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REVACC SCIENTIFIC

JOINT EVENT ON

VACCINES AND INFECTIOUS DISEASES

23-25 OCT, 2023

BOSTON, MASSACHUSETTS, USA

Venue:
Hilton Boston/Woburn 2 Forbes Road, Woburn,
Massachusetts, 01801, USA

BOOK OF ABSTRACTS

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23-25 OCT

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ABSTRACTS

JOINT EVENT ON

VACCINES AND INFECTIOUS DISEASES

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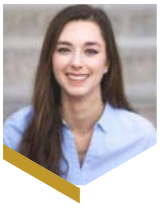
Medical University of Warsaw, Poland

Anju Kaushal
Member of New Zealand Organization For Quality, New Zealand

Austin Auyeung
University of Central Florida College of Medicine, United States

Brandon Lucke-Wold
Baylor University, United States



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Osmania Medical College, India

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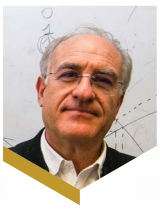

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University of Milan, Italy

Megha Priyadarshi
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Michael Silverman
Western University, Canada

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Nicole Vieira-Pires
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University of the Free State, South Africa

Nzolameso Makaya Jennifer
Medecin Generaliste, Democratic Republic of Congo

Olivia Viscuso
The University of Texas at Austin, United States

Paul Van Buynder
Griffith University, Australia

Rabab Elsadek
University of Central Florida College of Medicine, United States

Rahul Gomez
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Rahul Kumar
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University of Regensburg, Germany

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Istituto Zooprofilattico Sperimentale della Sicilia, Italy

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University of Wolverhampton, United Kingdom

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Stephen Brand
Mycovia Pharmaceuticals, United States

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Taipei Medical University, Taiwan

Thea Elisabeth Hein Petersen
Technical University of Denmark, Denmark

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International Clinical Laboratories, Ethiopia

Valeria Blanda
Istituto Zooprofilattico Sperimentale della Sicilia, Italy

Whegang Youdom Solange
University of Dschang, Cameroon

William Song
Ochsner Health System, United States

Anna Kloc
University of New Haven, United States

Speakers

Artemisia Ntoula
University of Crete, Greece

Chital Naresh
School of Health System Studies, India

Francesca Gucciardi
Istituto Zooprofilattico Sperimentale della Sicilia, Italy

Nhlayiso Atalia Maswanganyi
University of Limpopo, South Africa

Thank You All...

Welcome Message

Dear congress attendees, it is my pleasure to write a few words to welcome you. Surveillance of healthcare-associated infections is one of the main challenge for infection control in hospitals worldwide. Indeed, these infections are responsible for significant mortality and extra-costs, especially when due to antibiotic resistant pathogens. Surveillance systems are needed whatever the income level of the country and should be adapted according to the HAI and the patients groups. Information issued from the surveillance systems is to be fedback to both healthcare providers and decision makers for implementing public health actions and prevention. Automation of such system is crucial in making effective, simple, and user-friendly as well as not too expensive data surveillance for the healthcare system. The development of information technologies is the main challenge fort the next few years.

Astagneau Pascal

Sorbonne University, France

Welcome Message

Dear Infection 2023 Participants,

COVID-19 caused by SARS-CoV-2, with its devastating health, social, and economic consequences, has brought new and rapidly spreading infectious diseases to the attention of the global population. Success with rapidly developed COVID-19 vaccines has been crucial for saving innumerable lives and controlling this pandemic. COVID-19 has also spawned new understanding of mechanisms of infection and evasion of immunity by viruses and other pathogens that infect humans. The study of animal and plant pathogens has also seen much recent progress. I expect your participation in this international conference, and the exchange of ideas and information that accompanies it, to benefit your own research into advancing knowledge and teaching in infectious diseases.

Ranjan Ramasamy

IDFISH Technology, United States

Welcome Message

Dear esteemed colleagues and fellow researchers,

On behalf of the Organizing Commitee, I warmly welcome you to the 5th World Congress on Infectious Disease here in Boston. Participating in such a pivotal gathering of experts and passionate professionals from the global infectious diseases' community is truly an honor. As we delve into the rich academic and scientific sessions ahead, I eagerly anticipate the cutting-edge discussions, research revelations, and innovative strategies that will emerge. The dynamic nature of our field underscores the importance of events like this, ensuring we remain at the vanguard of medical and scientific progress. Together, we have the capacity to drive transformative change in patient care, disease prevention, and global health strategies. I invite all of us to embrace this moment, foster collaborations, and champion advancements in infectious disease management.

I wish all participants a rewarding and inspiring experience throughout the conference.

Sincerely,

Yongqing Li

University of Michigan Medical School, United States

Welcome Message

Esteemed Vaccinology Colleagues,

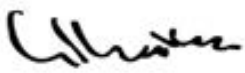
It's not just the bacteria or viruses that most commonly cause life-threatening disease in human, some of them could be fungal pathogens. Globally, over 300 million people are afflicted with a serious fungal infection Fungal infections kill more than 1.5 million people every year. That amounts to more than are killed by malaria, or breast cancer, and almost as many as those claimed by HIV or tuberculosis. The major burden of serious invasive fungal infection is borne by low- and middle-income countries.

The substantial morbidity and mortality rates highlight the relevance of developing effective vaccines to control fungal pathogens. Approximately, 80% of this mortality are due to infections caused by opportunistic fungi. Majority of these patients die due to fungal sepsis caused by uncontrolled fungal growth.

During my session, I will talk about the prevalence of fungal infections, category of vaccines, and challenges developing a fungal vaccine.

In participation, I hope to hear your experiences in the domain of your expertise and learn from you as well.

Hope to virtually meet you at IVC-2023.



