laparotomy, aneurysmectomy, and ilio-iliac bypass grafting.

Objective: To detail the clinical presentation, diagnostic challenges, and successful multidisciplinary management of an infected pseudoaneurysm of the common iliac artery in a 75-year-old hypertensive and diabetic male.

Case Presentation: The patient, a 75-year-old male with hypertension and diabetes, presented with a two-week history of fever and chills, body malaise, and a three-day history of bilateral knee pain with difficulty ambulating. Previously treated for community-acquired pneumonia and hepatic abscess, he presented afebrile with a swollen, tender left knee and decreased pulses in the left dorsalis pedis. Laboratory findings included a high procalcitonin level of 73.8, CRP of 317.3, and significant pyuria. A CT scan revealed a hepatic abscess and an abscess formation along the left common iliac artery, causing significant stenosis. Blood and urine cultures were positive for Klebsiella pneumoniae, sensitive to Meropenem. Despite initial improvement with Meropenem, a follow-up CT scan revealed a mycotic pseudoaneurysm of the left common iliac artery. The patient underwent successful laparotomy, debridement, aneurysmectomy, and ilio-iliac bypass grafting, recovering well post-operatively without complications.

Biography

John Luis R. Wee is a medical professional currently deepening his expertise through an Internal Medicine Residency at Chong Hua Hospital, which he began in 2024. He passed the Philippine Physician Licensure Examination in 2023 (Lic. No. 0165924) after completing his Post-Graduate Internship at Chong Hua Hospital from 2022 to 2023. He earned his medical degree from Cebu Doctors' University Medicine (2018-2022). Dr. Wee's foundational education is in laboratory science, holding a Bachelor of Science in Medical Technology from Velez College (2013-2017), and he also successfully passed the related Medical Technology Board Exam in 2017.

John Matthew S. Tan* RMT, MD; Ma. Cecilia Momville MD, FPCP, FPCCP; Patricio Palmes MD, FPCP, FPCC, FPSE, FPSVM

West Visayas State University Medical Center, Jaro, Iloilo City, Philippines

Knowledge, attitude, and practices pertaining to latent tuberculosis among household contacts of patients diagnosed with bacteriologically-confirmed pulmonary tuberculosis in the seven districts of Iloilo city

Background: Latent Tuberculosis Infection (LTBI) reflects a sustained immune response to *Mycobacterium tuberculosis* without active disease. Despite global progress toward the WHO "End TB Strategy," household contacts of TB patients remain at high risk of infection. Gaps in Knowledge, Attitudes, and Practices (KAP) continue to limit early prevention and adherence to LTBI management, particularly in high-burden urban settings.

Objective: Assess the level of knowledge, attitude, and practices pertaining to latent TB among household contacts of patients diagnosed with bacteriologically-confirmed pulmonary tuberculosis in the seven districts of Iloilo city.

Methodology: A descriptive cross-sectional analytical study was conducted from September to October 2025 among 278 household contacts selected through simple random sampling. Data was gathered using a structured self-administered questionnaire. The Kruskal-Wallis test determined differences in KAP across sociodemographic groups, while Spearman's rank correlation and logistic regression identified associations and predictors. Statistical significance was set at 0.05.

Results: A total of 278 respondents (male 129 & female 149) were included in the study. Respondents demonstrated low knowledge (mean=3.6/10), fair attitudes (mean=32.7/50), and fair practices (mean=35.4/50) toward LTBI. Educational attainment, district of residence, and proximity to health facilities were significant factors influencing KAP levels. Spearman's correlation showed moderate positive relationships between knowledge–practice (r=0.30)

and attitude–practice (r=0.36), and a weak positive link between knowledge-attitude (r=0.27). Logistic regression identified education and accessibility as significant predictors of higher KAP scores.

Conclusion: Household contacts in Iloilo city exhibited limited understanding of LTBI but showed fair preventive behaviors. Knowledge alone did not translate into consistent practice, suggesting the influence of access and structural factors. Strengthening community-based education and equitable health service delivery may enhance LTBI prevention and align local efforts with the WHO's "End TB Strategy".

Keywords: Latent Tuberculosis Infection, Knowledge, Attitude, Practices, Household Contacts.

Biography

Dr. Matthew studied Medical Laboratory Science at the University of San Agustin, Iloilo City, Philippines and is a registered Medical Technologists. He pursued his medical degree at the West Visayas State University College of Medicine, Iloilo City, Philippines and finished his Internal Medical Residency Training at the West Visayas State University Medical Center. His research "Knowledge, Attitude, and Practices Pertaining to Latent Tuberculosis among Household Contacts of Patients Diagnosed with Bacteriologically-Confirmed Pulmonary Tuberculosis in the Seven Districts of Iloilo City" has been awarded 2nd place in the Philippine College of Physicians Western Visayas Chapter Descriptive Category.

Kate Cassandra Digaum* MD, Kenneth Tee MD, Arlene Macabaya MD

Chong Hua Hospital Cebu, Philippines

Surviving a rare, multifocal musculoskeletal infection with concomitant septic myocarditis from *S. dysgalactiae* bacteremia in a 50 year old male filipino: A case report

Background: *Streptococcus Dysgalactiae* (SD) is an uncommon human pathogen and its invasive course and clinical outcomes remain unknown. Bacteremia due to SD with systemic complications is rare with an incidence rate of 7/100,000, and survival in such cases is even rarer. Here, we report a unique case of disseminated SD infection with multi-organ involvement who survived despite extensive disease burden.

Case: We report a case of a 50-year-old male who initially presented with fever, severe bilateral upper and lower extremity pain, and new onset heart failure. Blood cultures taken showed growth of *Streptococcus dysgalactiae*, hence IV Penicillin G was initiated. With increasing myalgia, patient developed acute rhabdomyolysis secondary to infectious myositis. Severe bacteremia eventually led to polyarticular arthritis, hence patient underwent knee arthrocentesis. Culture showed growth of SD-confirming septic arthritis, hence a STAT bilateral arthrotomy with synovectomy was performed. Further work up showed an incidental finding of a 7.0x4.1x9.0cm organized abscess in the left gluteus medius. Patient succumb to ARDS, but eventually recovered. Repeat cultures showed clearing of the bacteremia and septic cardiomyopathy from SD bacteremia was confirmed with the reversal of the new onset heart failure upon full recovery.

Discussion: *Streptococcus Dysgalactiae* (SD) is a gram-positive coccus that belongs to the Lancefield group C/G *Streptococci.* Data on SD bacteremia is scarce due its rare incidence, which hinders timely diagnosis and contributes to high mortality rate. Polyarticular septic arthritis from SD bacteremia accounts a 50% mortality rate-but with only 3 documented cases at present. Only 1 case of infectious myositis with muscular abscess formation from

SD infection is reported-adding to the difficulty in identifying this disease complication. No documented cases of SD septic cardiomyopathy is reported, making this case an addition this bacteria's invasive potential.

Conclusion: This case adds to the limited literature on SD invasive infection and clinical presentation. Further studies and systematic reporting are essential to better define the disease spectrum for this uncommon yet potentially life-threatening pathogen.

Biography

Kate Cassandra Digaum 27, is a dedicated healthcare professional and a registered Medical Technologist who has built a strong foundation in clinical diagnostics and patient care. Driven by her passion for medicine and her commitment to serving others, she is currently undergoing training as an Internal Medicine resident. Known for her diligence, compassion, and strong work ethic, Kate continues to refine her clinical skills while striving to make meaningful contributions to patient outcomes and the medical community.

Alexandra Tabaran[1], Oana Lucia Crisan-Reget[1], Dana Alina Magdas[2], Mihai Borzan[1], Sergiu Condor[1], Caroline Lăcătuș[1]*, Sorin Daniel Dan[1]

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Public health risks associated with polycyclic aromatic hydrocarbons and microbial contamination in traditional pork products

Traditional Romanian pork products, including smoked sausages, dry-cured ham, and smoked bacon, are widely appreciated for their cultural and sensory value. However, their production in small-scale and artisanal settings may present important public health concerns due to limited control over processing conditions and hygiene practices.