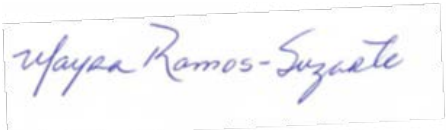
Regards,

Sudhakar Bangera

AILEEN Clinical Research Services, India

Welcome Message

Dear delegates of the “3rd Edition of International Vaccines Congress” (IVC 2023) the congress “SAVED: Spearheading Advancements in Vaccine Evolution and Development”. It is an honor and a pleasure to write you some welcome notes. The Covid-19 pandemic has subjected us to indescribable challenges in the last three years to save humanity. We had to reposition knowledge in order to stop the severity of this disease and reformulate the way we find vaccines and therapeutic options in record time. The development achieved up to 2019 in biotechnology allowed us to stop this phenomenon and has left us with new methodologies for future actions. On the other hand, chronic non-communicable diseases have been taking over the world not only due to population aging but also due to social development itself that leads to changes in our planet that challenge the human species to survive in it, with inevitable changes in the systems Biological at all levels. We are here to exchange experiences, learn from everyone and propose new prophylactic, therapeutic and technological alternatives. No matter where we come from, humanity demands more of us to survive. Let's give him then not only hope but the tools to do it. Together we can achieve it.



Mayra Ramos-Suzarte

Center of Molecular Immunology, Cuba

Welcome Message

Dear fellow researchers, physicians, and distinguished guests,

On behalf of the organizing committee, it is my pleasure to extend a warm welcome to the World Congress on Infectious Diseases 2023. This congress brings together leading experts, researchers, and healthcare professionals from around the globe to share their knowledge and expertise on the latest advances in the field of infectious diseases.

As a member of the scientific committee and the session chair for the Infection, Immunity, and Inflammation session, I am excited to engage in stimulating discussions and explore new insights into the basic research, diagnosis, prevention, and management of infectious diseases and inflammation. Our aim is to provide a platform for interdisciplinary exchange of ideas, which we hope will lead to new and innovative solutions for the global health challenges we face.

We have prepared a comprehensive program featuring keynote speakers, oral presentations, and more, as well as a range of networking opportunities for you to connect with your peers and colleagues. I am confident that this congress will inspire fruitful collaborations and provide a platform for new and meaningful relationships to be formed.

Thank you for being a part of this important event, and I wish you all a productive and enjoyable congress.

Cheers!

WenQing Yang

Clinbridge Biotech Co. Ltd, China

Welcome Message

Dear Delegates at WCID 2023, I gives me immense pleasure welcome you in this very prestigious infectious diseases meeting. Lectures and presentations from renowned ID specialist is the hallmark of this meeting. I am sure you will enjoy attending these discourses. Do not forget to visit the beautiful sites of this academic city Boston. Although it is a hybrid meeting, I urge you to attend this meeting physically and meet the bigwigs of Infectious Disease. It is a wonderful opportunity to keep abreast with the new knowledge in the field of infectious diseases.

Shyam Sundar

Banaras Hindu University, India

ABOUT
MAGNUS GROUP

Magnus Group (MG) is initiated to meet a need and to pursue collective goals of the scientific community specifically focusing in the field of Sciences, Engineering and technology to endorse exchanging of the ideas & knowledge which facilitate the collaboration between the scientists, academicians and researchers of same field or interdisciplinary research. Magnus Group is proficient in organizing conferences, meetings, seminars and workshops with the ingenious and peerless speakers throughout the world providing you and your organization with broad range of networking opportunities to globalize your research and create your own identity. Our conferences and workshops can be well titled as 'ocean of knowledge' where you can sail your boat and pick the pearls, leading the way for innovative research and strategies empowering the strength by overwhelming the complications associated with in the respective fields.

Participation from 120 different countries and 2000+ different Universities have contributed to the success of our conferences. Our first International Conference was organized on Oncology and Radiology (ICOR) in Dubai, UAE. Our conferences usually run for 2-3 days completely covering Keynote & Oral sessions along with workshops and poster presentations. Our organization runs promptly with dedicated and proficient employees' managing different conferences throughout the world, without compromising service and quality.

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The expertise of ReVacc Scientific is manufacturing pseudovirus reporter, a tool to evaluate vaccine efficacy, screen drugs (including neutralizing antibodies) or study viral entrance mechanism. We have multiple technologies for the development of pseudovirus reporter, covering fields of Arenavirus, Coronavirus, Filovirus, Flavivirus and more. Besides, test kit, antibody and recombinant protein products are available.

Besides products, we provide services, including 1), Customized pseudovirus generation; 2), Customized protein generation; 3), Antibody discovery and 4), Neutralizing antibody titer evaluation.

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DAY 01

KEYNOTE FORUM

JOINT EVENT ON

VACCINES AND INFECTIOUS DISEASES

Ongoing journey – targeting citrullinated histone H_3 ($CitH_3$) for early diagnosis and treatment of sepsis

Over the past decade, my research team and I have dedicated our efforts towards studying protein post-translational modifications with the goal of early diagnosis and treatment of sepsis. Our comprehensive and intensive research has culminated in the publication of approximately 40 manuscripts on the topic (click to see our sepsis project).

Citrullination of histone H_3 by nuclear-localized Peptidylarginine Deiminase (PAD) is recognized as an early phase in a distinct form of cell death, known as "neutrophil extracellular traps" or NETosis. Histone H_3 citrullination acts as a convergence point for a variety of inflammatory signals, triggering the neutrophil response to infections. Hyper-citrullinated histone H_3 ($CitH_3$) is detected in immune cells and the bloodstream during sepsis (infectious), but not subsequent hemorrhagic shock (non-infectious), according to rodent models and human studies (our preliminary data). Furthermore, septic mice treated with a pan-PAD inhibitor or an anti-$CitH_3$ antibody exhibit a significant improvement in survival, thereby illuminating the pathway for the proposed clinical discovery study.

Our team initially pinpointed $CitH_3$ as a potential serum protein biomarker in a lethal mouse model subjected to Lipopolysaccharide (LPS)-induced shock in 2011. Since then, we have persevered in this research direction, generating substantial data that reinforces the notion of $CitH_3$ acting not only as a biomarker but also as a contributing factor for endotoxic/septic shock and associated organ damage.

Over the past decade, we have tackled a substantial concern regarding the use of commercial anti-$CitH_3$ antibodies in research. A range of studies highlighted the limitation of commercially available $CitH_3$ monoclonal Antibody (mAb) (with the epitope of 3 Cit at R2/R8/R17) in accurately quantifying serum $CitH_3$ levels. This antibody has been employed to link $CitH_3$ with advanced cancer patients displaying an intensified inflammatory response, suggesting its potential as a diagnostic and prognostic blood marker. Nonetheless, the conflicting findings reported in these studies are predominantly due to the limitations inherent in the commercial antibody.

One significant contribution from our lab is the development of a novel anti-$CitH_3$ antibody, which contains an epitope of 4 Cit at R2/R8/R17/R26 and offers a more precise diagnosis and prognosis of sepsis. This $CitH_3$ mAb (4 Cit) recognizes epitopes on $CitH_3$ generated by both PAD4 (R2/R8/R17) and PAD2 (R26). Our team has proven that this antibody can enhance survival rates in a mouse sepsis model. Upon evaluating the specificity and sensitivity of our $CitH_3$ mAb (4 Cit), we found it to be superior to the commercial $CitH_3$ mAb (3 Cit) in specificity. Our antibody

Yongqing Li MD, PhD*, Hasan B. Alam MD, FACS

University of Michigan Medical School, United States of America

Biography

Dr. Yongqing Li, M.D., Ph.D., is an Associate Professor of Surgery, the University of Michigan Medical School at Ann Arbor, Michigan. He obtained his M.D. and M.S. in Pharmacology in China before earning a Ph.D. in Biochemistry and Molecular Biology from the University of Miami School of Medicine. His postdoctoral training was completed at the University of North Carolina at Chapel Hill and Harvard Medical School. Subsequently, he was appointed as an Instructor of Medicine at Harvard, leading a scientific team until 2003. In 2005, he joined the Department of Surgery at Massachusetts General Hospital (MGH). In 2011, Dr. Li was promoted to Assistant Professor of Surgery at Harvard Medical School, where he also served as the Director of the Trauma Surgery Research Laboratory at MGH. He joined the University of Michigan (UM) in 2013. Dr. Li's academic career began with cancer research in the 1990s, and his work has been recognized in prestigious journals. Since 2005, his focus has shifted to the pharmacological treatment of sepsis, traumatic hemorrhagic shock, and traumatic brain injury (TBI), with a special emphasis on

binds to all circulating $CitH_3$ produced by PAD2 and PAD4, thereby addressing the deficiency of commercial $CitH_3$ antibodies. In fact, our antibody fills the void identified by Neeli and Radic in their research on citrullinated histone antibodies (Current Challenges and Limitations in Antibody-Based Detection of Citrullinated Histones, Frontiers in Immunology, 2016). Utilizing an assay based on our $CitH_3$ mAb (4 Cit), we established that $CitH_3$ is a dependable blood biomarker for the diagnosis and treatment of endotoxic shock (Pan et al. Scientific Reports 7: 8972 PMID: 28827548; Deng et al. Frontiers in Immunology. 2020;10: 2957. PMID: 32943500). Other scientists have noted in Commentary that our findings could facilitate early detection and monitoring sepsis progression.

We've created a sandwich Enzyme-Linked Immunosorbent Assay (ELISA) utilizing our novel $CitH_3$ mAb as the capture antibody. This ELISA shows greater sensitivity in comparison to commercially available ELISA kits. Utilizing our kit, we've recently shown that $CitH_3$ levels can effectively distinguish between patients with septic and non-septic shock, as well as correlate with the severity of the disease. These recent findings have been published in Infection.

The University of Michigan (UM) holds the patent for this innovative $CitH_3$-ELISA kit and is actively collaborating with a pharmaceutical company to bring it to clinical use. The successful commercialization of this kit will significantly benefit the University. Concurrently, we have partnered with Dr. Katsuo Kurabayashi's team from the Department of Mechanical and Aerospace Engineering at NYU Tandon School of Engineering. Together, we have engineered an integrated plasmo-photoelectronic biosensor for the rapid detection (within 15 minutes) of the $CitH_3$ biomarker. This biosensor aids in the prompt diagnosis of sepsis in mice, as discussed in our publication in Small, and it holds promise for clinical applications in point-of-care precision medicine.

Beyond the creation of a novel anti-$CitH_3$ mouse monoclonal Antibody (mAb), we've also developed a humanized version of the $CitH_3$ mAb ($hCitH_3$ mAb). Our findings indicate that the $hCitH_3$ mAb demonstrates a significantly stronger binding affinity to Citv when compared with the control mAb.

histone modifying enzymes. His team developed a novel antibody against citrullinated histone H_3 ($CitH_3$), distinct from commercially available variants. His pioneering work on $CitH_3$ for early diagnosis and treatment of sepsis is currently under clinical translation.