This study assessed both chemical and microbiological hazards in traditionally processed pork products from rural regions of Transylvania. Particular focus was placed on Polycyclic Aromatic Hydrocarbons (PAHs), compounds with known carcinogenic potential, and on microbiological contamination, including hygiene indicator bacteria and major foodborne pathogens.

While most samples complied with current European limits for PAHs, variability in traditional smoking practices led to occasional exceedances, highlighting potential long-term exposure risks. From a microbiological perspective, the detection of hygiene indicator bacteria such as coliforms and Enterobacteriaceae suggests deficiencies in sanitation, handling, and storage conditions. More importantly, the identification of pathogens such as *Salmonella spp.* and *Listeria monocytogenes* in certain products—particularly smoked sausages—raises significant public health concerns, as these microorganisms are responsible for foodborne infections that can range from mild gastrointestinal illness to severe, life-threatening conditions in vulnerable populations.

The coexistence of chemical contaminants and pathogenic bacteria in traditional pork products underscores a dual risk to consumers, combining chronic exposure with the potential for acute foodborne disease. These findings highlight the need for improved hygiene education, better process control, and strengthened surveillance systems in artisanal production, in order to safeguard public health while preserving traditional food practices.

Biography

Lăcătuș Caroline-Maria is currently a PhD student in the Department of Public Health and Food Hygiene at the Faculty of Veterinary Medicine, University of Agricultural Sciences and Veterinary Medicine Cluj-Napoca, Romania. Caroline's doctoral research focuses on veterinary public health, with particular emphasis on food safety, environmental contamination, and the impact of risk factors on animal and human health. Caroline is also currently involved as a member of a UEFISCDI-funded research project aimed at optimizing the processing of traditional pork meat products, contributing to enhanced food safety and quality standards. Caroline is a motivated and detail-oriented individual, with a strong interest in research and continuous learning. Caroline is highly organized, responsible, and able to manage my time effectively in both academic and research settings.

Milagros Neyra Blatz[1*], Nicole Pulido[1], Michelle Asiedu Danso[1], Dustin Hill[1], Margaret Grace Rose[1], Yifan Zhu[1], Keshia M. Pollack Porter[2], David A. Larsen[2]

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Equities and inequities inherent in wastewater surveillance systems for public health

Objective: To examine the equity and inequity inherent in wastewater surveillance systems under different design specifications, using New York State as a case study.

Methods: In addition to evaluating the equity of inclusion, we introduce two novel measures of equity in infectious disease surveillance: 1) Equity of outbreak detection and 2) Equity of disease forecasting. We considered equity in terms of demographics, environmental justice, and social vulnerability.

Results: Communities with higher social and environmental vulnerabilities are included in the NYS wastewater surveillance network; however, these same communities are often served by larger wastewater treatment plants resulting in inequity in outbreak detection as outbreaks must grow larger in these communities before they can be detected in their wastewater. Conversely, regions with smaller populations or a higher proportion of households not connected to public sewer may experience an inequity in disease forecasting.

Conclusions: This assessment of equity and inequity, including outbreak detection and disease forecasting, can be applied to improve both the design of wastewater surveillance systems and the understanding of infectious disease risk derived from wastewater surveillance.

Biography

Mila Neyra Blatz is the Program Director of the New York State Wastewater Surveillance Network at Syracuse University. She leads efforts to strengthen wastewater surveillance, collaborating with academic, government, and community partners to advance data equity, public health response, community engagement and communications initiatives. Mila has a bachelor's degree from New York University and a Master of Public Health from the Johns Hopkins Bloomberg School of Public Health, where she was a fellow of the Bloomberg American Health Initiative.

Mohammed Sayeemuddin*, Nandana Syam, Saranya Ravi, Abhinav Nair, Rashmi Gandhi

King's College Hospital NHS Foundation Trust, Neonatology, United Kingdom

Does KP sepsis calculator provide more reliable, accurate and efficient screening and treatment for early onset neonatal sepsis as compared to NICE guidelines? KCH experience

Background: Early onset sepsis is a leading cause of morbidity and mortality in neonates requiring early detection and treatment. However, often it can present with non-specific clinical signs and symptoms. It is therefore important to have an effective screening tool which can be used to assess the risk of infection at birth.

Aim: The aim for this quality improvement project was to compare the effectiveness of using King's College Hospital (KCH) Trust guidelines (based on the NICE for neonatal sepsis 2024) against the Kaiser Permanente (KP) calculator across both units at KCH and Princess Royal University Hospital (PRUH).

Method: This study looked at 199 patients who were started on intravenous antibiotics based on Trust guidelines at KCH and PRUH between August 2024 to January 2025, excluding those who required admission to NICU. Data was collected from electronic records and KP sepsis calculator recommendations were generated. Culture Negative Sepsis (CNS) was defined as first or 24 hour CRP >10mmol/l PLUS 2 or more risk factors/clinical indicators for sepsis.

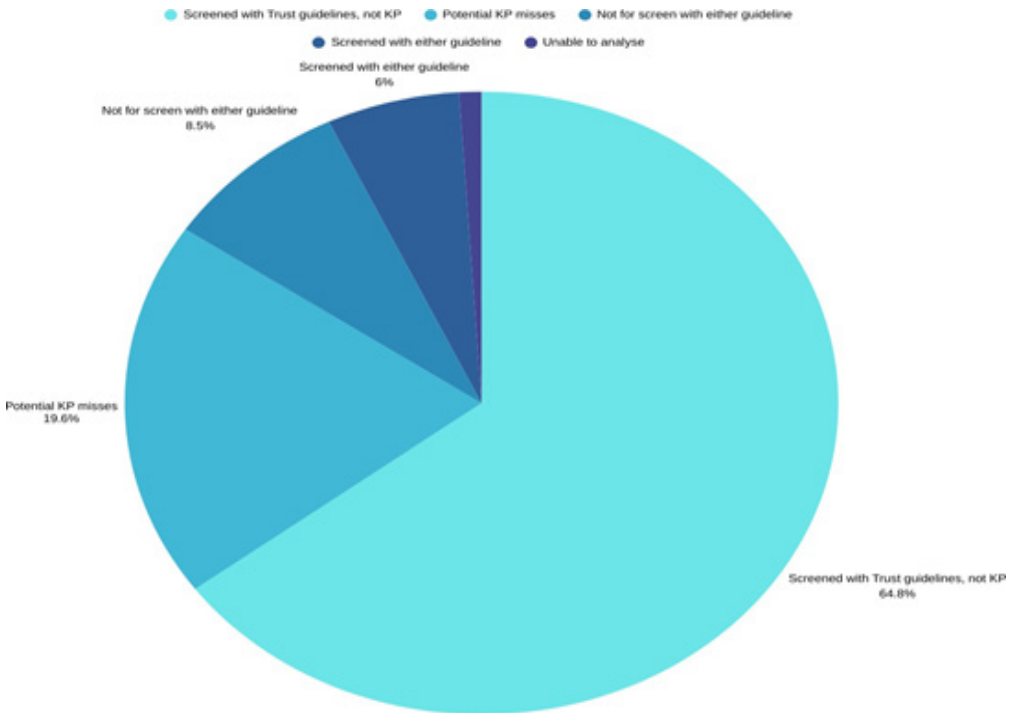
Results:

1. **At PRUH (100 Babies):** 58% overtreated (defined as well babies with negative CRP) using Trust guidelines, 22% potential missed CNS using KP, 14% not for screen based on either guideline and 6% screened using either guidelines. 3% had positive blood culture with high CRP.

2. **At KCH (99 Babies):** 71.2% overtreated using trust guidelines, 17.4% potential missed CNS sepsis using KP, 3.1% not for screen using either guideline and 6.1% treated with either guideline. 2% was not suitable for analysis. 3% had positive BC with high CRP.

Conclusion: In the population of patients at KCH and PRUH, use of KP protocols would result in a large proportion of potential cases of missed CNS sepsis and this study does not currently recommend switching to KP guidelines currently.