Surveillance of healthcare-associated infections: New challenges for the next decade

Healthcare-Associated Infections (HAI) are one of the most frequent adverse events in hospitalized patients. Their potential outcomes could be fatal or severe and represent a significant disease burden. In addition, a part of HAI is due to Multidrug-Resistant Organisms (MDRO), which extension represents a threat for both the hospital and the community. For the last three decades, most HAI and AMR pathogens are targeted by Infection Control (IC) programs in many countries including European countries. Since surveillance is historically the trigger for launching IC programs, the World Health Organization (WHO) has reminded recently that an HAI surveillance system is crucial for both national and hospital IC programs, being one of the eight core components defined for effective HAI control (Storr J, Antimicrob Resist Infect Control 2017, 6:6). The surveillance systems which are rolled varies according to the HAI targeted (Surgical-Site Infections (SSI), bloodstream infections, ventilator-assisted pneumonia, Antimicrobial Resistant Pathogens (AMR)), patient groups and allocated resources. However, they are all fostered to develop feedback and automation using Information Technology (IT).

Surveillance systems are aimed to provide evidenced-based information for acting and orienting prevention. Therefore, the feedback of surveillance data to caregivers and policymakers is a key issue to decrease HAI and AMR incidence rates. For decades, many surveillance networks at the national level have demonstrated that participation can truly contribute to a reduction of HAI or AMR rates (Abbas M, J Hosp Infect, 2019, 102:267e76). However, to get stakeholders' adhesion to a surveillance program presupposes the existence of a simple, effective, and reactive system. The main issue is then to develop a user-friendly system for caregivers, which will not be too time-consuming, but also informative for decision makers, and yet, not too costly in terms of human and financial resources. To date, different countries propose pilots of automated surveillance systems based on the methods of the PRAISE European initiative (Providing a roadmap for automated infection surveillance in Europe) (Van Mourik MSM, Doi: 10.1016/j.cmi.2021.02.028). In this context, France has launched at the national level different automated surveillance systems focus primarily on SSI and AMR.

Overall, the future development of automated HAI surveillance systems depends primarily on the ability of the hospitals to get their own resources and expertise in IT, but also on the awareness of healthcare staff to be involved in infection control.

Astagneau Pascal

Centre for Prevention of Healthcare-Associated Infections (CPIAS), Institute of epidemiology and public health, INSERM / Sorbonne University, Paris F75013, France

Biography

Prof. Astagneau is medical doctor, infectious diseases specialist, graduate at Pitié-Salpétrière School of medicine, Paris, in 1991, and received a PhD degree in epidemiology and public health in 1994. His main research activity focused on infection control (more than international 150 publications - ref. ORCID). He is now professor of medicine, head of the Centre for prevention of healthcare-associated infections and associated researcher at the Institute of epidemiology and public health at Sorbonne University, Paris, France. He participates to infection control initiatives at the Ministry of health, Public Health France, and the European Centre for disease prevention and control.

Audience Take Away Notes

- To update knowledge of HAI in terms of magnitude, trends and burden
- To improve knowledge about HAI surveillance systems existing in different countries
- To better understand the potential benefits and limits of automated surveillance in hospital settings
- To discuss perspectives and future of such systems

BOOK OF ABSTRACTS

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23-25 OCT

DAY 01

SPEAKERS

JOINT EVENT ON

VACCINES AND INFECTIOUS DISEASES

Jacob F. Kocher Ph.D*, Tammy Carrea, M.S., R.A.C, David Emerson Ph.D., Jonathan Smith Ph.D., Nathan Stasko Ph.D., Max Stockslager Ph.D., Thomas M. Womble M.S., John McNeil M.D., Ph.D

EmitBio Inc; Morrisville, NC, USA; 2Adaptive Plus LLC; Durham, NC, United States of America

A phase II, randomized, sham-controlled dose-finding study of the RD-X19 treatment device in individuals with mild-to-moderate COVID-19

The EmitBio RD-X19 is a handheld, self-administered device that delivers doses of 425 nm visible light to the posterior oropharynx and surrounding tissues to serve as a potential new treatment option for outpatients with COVID-19. A Phase II, sham-controlled dose-finding study was conducted in 216 subjects at nine clinical sites across the United States in order to (1) evaluate the safety and efficacy of the RD-X19 in ascending doses and (2) identify a suitable subject population and dose for a subsequent pivotal trial. Enrolled subjects had mild-to-moderate COVID-19 with at least two moderate or greater symptoms <72 hours from onset and a positive SARS-CoV-2 rapid antigen test. Subjects were randomized to receive the RD-X19 device delivering either 24 J/cm2 (Cohort A) or 32 J/cm2 (Cohort B) or a sham device. RD-X19 and sham treatments were delivered in five-minute doses twice daily for seven days. Eight COVID-19 symptoms were self-evaluated daily on a numeric score ranging from absent (0) to severe (3) and were monitored for 14 days. The primary efficacy endpoint was the time to the sustained resolution of COVID-19 signs and symptoms (defined as all symptoms being scored as absent (0) or mild (1) and remaining at this level through Day 14) in mild-to-moderate or mild COVID-19 subjects.

No serious treatment-related adverse events were observed among subjects receiving the 32 J/cm2 (highest) light dose; this dose was found to be well-tolerated when compared to sham. Measures of the primary efficacy endpoint were not statistically significant in the full analysis set; however, a treatment benefit was observed in subjects with mild COVID-19. Consistent with studies of other COVID-19 therapies where greater treatment was observed in older subjects, post-hoc analyses suggested the greatest treatment benefit was in subjects aged 40 years or older with “FDA/NIH” definition of mild COVID-19 (hazard ratio 0.343; median times to sustained symptom resolution 111 hours [active] vs. 188 hours [sham]; N = 40 subjects; nominal log-rank p = 0.008). Quantitative PCR assessments of SARS-CoV-2 viral load at each visit and change in α and β diversity in microbial flora from baseline on day 8 and day 14 as analyzed by 16S rRNA subunit analysis will also be presented. Importantly, there was a greater reduction in the SARS-CoV-2 nasopharyngeal viral load in subjects treated with RD-X19 compared to sham at all timepoints with no corresponding disruption of the oral microbiome.

Audience Take Away Notes

- Certain wavelengths and doses of visible light have antiviral effects by inactivating cell-free SARS-CoV-2 and reducing viral titers in productive infection models of the human airway
- In a clinical study, visible light (425 nm) had antiviral effects at doses that did not disrupt the oral microbiome
- In the same clinical study, symptomatic relief was greatest in subjects ages 40 and above with mild COVID-19 when compared to the sham control. Age has been shown to be both a predictive and prognostic indicator for treatment benefit for COVID-19 therapeutics

Biography

Dr. Kocher is the Director of Virology at EmitBio and is responsible for the preclinical evaluation of EmitBio's proprietary visible-light based technology platform targeting upper respiratory viruses. He conducted his post-doctoral training in Dr. Ralph Baric's group in the Gillings School of Public Health at the University of North Carolina at Chapel Hill. Prior to his post-doctoral work with betacoronaviruses (MERS-CoV and SARS-CoV), he obtained his Ph.D. in Biomedical and Veterinary Sciences from the research group of Dr. Lijuan Yuan at Virginia Polytechnic Institute and State University studying norovirus. He received his B.S. in Biology from St. Vincent College.

William Song M. D[1]*, Raina Saxena D. O[2], Rebecca Bernheimer B. A[2], Rubina Khan M. D[3], Jose Posas III M. D[4]

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[4]Department of Neurology, Ochsner health System, New Orleans Louisiana, United States of America

A case of SARS-CoV-2 induced guillain-barre syndrome in a patient with concurrent bacterial infection while undergoing chemotherapy

Guillain-Barre Syndrome (GBS) represents a spectrum of lmmune-mediated neuropathies that affect 1 to 2 in 100,000 people annually worldwide. Known triggers include infections, vaccinations, trauma, bone marrow transplants, systemic diseases, and medications. Recently, SARS-CoV-2 infection has emerged as an etiology for GBS as well as other neuropathies.

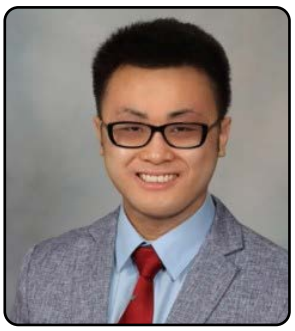
A 68-year-old woman undergoing neoadjuvant chemotherapy for breast cancer was admitted to the hospital with gait abnormality and bilateral lower extremity numbness and paresthesias. She had recently been hospitalized for sepsis due to SARS-CoV-2 and Klebsiella pneumoniae Urinary Tract Infection (UTI); she received remdesivir and ceftriaxone therapy for 3 days and she was discharged on ciprofloxacin. Notably, she was fully vaccinated agalnst SARS-CoV-2, however she was overdue for a booster dose. She subsequently developed worsening weakness of both lower extremities that ascended to involve her upper extremities as well. Lumbar Puncture (LP) Showed Cerebrospinal Fluid (CSF) studies consistent with albuminocytologic dissociation; combined with the clinical progression, we diagnosed her with GBS. Plasmapheresis was initiated and she responded well.

In this case, the patient's diagnosis was complicated by several factors that could be potential triggers for GBS. Notably, her recent SARS-CoV-2 infection was the most likely trigger, however further study is warranted to determine the impact of SARS-CoV-2 severity and vaccination status on the development of GBS. We also considered if 1) concomitant Klebsiella pneumoniae lnfection, 2) concurrent use of paclitaxel, a chemotherapy agent known to cause peripheral neuropathy, and 3) chemotherapy-induced pancytopenia could have increased the risk of GBS in this patient with SARS-CoV-2 infection.

Objective: To describe the clinical course of SARS-CoV-2-induced GBS. To illustrate the increased risk of developing GBS in patients with concurrent bacterial infections. To illustrate the increased risk of developing GBS in patients concurrently undergoing chemotherapy. To raise awareness of the increased risk of developing GBS in patients with chemotherapy-induced pancytopenia.

Biography

William Song, M.D. is a resident physician in Internal Medicine at the Ochsner Clinic Foundation in New Orleans, Louisiana, United States. He is clinically interested in the fields of infectious diseases, oncology, and critical care medicine.



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A case of leprosy in North Florida

Introduction: The global prevalence of leprosy, also known as Hansen's disease is <1/10 000, with the majority of new cases in India, Brazil and Indonesia. It can be broadly categorized as tuberculoid or lepromatous based on histopathological analysis. The USA continues to have approximately 200 new cases a year, concentrated in the southern states and data suggest that leprosy may be endemic to Florida. Human-to-human contact is a potential mode of transmission. However, exposure to armadillos and the Eurasian red squirrel have also been linked to zoonotic spread. We present a case of leprosy in North Florida without travel to an endemic area, contact with a known case or zoonotic exposures.

Case Presentation: A 55-year-old female, living in North Florida, presented with lesions on her arm that she noticed a year ago. Initial biopsy and clinical examination revealed probable granuloma annulare. Twelve months later, the patient was informed that the initial biopsy was positive for Hansen's disease and she was recalled for follow up and additional biopsies, which confirmed this diagnosis.

Past history was negative for direct exposure to armadillos, gerbils or squirrels. She denied any international travel or exposure to known cases of Hansen's disease. She had previously lived in central Florida where there was an infestation of tree rats in the attic of her house. She currently lives with two dogs, works in finance and denies participating in any outdoor occupational or recreational activities.

Physical examination revealed multiple itchy macules and patches with central clearance and erythematous borders on the right arm and shoulder. She reported right knee swelling and pain but denied hypoesthesias over the lesions, fever, chills or abdominal pain.