Graphs:



Biography

Mohammed Sayeemuddin is a Senior Clinical Fellow in the Neonatal Medicine at King's College Hospital, London with over 10 years of experience in neonatal and Paediatric medicine. He holds MBBS, DNB, DCH, and MRCPCH, reflecting comprehensive postgraduate training in paediatrics and neonatology. His clinical and academic interests focus on neonatal medicine, particularly the prevention, early diagnosis and management of neonatal infections. He has led and contributed to multiple QIP aimed at enhancing patient safety, optimizing clinical outcomes and improving service delivery within neonatal services. He is committed to evidence-based practice, multiprofessional collaboration and continuous professional development in neonatal care internationally.

Nilton Gabriel Vicente Fernandes da Silva*, Adriana Gibotti, Carlos Alberto Fonte de Souza, Daniela Martins da Silva, Geraldo Alécio de Oliveira, Bárbara Alves Rhomberg

UNOESTE University, Brazil

Community-associated invasive infection by methicillin-resistant *Staphylococcus aureus* in an immunocompetent adolescent–case report

Community-associated methicillin-resistant *Staphylococcus aureus* infection is a rare condition, with pneumonia being an uncommon manifestation, especially in previously healthy individuals. A 13-year-old male patient with no previous medical history was admitted to an infectious disease hospital with severe pain in his groin, thigh, and left calf, which was tight, continuous, aggravated by walking, and relieved by rest. He reported that the complaint began five days earlier after sports activity. After two days, it progressed with uncontrollable vomiting, the appearance of a rash on the lower limbs, jaundice in the extremities, fever (38°C), pleuritic pain, and tachypnea. Non-contrast tomography showed hepatomegaly and diffuse bilateral reticulonodular infiltrate. Treatment was started with Ceftriaxone, later escalated to Piperacillin with Tazobactam and Vancomycin, and cultures were requested. Admission laboratory tests revealed pancytopenia, renal dysfunction, and a significant increase in inflammatory tests. Serology for human immunodeficiency virus, syphilis, Hepatitis B, and Hepatitis C were non-reactive. Five hours after admission, he developed acute respiratory failure and septic shock, likely of pulmonary origin. Fifteen hours after admission to the intensive care unit, he became refractory to treatment, went into asystolic cardiac arrest, and died. He was referred to the death verification service, and the death certificate was issued with a diagnosis of septic shock and bacterial pneumonia. The four blood culture samples collected on admission showed growth of methicillin/oxacillin-resistant *Staphylococcus aureus,* confirming severe community-acquired invasive infection by a multidrug-resistant microorganism in a previously healthy patient.

Biography

Nilton Gabriel Vicente Fernandes da Silva is a student and teaching assistant of infectology at a medical school.

Nilton Gabriel Vicente Fernandes da Silva*, Adriana Gibotti, Geraldo Alécio de Oliveira, Flávio Rossi de Almeida, Daniela Martins da Silva, Beatriz Medeiros Correa, Bárbara Alves Rhomberg

UNOESTE University, Brazil

Rifampicin-resistant meningeal tuberculosis in an immunocompromised patient with HIV: Case report

Male patient, 35 years old, with a personal history of HIV diagnosis one year ago with irregular treatment, and pulmonary tuberculosis infection with complete treatment and discharge due to cure two years ago, resident of a free area, cocaine user, with grade III malnutrition. He was admitted to an emergency room with a history of asthenia, general decline, and loss of appetite. During treatment, he developed decreased consciousness and decorticate posture, undergoing orotracheal intubation for airway maintenance. Initial laboratory tests showed mild anemia, leukocytosis with left shift, and hyponatremia. Non-contrast cranial tomography showed a faint hypoattenuating area in the right thalamocapsular region, heterogeneous and poorly defined, with no significant expansive or retractive effect. Mild diffuse brain atrophy and calcified carotid and vertebrobasilar atheromatosis were also observed. Empirical antibiotic therapy with ceftriaxone was initiated. Given the suspicion of neuroinfection, the patient was transferred to a referral hospital for infectious diseases. Upon admission, he was hemodynamically stable, under invasive mechanical ventilation in pressure-controlled mode, with continuous sedation and analgesia, and low ventilatory parameters. Treatment with sulfamethoxazole-trimethoprim (due to suspected pneumocystosis), COXIP regimen, and corticosteroid therapy with dexamethasone was instituted. Laboratory tests on admission showed mild anemia (Hb:10.9mg/dL), elevated ferritin (2,000ng/mL), and increased CRP (116mg/L). Cerebrospinal fluid obtained by lumbar puncture revealed elevated protein (185mg/dL), reduced glucose (12mg/dL), increased lactate (62.6mg/dL), and leukocytosis (295cells/mm^3) with a predominance of neutrophils (55%). Gram staining showed Gram-positive cocci, India ink staining was negative for encapsulated yeasts, and the bacterial capsular antigen (latex) test was nonreactive. The GeneXpert molecular test detected rifampicin-resistant Mycobacterium tuberculosis in both the cerebrospinal fluid and tracheal secretions. BAAR testing in tracheal secretions was positive (2 crosses). The viral load for HIV was 314,000

copies, with CD3 count: 424, CD4: 130, and CD8: 275cells/mm^3. The patient, who was immunocompromised and severely malnourished, had an unfavorable outcome, with difficult weaning from ventilation due to neurological impairment. He underwent tracheostomy after 13 days of orotracheal intubation and died after 21 days of hospitalization.

Biography

Nilton Gabriel Vicente Fernandes da Silva is a student and teaching assistant of infectology at a medical school.

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Opportunistic Central Nervous System (CNS) infections and transplant rejection in Solid Organ Transplant (SOT) recipients: A scoping review

Background: Opportunistic Central Nervous System (CNS) infections are uncommon but devastating complications of Solid Organ Transplantation (SOT). Although individual pathogens are relatively rare, CNS infections collectively account for up to 10% of transplant-associated complications and carry disproportionate morbidity and mortality. Management is further complicated by atypical clinical presentations in immunosuppressed hosts and the absence of standardized guidelines for balancing antimicrobial therapy with immunosuppression reduction. While prior studies have focused on short-term neurological outcomes following CNS infection, the impact of immunosuppressive modulation on graft rejection and longer-term outcomes remains poorly characterized.

Objective: To map the existing literature describing transplant rejection in the setting of opportunistic CNS infections among SOT recipients, with emphasis on pathogen profiles, immunosuppressive management strategies, and clinical outcomes.

Methods: A scoping review was conducted in accordance with the Arksey and O'Malley framework, refined by the Joanna Briggs Institute, and is reported in accordance with the PRISMA Extension for Scoping Reviews (Figure 1). MEDLINE (PubMed), EMBASE, and Scopus were searched from inception through October 2025. Eligible studies included human experimental and observational designs (randomized trials, cohort studies, case series, case reports, and reviews) describing both CNS opportunistic infection and transplant rejection in SOT recipients of any age. Two reviewers independently screened studies and extracted data using a standardized form. Findings were synthesized narratively using the Population-Concept-Context framework.

Results: Of 1,008 records identified, 26 studies met inclusion criteria. Across cohort and case–control studies of opportunistic CNS infections in SOT recipients, infection and rejection were closely linked temporally and therapeutically. CNS infections often occurred years after transplantation, frequently following intensified immunosuppression for rejection. In large toxoplasmosis series, 35-70% of patients had prior rejection treated with high-dose corticosteroids, with diagnoses often delayed months to years; mortality remained high, particularly with delayed recognition. Immunosuppressive regimens-including calcineurin inhibitors, antimetabolites, and corticosteroids-were consistently associated with pathogen-specific CNS infections. High calcineurin inhibitor levels and recent corticosteroid exposure were independent risk factors. Reduction of immunosuppression during infection management was followed by acute rejection in approximately 25-35% of patients within one year. Neurologic outcomes ranged from full recovery to permanent neurologic injury and graft dysfunction, with diagnostic delays common due to overlapping features of rejection and infection.

Conclusions: The literature describing transplant rejection in the context of opportunistic CNS infections is limited and heterogeneous. Significant gaps exist regarding standardized immunosuppressive management, and long-term graft and neurological outcomes. These findings highlight the need for prospective studies and consensus-based guidance to optimize outcomes in this high-risk population.

Figure 1. PRISMA flow diagram illustrating study identification, screening, eligibility assessment, and inclusion for the scoping review of opportunistic CNS infections and transplant rejection in solid organ transplant recipients.