Serum vitamin D levels were in the optimal range, and negative for hepatitis and TB. Patient was prescribed rifampin 600 mg, moxifloxacin 400 mg and minocycline 100 mg monthly.

One month later, new lesions were noted on the arms, forehead and right foot. Treatment plan remained unchanged. At the two-month follow-up visit, number and size of lesions remained unchanged, but she reported paresthesias in her hands. Adjunctive methotrexate and low dose prednisone were added to the patient's regimen.

Discussion and Conclusion: Cases of leprosy in the USA have doubled since 2000, concentrated in the southeastern states. Our patient did not have any of the traditional risk factors, including travel to an endemic area, exposure to armadillos, squirrels, contact with someone who has been to an endemic area or a confirmed case of leprosy. This case adds to the body of literature that supports leprosy being endemic to Florida. Travel to Florida should be considered when investigating for leprosy within the USA, in addition to the typical risk factors. Given the slow progression of leprosy, the possibility of other undiscovered zoonotic reservoirs should also be considered.

Audience Take Away Notes

- Leprosy, also known as Hansen's disease is an ancient chronic bacterial disease caused by Mycobacterium leprae or Mycobacterium lepramotosis. While the majority of new cases are in India, Brazil and Indonesia, the United States continues to have approximately 200 new cases a year concentrated in the southeastern states. We present a case of leprosy in North Florida without travel to an endemic area, contact with a known case or zoonotic exposures, providing further evidence that leprosy is now endemic to Florida.

Biography

Austin Auyeung graduated from the Royal College of Surgeons in Ireland in 2022. He is currently an Internal Medicine resident physician at the University of Central Florida College of Medicine, Graduate Medical Education / HCA Florida North Florida Hospital.

Rebecca Yao M.D., M.P.H[1]*, Priscila Santiago Liberato de Mattos M.D[2], Karan Chohan M.D[1], Mary Labib M.B., B.Ch., B.A.O., M.D[1], Karthik Ravi, M.D[2]

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Disseminated histoplasmosis presenting as isolated acute liver injury: A case report

The various manifestations of disseminated histoplasmosis can involve nearly any organ system, including the CNS, skin, and adrenal glands. We present a case of disseminated histoplasmosis in an immunocompromised host presenting with isolated acute liver injury.

A 59-year-old woman from Minnesota with a history of pulmonary sarcoidosis on methotrexate and infliximab presented with a 10-day history of fevers, myalgias, and generalized weakness. Symptoms were associated with nausea and small volume emesis, without abdominal pain, constipation, or diarrhea. A week prior to presentation, she was evaluated in the urgent care setting with laboratory work demonstrating AST 106 IU/L, ALT 105 IU/L, total bilirubin 1 mg/dl, alkaline phosphatase 203 IU/L. Hepatic biochemistries had never previously been outside of normal range. She was initiated on a course of doxycycline for suspected sinusitis and continued on acetaminophen for symptom management, however, symptoms continued to worsen. On presentation, she was febrile to 39.2oC, in moderate distress with marked nausea and dry heaves, mild conjunctival icterus, and unremarkable abdominal exam. Lab work revealed mixed hepatocellular and cholestatic liver injury with ALT 599 IU/L, AST 608 IU/L, total bilirubin of 2.3 mg/dl, ALP 585 IU/L, and INR 1.3. CT chest/abdomen/pelvis demonstrated splenomegaly along with stable features of pulmonary sarcoidosis. Right upper quadrant ultrasound revealed a normal-appearing liver with patent hepatic vasculature. Prior medications were held due to concern for drug-induced liver injury. In the context of her immunosuppression, a broad infectious and autoimmune workup was performed, ultimately revealing positive histoplasmosis urine antigen further confirmed by consistent Histoplasma antigen and antibody positivity in the blood. Ferritin was also measured and found to be over 36,000 mcg/L, raising suspicion for Histoplasmosis-induced hemophagocytic lymphohistiocytosis. She clinically improved on IV amphotericin B and was transitioned to long-term itraconazole after two weeks.

Discussion: Histoplasmosis presents in many forms and is most commonly asymptomatic in immunocompetent hosts. Immunosuppression, particularly secondary to solid organ transplant, HIV, or TNF-α inhibitor therapy, significantly increases the likelihood of developing disseminated histoplasmosis. Though hepatic involvement is common in disseminated histoplasmosis, it is rarely seen in isolation, particularly in the absence of pulmonary findings. As the fatality rate of untreated disseminated histoplasmosis in an immunocompromised patient is 100%, a high index of suspicion for disseminated histoplasmosis is necessary for those who present with fever of unknown origin, jaundice, elevated liver enzymes, or other features of acute or chronic liver disease.

Biography

Rebecca Yao graduated from Drexel University College of Medicine in 2021. She currently is an Internal Medicine resident physician at Mayo Clinic Rochester.

Benoît LEVAST
BIOASTER, LYON, FRANCE
HCL, LYON, FRANCE
ULB, BRUXELLES, BELGIQUE

System serology approach on COVID-19 patients' sera reveal specific immune pattern in the heterogeneous population: The COVIDAuRA study

The emergence of multiple SARS-CoV-2 variants as well as the implementation of different vaccination strategies gave rise to multiple immunization schemes in the population and related questions: which immunization strategy leads to the most effective long-term immune response against SARS-CoV-2? What is the impact of the emergence of new variants? To this aim, we evaluated the humoral immune response 6 months post last immunization (infection or vaccination) in nine groups of individuals with different immunization schemes:

Group number	Name	Short name
1	Convalescent mild patients	ConMild
2	Convalescent severe patients	ConSev
3	Vaccinated Convalescent: ChAdOx1-S-nCoV-19 vaccine only	Con-ChAd
4	Vaccinated Convalescent: BNT162b2 vaccine only	Con-BNT
5	Vaccinated Convalescent: BNT162b2 vaccine – 2 doses	Con-BNT(2)
6	Vaccinated Naïve: ChAdOx1-S-nCoV-19 and BNT162b2 vaccines received	ChAd-BNT
7	Vaccinated Naïve: BNT162b2 vaccine – 2 doses	BNT(2)
8	Vaccinated Naïve: BNT162b2 vaccine – 3 doses	BNT(3)
9	Vaccinated Breakthrough Infection	BNT-BA.1

This study was conducted on 180 individuals from different cohorts subdivided into: i) convalescent patients after severe or mild COVID-19 during the first wave of the pandemic. ii) vaccinated convalescent patients (after mild COVID-19 during the first wave of the pandemic) who received either one dose of the adenoviral-based vaccine ChadOx1, or one/two doses of the Pfizer BNT162b2 mRNA vaccine. iii) COVID-19 naïve individuals fully vaccinated with two or three doses of BNT162b2 or one dose of ChadOx1 followed by one dose of BNT162b2. iv) individuals vaccinated with two or three doses of the BNT162b2 vaccine followed by a breakthrough infection during the Omicron BA.1 wave. The humoral immune response of each individuals was monitored at 6 months post last immunization, i.e. 6 months post infection or last vaccine dose. We performed anti-RBD IgG titers, neutralization activity, ADCC activity and Fc binding analyses on sera samples. A multivariate analysis of the different technologies provided a comprehensive description of the immune status of individuals at 6 months post last immunization. The results could potentially help to better identify vaccination strategies for the different populations.

Audience Take Away Notes

- SARS-CoV-2 serology; anti-viral immunity; vaccination strategy
- Next SARS-CoV-2/viral epidemic management
- Patients management from a clinicians standpoint
- Yes, from technological point of view to scientific knowledge

- The results provide information for the management of populations considering next pandemic events (notion of rationale vaccine selection; better address heterologous approaches)
- It provides new information to assist vaccination strategy design
- List all other benefits
    - The presentation aims to identify technologies of interest to drive serological analyses in the context of COVID-19 epidemiology and variants of concern. The results and further analyses of correlates of protection could support the rationale selection for vaccine characterization & formulation

Biography

Dr. Levast studied Chemistry at the Grenoble1 University, France and graduated as MS in 2006. He received his PhD degree in 2010 at the François Rabelais University of Tours within the INRAE institute. After five years of postdoctoral fellowship at VIDO, University of Saskatchewan, to study PRRSV vaccination in swine; and at McGill to study immunity against S. aureus, he joined MaaT Pharma in 2016 to develop gut-derived microbiotherapeutics in infectious and oncological diseases. He joined BIOASTER in 2022 as project lead in the vaccines program.

Regina Au
BioMarketing Insight, Boston, Massachusetts, United States of America

Lessons learned from the Covid-19 vaccine and what is needed when developing a vaccine for a successful rollout

When the COVID-19 Vaccine was developed, time was crucial and the pharmaceutical and biotechnology companies primary goal was to get a vaccine out as soon as possible so people to get vaccinated in saving lives. What wasn't considered which most large companies conduct and develop, was the Target Product Profile (TPP) from a business/commercial perspective which looks at safety, efficacy and compliance for all stakeholders to achieve product adoption. This includes healthcare institutions and professional who administer the vaccine, and the patients and front line works acceptance or willingness to get the vaccine.

For example, the vaccine originally had to be stored in an ultra cold freezer 90°C and -60°C (-130°F and -76°F) which required special freezers that many of the healthcare institutions did not have and they had to buy one which was an unanticipated cost for the institution. This also delayed the rollout of the vaccine.

Vials at room temperature or once punctured had to be used within 12 hours, creating potential waste if not used within this time. While there was an initial surge of patients wanting to get the vaccine, once these patients were vaccinated, the people signing up for the vaccine, dramatically dropped. Some places were taking walk-in vs. appointments only, or asked people if they knew others who wanted to get vaccinated so that the vaccine wouldn't be wasted.

The challenges were magnified significantly during the pandemic to demonstrate the importance of incorporating a business/commercial TPP. While the COVID-19 vaccine was an exception to the rule because time was of essence in saving lives, these challenges could have been mitigated or reduced during product development for non-pandemic vaccines. Even if a pandemic has already occurred, future pandemic preparedness in planning the TPP (R&D and business) can still be done ahead of time.

Find out more on the lessons learned in how to develop a better vaccine for a successful rollout and uptake of the vaccine by patients and other front line workers.

Audience Take Away Notes

- The audience can incorporate the lessons learned from the COVID-19 vaccine rollout and uptake by patients into their product development process by defining a business TPP that will address the issues encountered during the COVID-19 vaccine rollout and acceptance
- The results are greater uptake of the vaccine which translates into greater sales revenue and setting the bar that other vaccine companies or competition have to meet in order to be successful
- The end result is that each company will strive to develop better vaccines over the other companies
- This will help everyone involved in the product development process and the commercial group once the product is launched in being successful

- List all other benefits
    - Having a strong TPP (R&D and business) helps the commercial/marketing group deliver a stronger and better message on the safety and efficacy of the vaccine to enhance acceptance and uptake of the vaccine and reduce hesitancy or rejection. More will be covered in the presentation

Biography

Regina Au, CEO at BioMarketing Insight with 20+ years experience in the life science industry. She helps companies define their target product profile (TPP) to be able to compete in the market and be better in meeting the company's goals. Ms. Au was a member of the Advisory Board for Regis College Master of Regulatory and Clinical Research Management Program, an Adjunct Professor at Northeastern University in the Biotechnology Program and currently on the Editorial Board for the International Journal of Clinical Pharmacology & Pharmacotherapy. She has published over 22 articles in scientific and business journals and given 29 presentations at international conferences. Regina has a BS in microbiology from the University of Michigan, an MBA in Marketing from the University of Connecticut and a Masters in International Management from Thunderbird, Global School of Management.