Biography

Priyanka Shekhawat MD is a neurologist at Mass General Brigham. Her clinical and academic interests include pediatric neurology, global neurology and complex diagnostic intersections between neurology and infectious diseases, particularly in TB-endemic settings.

Chaabi Safia*, Chiguer Chaimae, El Mostadi Abderrahman, Nsiri Afak, Al Harrar Rachid

Surgical Emergency Department P33, Ibn Rochd University Hospital, UH2C, Morocco

Peritonitis complicating body packing: A case report

Cocaine body packing, which is the intentional ingestion of drug-containing packets, has been a major risk factor for fatal consequences if a packet ruptures. Of these, peritonitis secondary to gastrointestinal perforation, though uncommon, is a surgical emergency with high mortality.

Case Report: A 35-year-old male with generalized peritonitis following ingestion of multiple cocaine capsules. This case was recorded by a thorough review of clinical, laboratory, radiological, surgical, and postoperative information found in the patient's documents. Emergency care was performed according to established medico-surgical guidelines. The patient had presented with acute abdominal pain and clinical presentation of diffuse peritonitis. Abdominal Computed Tomography (CT) showed 57 intracorporeal drug packets. The exploratory laparotomy finally resulted in the extraction of 85 cocaine capsules, several of which were fissured. The surgical procedure revealed a perforated cecal fistula with widespread purulent peritonitis. Despite timely surgical intervention and intensive care, the patient developed refractory septic shock and died on the fourth postoperative day. Here we see the exceptional but catastrophic complications that are expected from body packing, with GI perforation resulting in peritonitis being the most common. CT imaging is still the backbone of diagnosis, allowing rapid identification of packet location and complications. Yet the threat of systemic toxicity, infection, and multiorgan failure is high, even when all visible packets have been successfully extracted. Complications associated with body packing, particularly in otherwise healthy young individuals, are critical, as highlighted in the case. Early identification, speedy surgical approach, and aggressive critical care are necessary to achieve better outcomes. Thus, the report highlights the fatal consequences of drug body packing in the setting of bowel perforation and peritonitis, advocating for highly specialized multi-disciplinary solutions at high pressure in an emergency.

Biography

Dr. Chaabi Safia, assistant professor in the anesthesia and resuscitation department of surgical emergencies at the Ibn Rochd University Hospital in Casablanca, Morocco.

Sarvin Youssefizad*, Eva Israyelyan*, Courelli Panayiota PhD

USC Keck School of Medicine, United States

The risk of hepatitis B reactivation during immunosuppressive therapy in B-cell cancers: The role of antiviral prevention

Background: Patients receiving immunosuppressive therapy for B-Cell cancers such as lymphoma and leukemia, may be at an increased risk for reactivation of Hepatitis B infections. Immune Checkpoint Inhibitors, (ICIs), weakens immune responses that control latent viruses. Reactivation of Hepatitis B leads to disruption of necessary cancer treatment, liver complications, increased morbidity. This qualitative study assesses clinical data to observe whether antiviral medications may reduce the likelihood of the reactivation of Hepatitis B in patients due to treatments for B-cell cancers, and to examine clinical strategies that can be used to manage these issues.

Materials and Methods: A qualitative review was carried out to evaluate the risk of Hepatitis B reactivation in patients with B-Cell malignancies who are currently receiving immunosuppressive Treatments. Literature included viral infection reactivation rates, antiviral treatments, and treatment outcomes. Specific data sets were reviewed comprising of 1,057 patients with chronic Hepatitis B infection receiving ICI, while another study reviewed 633 patients with Hepatitis B infection and cancer who are also undergoing ICI therapy. Across these trials, reactivation incidents were evaluated and statistical comparisons were made between patients receiving antiviral treatments and those who weren't. These clinical trials revealed that reactivation was statistically higher for patients with chronic Hepatitis B infection compared to those without. Additionally, a multinational survey of 56 oncology centers throughout Europe including Italy, France, and Spain assessed the clinical practices needed in order to manage patients suffering from Hepatitis B, allowing them to receive immunotherapy.

Results: Across examined studies, reactivation was statistically higher in those with chronic infection compared to those with a past infection. It was evident that the absence of antiviral treatments was associated with increased rates of reactivation risk. Antiviral prophylaxis significantly reduced the risk of viral reactivation. HBV prophylaxis is recommended by European and American medical societies, for managing HBV infection in patients receiving ICIs. It is clear that screening cancer patients for HBV before beginning ICIs is crucial. By monitoring HBV biomarkers, it reduces the likelihood of complications and inhibits potential mortality amongst these patients.

Conclusions: Our qualitative study concluded that cancer treatment with ICIs has been associated with the reactivation of the Hepatitis B virus, particularly among patients with chronic infection. When antiviral prophylaxis is not administered to patients, studies show the clinical studies we reviewed reflected that there is a significantly higher rate of reactivation without prophylaxis compared to minimum rates of reactivation for patients receiving prophylaxis treatment. Across examined studies, cancer patients receiving immunotherapies reflected relatively low reactivation rates, yet almost all cases occurred in patients with chronic HBV infection. HBV screening before initiation of Immunotherapy or ICI treatment is crucial. Consequently, expansion of screening and antiviral therapy may reduce hepatitis reactivation incidents during Immunosupressive treatment in patients with B cell cancers. Therefore the conclusion of our qualitative study emphasizes that patients who are receiving antiviral treatments are not likely to have reactivation of Hepatitis B. Strategically, European Oncologists are in the process of developing methodical and systematic treatment improvements aiming at optimum treatment outcomes.

Biography

Sarvin Youssefizad is a pre-medical student at the University of Southern California pursuing a degree in Global Health. She is committed to pursuing a career in medicine with an emphasis on Neurology. Sarvin's academic and research goals are focused on patient centered care, infectious disease, and neurological health. She is passionate about making a change in medicine and advancing equitable care for diverse patient groups through both clinical work and research.

Eva Israyelyan is a sophomore at USC. She is on the pre medical track and is currently majoring in global health. She currently volunteers at Glendale Adventist hospital and is interested in become a physician in the future. Eva is also very interested in health regarding research.

Sasha Leibholz[1,2*] MD, Lauren Gruffi[1,2] MD, Barbara Magid[1] MD

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Severe legionella pneumonia case series at an urban academic medical center

An outbreak of Legionnaires' disease began in New York City in July 2025. In this abstract we present a series of three severe cases of Legionella pneumonia seen in an urban academic emergency department:

Case 1: A 71-year-old male with a history of hypertension, hyperlipidemia, and prior cerebrovascular accident presented to the Emergency Department for decreased level of alertness and slowed, incoherent speech. His initial vital signs were notable for heart rate 150bpm and oxygen saturation 91% on room air. Laboratory results were notable for acute renal failure, with a creatinine level of 8.7mg/dL from a baseline of 1, as well as significant transaminitis. Creatine kinase was 69,907 U/L; there was no reported downtime. Chest X-ray showed bibasilar opacities concerning for pneumonia. Urine antigen testing resulted positive for Legionella. The patient was admitted to the Medical Intensive Care Unit (MICU) where he required intermittent hemodialysis.

Case 2: A 38-year-old male with no significant history presented to the ED with five days of nausea, diarrhea, and shortness of breath. Vital signs were notable for heart rate 135 bpm and oxygen saturation 97% on room air. Labs were notable for sodium 122mmol/L, potassium 2.5mmol/L. Chest imaging demonstrated right upper lobe consolidation. He became progressively more confused in the ED. Repeat bloodwork showed his sodium acutely declined to 107mmol/L. Hypertonic saline was initiated in the ED and he was transferred to the MICU, where desmopressin was given for severe hyponatremia secondary to SIADH. Urinary antigen returned positive for Legionella.

Case 3: A 64-year-old male with a history of obesity presented to the ED for a week of diarrhea and dyspnea. His vital signs were notable for heart rate 113 and oxygen saturation of 81% on room air. Cross-sectional imaging demonstrated multifocal pneumonia. He was admitted to the MICU for acute hypoxic respiratory failure requiring escalating settings of non-invasive ventilation. He was consented for Extracorporeal Membrane Oxygenation (ECMO) and cannulated on Day 3 of admission.

Discussion: Legionnaires' disease is associated with significant morbidity and mortality with nearly half of patients diagnosed with Legionella pneumonia requiring intensive care. Legionella causes infection through inhalation of water droplets contaminated by the bacteria. In the recent outbreak in New York City, Legionella bacteria was released into the air as aerosols from cooling towers in multiple buildings. As global temperatures continue to rise, Legionella, which thrives in warm water, will be a continued public health threat. In our case series, patients ultimately diagnosed with Legionella pneumonia presented to an academic medical center with different chief complaints and had multiple manifestations of the disease.

Chief complaints in our case series included confusion, cough, dyspnea, and diarrhea. Legionella most commonly causes pulmonary and gastrointestinal manifestations but can have multiple extra-pulmonary manifestations as well. One patient in our case series developed rhabdomyolysis secondary to Legionella, which is a rare but serious complication of Legionella secondary to an endotoxin released by Legionella that directly damages muscle tissue. Additionally, one patient developed profound hyponatremia secondary to SIADH, a well-documented but potentially life-threatening complication of Legionella infection. Our cases highlight the importance of recognizing broad laboratory abnormalities as an early clue to Legionella pneumonia, even before respiratory symptoms predominate.

Biography

Drs. Sasha Leibholz and Lauren Gruffi are PGY-3 Emergency Medicine residents at the Columbia-Cornell/NewYork-Presbyterian program. Both share a strong interest in global health and the intersection of infectious diseases and emergency care delivery in resource-limited settings. They aim to improve access to acute and preventive care in international and underserved communities, combining clinical excellence with a commitment to health equity and education.

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Unexpected pulmonary cryptococcosis in an immunocompetent individual: Case report and clinical analysis

Pulmonary cryptococcosis in immunocompetent individuals represents an underestimated diagnostic and therapeutic challenge, with growing relevance in clinical practice and global public health. Although historically associated with advanced immunosuppression-particularly HIV infection, solid organ transplantation, or prolonged corticosteroid use-cases are increasingly reported in patients without apparent risk factors, especially when related to *Cryptococcus gattii,* an emerging pathogen with a distinct epidemiological profile.

We present the case of a 73-year-old immunocompetent man from northern Mexico with a three-year history of chronic cough, significant weight loss, mild hemoptysis, and constitutional symptoms, initially interpreted as chronic inflammatory lung disease or possible pulmonary neoplasm. Chest CT revealed mediastinal lymphadenopathy and irregular consolidation, raising strong suspicion for malignancy. Bronchoscopy demonstrated grade III endobronchial infiltration, and multiple biopsies were required to establish the definitive diagnosis of pulmonary cryptococcosis. Serologies for HIV, HBV, HCV, and syphilis were negative, and the patient had no history of immunosuppression, recent travel, or high-risk exposures other than environmental contact with pigeons. CT imaging reported a lymph node conglomerate up to five centimeters in stations 2R and 4R, associated with an irregular area with air bronchogram in the right upper lobe. Bronchoscopy revealed grade II and III mucosal infiltrations, anthracotic mucosa, and extrinsic compression in segmental bronchi. Bronchial lavage cytology showed nonspecific inflammatory changes; however, endobronchial biopsies confirmed cryptococcosis, prompting antifungal therapy initiation.

This case highlights the global diagnostic challenge of pulmonary cryptococcosis in immunocompetent hosts. The disease can mimic tuberculosis, lung cancer, sarcoidosis, and other chronic granulomatous processes. Diagnostic delays are common due to nonspecific symptoms, variability in radiologic findings, and low clinical suspicion in non-endemic regions. In this patient, deep endobronchial biopsies were essential to differentiate fungal infection from malignancy given the extent of mucosal infiltration.

Therapeutic decision-making in this context is also complex. Although mild to moderate pulmonary cryptococcosis is typically managed with fluconazole, the persistence of hemoptysis, severe endobronchial involvement, and radiologic burden justified induction therapy with amphotericin B deoxycholate followed by high-dose fluconazole. This reflects the limitations of current guidelines-largely derived from immunocompromised populations-which offer limited precision for extensive endobronchial disease in immunocompetent hosts.

Beyond the individual case, this report addresses emerging epidemiological concerns: The geographic expansion of *C. gattii* as a primary pathogen, environmental changes altering fungal distribution, and the need to strengthen mycological surveillance in regions previously considered low risk. Clear opportunities exist to improve care through enhanced clinician awareness, early incorporation of fungal diagnostics in chronic pulmonary syndromes, standardization of therapeutic algorithms, and expansion of diagnostic capacity in resource-limited healthcare systems.

Biography

Dr. Sergio Silvestre Soto Sánchez is a third-year Internal Medicine Resident at the General Hospital of Zone No. 33 of the Mexican Social Security Institute (IMSS) in Monterrey, Nuevo León, Mexico. He obtained his medical degree from the Universidad Autónoma de Baja California. His clinical and academic interests focus on infectious diseases, particularly the epidemiology, diagnosis, and resistance mechanisms of pathogens relevant to northern Mexico. Dr. Soto Sánchez actively participates in research initiatives within his medical unit, promoting the integration of evidence-based infectious disease practices and antimicrobial stewardship into everyday clinical care. He is committed to strengthening regional infectious disease research and enhancing public health responses through early recognition, timely diagnosis, and multidisciplinary collaboration. Dr. Soto Sánchez aims to contribute to the development of local and national strategies addressing emerging infections and improving healthcare outcomes in Mexico.

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A case of neurosyphilis presenting as dyschromatopsia in an immunocompetent filipino adult

Background: Syphilis, caused by *Treponema pallidum,* is a multisystemic sexually transmitted infection recognized as a "great imitator." Ocular syphilis, a manifestation of neurosyphilis, can occur at any stage and affect nearly all ocular structures presenting with symptoms ranging from pain and blurred vision to complete blindness. In the Philippines, syphilis accounted for 1,157 deaths in 2020, ranking 39th globally, yet epidemiologic data on neurosyphilis in Asia and in the Philippines remain scarce up until today. Although commonly associated with HIV infection, ocular syphilis may also occur in immunocompetent individuals. We present a case of neurosyphilis manifesting as dyschromatopsia, highlighting the challenge in committing to treatment in the setting of inconclusive diagnostics in order to avoid permanent visual loss.

Case: This is a case of a 37-year-old, male, Filipino with history of sex with men who had three months of constitutional symptoms, including fatigue, fever, sore throat, and a generalized maculopapular rash. Two weeks before admission, he developed progressive dyschromatopsia, initially affecting red-green perception, leading to bilateral blurring of vision. Physical exam showed generalized lymphadenopathy, patchy alopecia and hyperpigmented macules. Visual acuity was 20/20 with Ishihara scores of 12/15 bilaterally. Baseline fundoscopic findings revealed right optic papillitis with bilateral retinal vasculitis and a left hemianopic defect on perimetry. No other pertinent neurologic physical finding was observed. Serology showed a reactive TPHA with non reactive VDRL/RPR, and negative results for HIV RNA, Hepatitis B surface antigen, and Hepatitis C. Brain with orbital MRI and visual evoked potentials were all normal. A lumbar tap was done and CSF analysis revealed lymphocytic pleocytosis, CSF total protein of 50mg/dl. However, CSF VDRL was non reactive. No pathogen was detected on Multiplex PCR meningitis and encephalitis assay. Based on strong clinical suspicion for ocular

syphilis, intravenous Penicillin G of 4 million units IV every 4 hours for 14 days was given with gradual improvement on the Ishihara scores at 15/15 and resolving optic neuropathy bilaterally at completion of 14 days of penicillin G infusion. No corticosteroid was given.

Discussion: Patients with ocular symptoms and reactive syphilis serology should undergo a comprehensive ophthalmologic exam. The most frequent findings are panuveitis-especially in HIV-positive patients-and posterior uveitis in HIV-negative individuals; chorioretinitis is also common. CSF analysis is indicated when cranial nerve deficits are present. Neurosyphilis is supported by neurologic symptoms plus CSF abnormalities (pleocytosis, elevated protein, or reactive CSF-VDRL) with positive treponemal serology. Because no single test is definitive, all results must be interpreted in the context of the patient's overall clinical picture and pretest probability.

Conclusion: This case underscores the challenges in diagnosing neurosyphilis. Prompt recognition and empiric treatment are critical in preventing irreversible visual loss.

Biography

Dr. Sharrah Mae Tan is a first year resident physician in the Department of Internal Medicine at Chong Hua Hospital in Cebu City, Philippines. Her clinical interests include infectious diseases, and atypical presentations of sexually transmitted infections. She has been participating in case-based presentations in the Philippines. She is committed to documenting and bringing attention to underreported infectious diseases to help strengthen data and improve understanding of rare conditions in the Philippines.

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Legionella pneumophila pneumonia: An underdiagnosed disease, but with a high impact

Legionella pneumophila is an aerobe, non-sporulated, facultative intracellular, mobile, gram-negative bacillus. It's the cause of pneumonia in immunosuppressed patients, usually in a severe form which can expand to multiple lobes, or occasionally, a self-limited mild form, mimicking a flu, called Pontiac fever. Legionella is an airborne microorganism, its main way of spreading being through contaminated water mists or droplets. It persists inside aquatic systems such as plumbing networks, air conditioners and can replicate using hosts like protozoa or amoebae. Medical studies lack of a single global report on Legionella's annual death tool, but in 2021 ECDS mentioned a total of 704 fatalities in EU/EEA territory. The clinical aspects of "Legionnaires' disease" include fever, dyspnea, nonproductive cough, accompanied by gastrointestinal symptoms. The identification method used in our clinic was urinary antigen test.

We've conducted a retrospective study on a lot of 39 patients hospitalized in our clinic between 2023-2025. The exclusion criterium was the age, patients under the age of 18 being removed from the study because we've been monitoring adults' department only. The aspects we've checked were age, sex, obesity or smoking background, total days of care in our clinic and mortality. We've made several comparisons between our whole study group and those suffering from obesity or smokers.

The limits of our study were the size of our study lot (only 39 patients) and the tendency of underreporting this germ because of diagnostic difficulties. Our data confirms the fact that Legionella is continuously threatening elderly population, highlighting the necessity of watchful supervision of water sources and high clinical vigilance while facing severe pneumonias with atypical evolution.

Biography

Simoiu Madalina is a Primary Care Physician in Infectious Diseases at “Prof. Dr. Matei Bals” National Institute of Infectious Diseases from Bucharest, Lecturer at “Carol Davila” University of Medicine and Pharmacy of Bucharest, Department of Parasitology, competence in travel medicine. Her professional activity has two sides: Clinical (treating patients at the hospital) and academical (teaching seminaries of Infectious Diseases and Parasitology at CDUMP). She is also a part of dissertation supervisors committee for Parasitology at CDUMP.

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Vancomycin levels in CSF versus brain ECF: Which compartment reflects the target site in postoperative meningoencephalitis?

Introduction: A fundamental principle of rational antimicrobial therapy is the ability of a drug to achieve concentrations at or above the Minimum Inhibitory Concentration (MIC) at the site of infection. In Central Nervous System (CNS) infections, Cerebrospinal Fluid (CSF) drug concentrations have traditionally been considered a surrogate for target-site exposure. However, accumulating evidence over the past decades suggests that drug concentrations in brain Extracellular Fluid (ECF), measured using cerebral microdialysis, may more accurately reflect antimicrobial exposure at the site of parenchymal infection.

Whether CSF and brain ECF represent interchangeable compartments-or fundamentally distinct pharmacokinetic spaces-remains clinically relevant, particularly in postoperative meningoencephalitis. In this report, we present comparative data on vancomycin concentrations in CSF and brain ECF in four patients with suspected or confirmed postoperative meningoencephalitis.

Methods: Four patients undergoing multimodal neuromonitoring, including cerebral microdialysis and External Ventricular Drainage (EVD), were included. Vancomycin concentrations were measured under predicted steady-state conditions in CSF obtained from the EVD and in brain microdialysate collected over the dosing interval. Sampling was performed on two consecutive days to account for interday variability.

Microdialysis was conducted using a 70 Microdialysis Bolt Catheter with a 10 mm semipermeable membrane (20kDa molecular weight cut-off) and a perfusion flow rate of 0.3µL/min. Vancomycin concentrations were determined using a homogeneous enzyme immunoassay (EMIT® 2000). Brain ECF concentrations were corrected for in vitro probe recovery, as previously described.

Results: Two of the four patients received systemic vancomycin only, while two received additional intraventricular vancomycin (10-20mg/day). In patients treated systemically only, vancomycin concentrations in CSF were extremely low or undetectable, whereas measurable concentrations were observed in brain ECF. Conversely, in patients receiving intraventricular vancomycin, CSF concentrations were markedly higher than those measured in brain ECF (Table 1).

Patient	Vancomycin Administration	Day	CSF (mg/L)	Brain ECF (mg/L)
1	Systemic only	Day 1	Undetectable	7.19
		Day 2	Undetectable	11.24
2	Systemic only	Day 1	1.59	1.68
		Day 2	Undetectable	2.22
3	Systemic + intraventricular	Day 1	27.83	10.06
		Day 2	20.43	10.98
4	Systemic + intraventricular	Day 1	117.27	5.24
		Day 2	114.93	5.63

Conclusions: CSF and brain ECF represent distinct pharmacokinetic compartments for vancomycin in postoperative meningoencephalitis. Drug concentrations in one compartment cannot be reliably used to predict exposure in the other. Clinicians and researchers should carefully consider the relevant target site when interpreting vancomycin concentrations to assess therapeutic adequacy and optimize dosing strategies.

Biography

Skaistė Žukaitienė is a physician-clinical pharmacologist at the Hospital of Lithuanian University of Health Sciences Kaunas Clinics and a PhD candidate at the Lithuanian University of Health Sciences. She is also a lecturer at the Institute of Physiology and Pharmacology, Lithuanian University of Health Sciences. Her clinical and research interests focus on rational antimicrobial therapy, therapeutic drug monitoring, and pharmacokinetics/pharmacodynamics in critically ill and neurosurgical patients, including studies using cerebral microdialysis. She has regulatory experience, having worked for several years as a clinical expert at the European Medicines Agency and at the State Medicines Control Agency of Lithuania.

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Coexisting rifampicin-resistant peritoneal tuberculosis and Ventriculoperitoneal (VP) shunt-related CSF pseudocyst presenting as a pelvic mass: A complex diagnostic intersection

Background: Ventriculoperitoneal (VP) shunts are a well-established treatment for hydrocephalus; however, distal shunt complications such as peritoneal Cerebrospinal Fluid (CSF) pseudocysts are uncommon and may present with misleading extracranial features. In Tuberculosis (TB)-endemic settings, identification of peritoneal TB may anchor diagnostic reasoning toward infection as the primary etiology, potentially obscuring underlying shunt-related pathology.

Case Presentation: We report a diagnostically complex case of a 22-year-old woman with childhood-onset obstructive hydrocephalus treated with a VP shunt 10 years prior to presentation. She had concurrent peritoneal tuberculosis and was receiving first-line antitubercular (AKT; isoniazid, rifampicin, pyrazinamide, and ethambutol [HRZE]), who developed progressive abdominal distension, ascites, pelvic pain, nausea and vomiting. Initial ultrasonogram and MRI pelvis revealed a cystic right adnexal (ovarian) mass with elevated CA-125, raising concern for ovarian neoplasm in the setting of infection. Ascitic fluid analysis and molecular testing identified Mycobacterium tuberculosis, which was initially presumed to account for the patient's abdominal findings and guided early management. Despite antitubercular therapy and close follow up, the lesion continued to enlarge, prompting further evaluation. Definitive diagnosis was established only after exploratory laparotomy six months after initial presentation which revealed a large peritoneal CSF pseudocyst encasing the distal VP shunt catheter. Although cytology demonstrated a non-malignant inflammatory process, molecular testing revealed trace Mycobacterium tuberculosis DNA in both omental and pseudocyst wall tissue, with inconclusive rifampicin resistance profiling due to very low

bacterial burden. Neurologic evaluation showed frontal intermittent rhythmic delta activity on EEG and chronic hydrocephalus on brain MRI, consistent with altered CSF dynamics.

Discussion: This case illustrates how peritoneal tuberculosis may dominate early diagnostic reasoning and delay recognition of VP shunt–related distal complications. The presence of TB, ascites, and elevated tumor markers reinforced an infectious or gynecologic framework, while the underlying shunt-related CSF pseudocyst remained unrecognized until surgical exploration. Management and follow-up in this case were further complicated by evolving antimicrobial considerations and shunt-related factors. The later identification of rifampicin resistance raised concern for inadequate initial mycobacterial control and necessitated reassessment of antitubercular therapy. Ongoing peritoneal inflammation poses a continued risk for impaired CSF absorption and pseudocyst recurrence, complicating interpretation of follow-up imaging. As a result, longitudinal management requires coordinated multidisciplinary follow-up, with vigilance for overlapping clinical signals rather than reliance on a single explanatory framework.

Conclusion: In TB-endemic settings, clinicians should remain vigilant for VP shunt–related complications even when peritoneal tuberculosis is identified. Peritoneal CSF pseudocysts should be considered in the differential diagnosis of pelvic masses and ascites in shunted patients, particularly when neurologic symptoms worsen despite appropriate antimicrobial therapy.

Biography

Sushmita Das is a recent MBBS graduate from Armed Forces Medical College, Pune, India, with a clinical interest in neurology and neuroinfectious diseases. She aims to pursue further research and training in neurology.

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Determinants of symptoms experienced following COVID-19 vaccinations among health workers at a tertiary hospital in southwestern Nigeria

Background: The COVID-19 pandemic has affected health workers as one of the groups most at risk of infection. Although vaccines have been manufactured and documented to be a mainstay in prevention and control, many frontline health workers were averse to vaccination due to reported symptoms experienced.

Objectives: The study aimed to describe the pattern of associated symptoms and determinants of developing adverse reactions to COVID-19 vaccinations among the staff of the University College Hospital, Ibadan (UCH).

Methods: This was a cross-sectional descriptive survey of UCH Ibadan staff who received COVID-19 vaccinations, and the study was conducted between June 2021 and April 2022. A semi-structured self-administered electronic and hard copy questionnaire were used.

Data Analysis: Descriptive and inferential statistics were used for the analysis, using Stata with the level of significance set at $p \leq 0.05$.

Results: A total of 1,252 were sampled, 37.5% were 31-40 years with a range of 20 to 69 years and a mean of 38.9±8.6. Males (53.6%), Medical doctors (23.1%), Craftsmen (8.5%), Administrative staff (8.4%), and Nurses (8.2%) were the prevalent genders and occupations. An even spread of work experience was seen from soon after employment to preretirement.

Most (64.0%) were not on routine treatment in the previous 12 months, while those on treatment were hypertensive, dyspeptic, had asthma/COPD, or had malaria (10.9%, 5.0%, 3.0%, 1.9% respectively). More staff had exposure to COVID-19 suspects (36.3%) compared to confirmed

cases at 27.0%. Using COVID-19 "protection" medicine was common practice among 26.0%. Ensuring protection against COVID-19 infection (69.7%) was the commonest reason for taking the vaccine, even though an adverse reaction was anticipated in 40.3%. Vitamin C was the most frequently used (55.3%), then Paracetamol (49.2%) by 44.6% of the respondents within 24 hours before vaccination, while Paracetamol was the most frequently used (73.4%), then Vitamin C (54.7%) by 17.5% of the respondents within 24 hours after vaccination.

Adverse reactions occurred in 56.2% of participants and included pain at the site, headache, fatigue, muscle aches/cramps, and fever. Less common were loss of taste/smell and appetite, increased hunger, urinary symptoms, nausea/vomiting, and rash.

Symptoms were reported as mild to moderate and mostly ignored (52.4%), although routine activity (44.4%) and sleep (33.5%) were hampered, and 13.6% were unable to go to work. Symptoms largely (39.8%) resolved within 2-3 days and 29.1% within 12-24 hours. The level of protection obtained from the vaccine was estimated at 41-60% by 29.4% of respondents, with 82.4% having received the 2nd dose with adverse reactions (53.7%), which was reported largely as more (30.4%) compared with the 1st dose.

Determinants of symptoms experienced were gender, age, body weight, blood group, anticipating side effects, ever having had a positive COVID-19 test, use of medication within 24 hours of vaccination, smoking, and use of alcohol within the last 6 months before vaccination. However, the use of alcohol was the only statistically significant factor (χ^2=0.024).

Conclusion: Symptoms experienced with the COVID-19 vaccinations were reported as common and mostly self-limiting and responded to the use of paracetamol.

Keywords: COVID-19, Vaccinations, Health Workers, Adverse Reactions, Infection Prevention and Control, Symptoms Experienced.

Biography

Dr. Tawakalit Olubukola Salam is a Consultant Family Physician at the University College Hospital, Ibadan, and Lecturer in Health Policy and Management at the University of Ibadan. With over a decade of leadership in clinical practice and public health, she holds multiple fellowships and advanced degrees, alongside specialized training in Sexual and Reproductive Health and Travel Medicine. She leads service improvement initiatives, mentors trainees, and contributes to global scholarship through peer review and ethics roles. An active member of several professional bodies, she is committed to women's health, preventive medicine, and community development. She is happily married.

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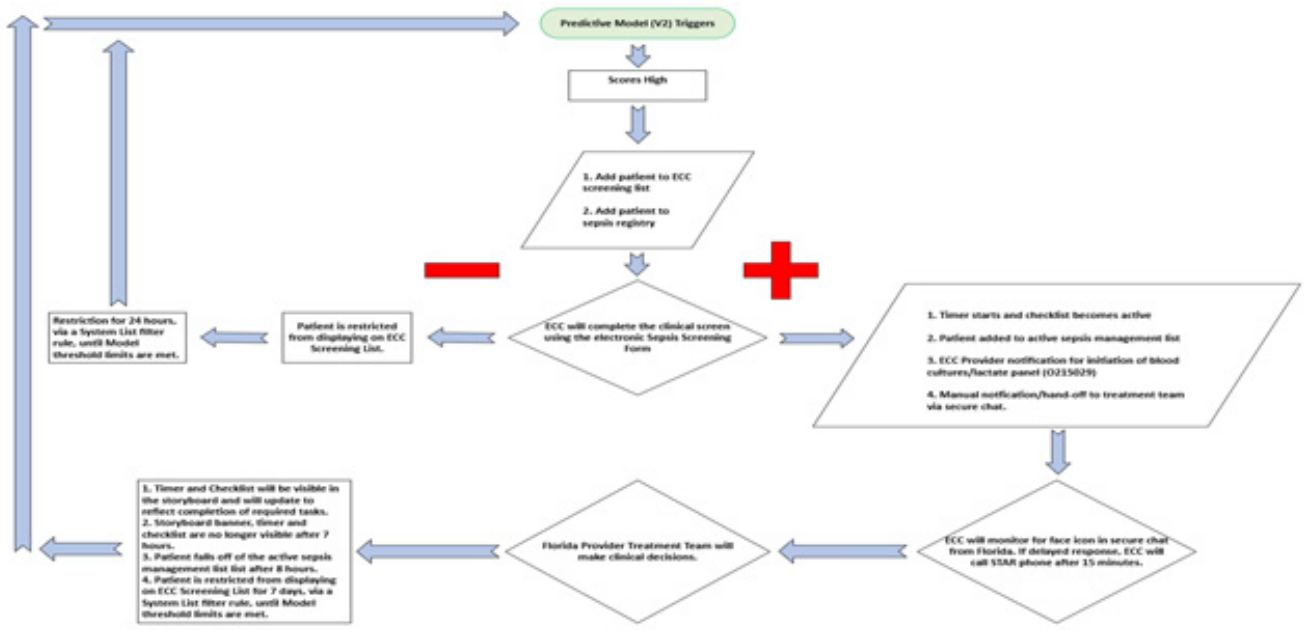
Sep-1 compliance metrics following the sepsis tool implementation project, utilizing the epic 2.0 sepsis prediction model

Mayo Clinic Florida (MCF) was one of the early adopters of Epic's 2.0 sepsis prediction tool nationwide. Beginning in early 2024, we launched the inpatient model, which included the implementation of an EHR integrated timer and checklist in July. These tools were deployed to support SEP-1 metric compliance as part of the Sepsis Tool Implementation Project (STIP).

SEP-1 is an all-or-nothing measure reflecting the organization's ability to deliver timed interventions within either a three or six-hour window, depending on the intervention item, for patients who are at high risk of sepsis. Early results indicate that the EPIC Sepsis Toolkit has aided in earlier detection of sepsis as well as delivering just in time reminders to providers to complete appropriate interventions in the designated timeframes. We are in the process of quantifying adherence to the three and six hour time windows from 2024-2025 to measure clinician uptake/buy in to STIP and the ability of the checklist and timer to improve performance on SEP-1 and patient outcomes.

We used the predictive model to alert an initial manual screening, conducted by our Enhanced Critical Care Registered Nurses (RNs), followed by onsite bedside care for patients manually screened as "possible sepsis" (Figure 1). There have been updates to our previous sepsis order sets and panels to improve documentation of clinical exceptions, and other lessons learned from this implementation that will inform similar efforts. We have also developed dashboard and reporting tools for both real time and retrospective tracking. The SEP-1 compliance for MCF has improved substantially since the inception of the STIP project, achieving 74.6% compliance in quarter 3 of 2024. We look forward to being able to share additional findings from the checklist and timer components of the STIP intervention with this audience.

Figure 1. Diagram demonstrating hospitalised patient sepsis workflow.



Biography

Terri Menser Ph.D., is a health services researcher in the Kern Center at Mayo Clinic Florida, focused on practice improvement and patient engagement. She specifically focuses her research on topics related to health disparities and chronic and complex disease management. Dr. Menser examines health outcomes based on differential treatments, interventions, and social determinants of health factors. She also assesses the implementation of care programs, targeted interventions, and artificial intelligence clinical decision aids. Dr. Menser collaborates with providers to develop interventions that engage and educate patients and their support networks to empower them and improve health outcomes.

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Coagulopathy, a hidden enemy in persistent organ dysfunction in post-septic rats

Background: Post-Sepsis Syndrome (PSS) affects up to 50% of survivors, with a mortality exceeding 82% at 5 years and annual costs exceeding $100 billion only in the United States. While immune dysregulation has dominated PSS research, coagulopathy emerges as a silent but critical driver of post-sepsis sequelae. However, mechanisms, biomarkers, and subsequently, therapies targeting PSS remain poorly characterized.

Objective: To evaluate the contribution of coagulopathy to organ dysfunction during the post-sepsis period.

Methods: Male Sprague-Dawley rats received Salmonella enterica serovar Typhi Outer Membrane Vesicles (OMVs) (n=17) or saline solution (n=11). Animals were euthanized at three temporal phases: Acute (6h), survivor (6d), and post-sepsis (20d) periods. Thirty-two parameters, including coagulation, renal, hepatic, immune, and metabolic markers were normalized as Z-scores against reference intervals from thirty untreated rats. An adapted SOFA score was used to define organ dysfunction. The predictive role of coagulopathy and associated markers was analyzed through relative risk (Fisher's exact), ROC/AUC, and logistic regression.

Results: OMVs induced organ dysfunction in 100% of animals at 6h (p=0.029) and 80% at 20d (p=0.048) versus 0% saline. SOFA trajectory showed a non-linear pattern, with 100% of animals presenting organ dysfunction at 6h, then a partial recovery at 6d, and re-emergence at 20d. INR independently predicted organ dysfunction (OR=6.6 [95%CI: 1.0–43.4], p=0.049;

AUC=0.903). Thrombocytopenia was the most persistent alteration on post-sepsis period (Cliff's δ=−1.0 at 20d), suggesting active platelet consumption by ongoing thrombus formation. Immune markers (LYMPHO% AUC=0.938; SEGMEN% AUC=0.920) and glucose (AUC=0.912) emerged as strong predictors of organ dysfunction, potentially attributable to NET formation, lymphocyte exhaustion, and hyperglycemia, possibly amplifying endothelial dysfunction and perpetuating the coagulopathic state.

Conclusions: Coagulopathy, specifically through elevated INR and thrombocytopenia, is associated with organ dysfunction during the post-sepsis period. Immune and metabolic dysregulation could act as amplifiers of these alterations. The S. Typhi OMVs model represents a robust platform for evaluating biomarkers and therapeutic strategies in post-sepsis syndrome.

Biography

Yolanda Prado is a biologist and Doctor in Molecular Biosciences. Currently a postdoctoral researcher at Universidad Andrés Bello, Chile. Her work focuses in three research lines: The pathophysiology of post-infectious sequelae, with a current focus on coagulopathy and organ dysfunction in post-sepsis syndrome; diagnostic and therapeutic innovation with a gender perspective in infectious diseases; and epidemiological surveillance of post-infectious sequelae at the territorial level.

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Decision-making regarding maternal vaccination: A multifactorial phenomenon from the perspective of pregnant women and healthcare staff

The WHO has identified vaccine hesitancy as one of the main threats to global health. Given that immunisation prevents around 4.4 million deaths worldwide each year, vaccination during pregnancy remains a key intervention for reducing the burden of disease in the first months of life and contributing to the achievement of maternal and neonatal survival targets.

Various studies indicate that vaccine hesitancy is not solely a matter of individual choice, but rather stems from the way in which emotions, knowledge and perceptions are shaped within specific social, institutional and territorial contexts. In Colombia, territorial and multi-ethnic diversity requires a multifactorial understanding of this phenomenon and its manifestation in specific practices of acceptance, delay or refusal of vaccination.

The CEIP is conducting a mixed-methods study, which began in May 2025, to understand decision-making regarding maternal vaccination from the perspective of pregnant women and healthcare staff, with a view to developing an intervention strategy. The study included the four cities with the highest maternal vaccination coverage and the four with the lowest coverage in Colombia. In the quantitative component, the GestVac questionnaire was designed and validated in the Colombian population, with 3,042 participants (1,570 pregnant women and 1,472 healthcare professionals); in the qualitative component, focus groups were conducted with 469 participants (274 healthcare professionals and 195 pregnant women).

In the questionnaire, pregnant women showed high adherence to the vaccination schedule (91.2%), attendance at appointments (85.7%), availability of the vaccine (85.3%) and receipt of information from healthcare staff (79.0%); lower proportions were observed in the active seeking

of information (52.6%) and in discussions with the doctor regarding concerns (58.7%). Among healthcare professionals, favourable practices centered on counselling and communication regarding maternal vaccination, including information on influenza (80.0%), Tdap (71.3%) and COVID-19 (74.1%), as well as guidance for family members (80.6%), the provision of educational materials (70.0%), recording in medical records (68.4%) and monitoring vaccination status (66.5%).

Regarding the qualitative component, the most frequently mentioned categories were knowledge regarding vaccination, unfavourable attitudes, favourable and unfavourable factors within the health system, healthcare provision, unfavourable sociocultural factors, access to vaccination, and proposals regarding receiving information and training. This highlights the need for an intersectoral approach that takes social determinants into account, enabling us to address vaccine confidence beyond education alone. This involves re-evaluating the influence of various stakeholders and creating multipliers who promote a culture of vaccination and informed decision-making.

Biography

Yurdey Fernanda Herrán Murillo is a PhD candidate in Psychology with dual training in Psychology and Nutrition and Dietetics from Pontificia Universidad Javeriana Cali. Her work integrates mental health, nutrition, and community-based research, focusing on food environments, social transformation and social determinants of vaccination. She has extensive experience in mixed-methods research, data analysis, and academic writing, contributing to high-impact publications and international conferences. She has led interdisciplinary projects, coordinated research teams, and supported evidence-based interventions in vulnerable communities. She currently teaches at the graduate level and actively promotes knowledge transfer, innovation, and participatory approaches to health and well-being.

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