Khursheed Anwer*, Subeena Sood, Majed, Meredyth Kinsella, Jessica Kim, John Henderson, Olivia Signer, Jeff Sparks, Joseph Rogers, Kempaiah Rayavara, Jean Boyer

IMUNON Inc., Huntsville, Alabama, United States of America

A DNA-based vaccine technology independent of a virus or device

This presentation describes the development of PLACCINE a novel DNA vaccine platform well-suited to overcome the limitations of the current vaccines. The PLACCINE platform leverages the inherent DNA advantages including design flexibility incorporating multi-antigen payload, durable antigen expression, strong cellular responses, stability at working temperatures (> 4C), and a rapid, scalable, and economical manufacturing process. A PLACCINE-based vaccine is independent of virus or device for delivery and is based on a plasmid DNA vector containing single or multiple antigens of a pathogen, a synthetic DNA delivery system, and an adjuvant. Proof of concept of monovalent and bivalent SARS-CoV-2 PALCCINE vaccines following prime and boost have been demonstrated in multiple animal models including rodents and non-human primates with the evidence of humoral and cellular responses and protection against viral challenge characterized by >95% clearance. The quality of immune response in mice or protection in non-human primates was comparable to a commercial mRNA vaccine with durable response maintain for at least up to 8 months. Analysis of cellular response showed increases in CD4 and CD8 cells in PLACCINE-vaccinated animals at higher cellular density than a commercial mRNA vaccine. Comparison of a single dose PLACCINE vaccine with an mRNA vaccine against a SARS-CoV-2 strain showed longer lasting antibody titers with the PLACCINE vaccine. The application of PLACCINE platform has also been demonstrated against other pathogens including monkey pox or flu virus. Vaccine stability studies at workable temperature (> 4C) shows PLACCINE vaccine is stably active for at least up to 9 months. These studies show potential for a DNA-based approach top vaccine that is independent of a virus or device.

Audience Take Away Notes

- An increased interest in DNA-based vaccines is expected
- Yes, of course. We are open to collaboration with research institutions or industry to better understand PLACCINE technology and expand its application
- Demonstrating the use of synthetic delivery systems for development of DNA vaccine may promote better and mor unique vaccine designs

Biography

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

William Song M. D[1]*, Nicholas Regnnitter M. D[2], Kelley Henely Frances Pharm D. M. P. H[2], Rebecca Bernherimer B. A[3], Allen Zhou B. S[3], Obinna Nnedu M. D[4]

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[2]University of pharmacology, Ochsner Health School, New Orleans Louisiana, United States of America
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A case of meningoencephalitis due to dual infection with streptococcus pneumoniae and herpes simplex virus 1

Meningoencephalitis is a serious and life-threatening infection with high mortality rates worldwide. Streptococcus pneumoniae is one of the most common infectious agents causing bacterial meningoencephalitis. Herpes Simplex Virus 1 (HSV-1) causes viral meningoencephalitis in an estimated 2 to 4 persons per 1,000,000 worldwide. Very rarely, meningoencephalitis can be due to dual infections with both bacterial and viral agents. A 69-year-old woman with diabetes and migraines was seen in the Emergency Department (ED) for headaches, treated with antiemetics and opioid pain medications, then discharged home. She was then found unresponsive and admitted with acute encephalopathy.

Work-up revealed Escherichia coli Urinary Tract Infection (UTI). On hospital day 5, she developed a new-onset generalized tonic-clonic seizure. Magnetic Resonance Imaging (MRI) of her brain revealed "extensive leptomeningeal enhancement overlying the frontal lobes bilaterally with a small focus in the left temporal lobe", consistent with meningoencephalitis. Cerebrospinal Fluid (CSF) was positive for S. pneumoniae with negative preliminary HSV PCR results. She responded well to vancomycin and ceftriaxone and was discharged home. 1 day after discharge, completed HSV PCR resulted positive.

Acyclovir was added to her antimicrobial regimen and she responded well. This patient's diagnosis was delayed and complicated due to multiple factors, including polypharmacy and a concurrent UTI, however her hospital course prompted further work-up which revealed meningoencephalitis, consistent with her initial presenting complaint of headaches. Interestingly, she was found to have both bacterial and viral infections. This complex case illustrates the importance of considering all differential diagnoses, including rare ones, and conducting a full diagnostic work-up while avoiding anchoring.

Objective: To illustrate the importance of a full diagnostic work-up. To highlight the value of avoiding anchoring on "most common" explanations and diagnoses. To raise awareness of initial false-negative polymerase chain reaction (PCR) results

Biography

William Song, M.D. is a resident physician in Internal Medicine at the Ochsner Clinic Foundation in New Orleans, Louisiana, United States. He is clinically interested in the fields of infectious diseases, oncology, and critical care medicine.

Whittle E[1]*, Yonkus J A[2], Alva Ruiz R[2], Horsman, S E[3], Suh G A[4], Patel R[5], Truty, M J[6], Chia, N[7]

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[5]Division of Clinical Microbiology, Mayo Clinic, Rochester, Minnesota, United States of America
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Answers in hours – a prospective clinical study for rapid detection of pathogens and antibacterial resistance in surgical patients using oxford nanopore sequencing

Surgical Site Infections (SSI) are a major source of morbidity in patients undergoing pancreatic head resection. Infections are often caused by organisms detected in the bile duct, resulting in many institutions using prolonged prophylactic antibiotics that are later optimized based on bile cultures. Standard cultures, however, can take days to complete, leaving many patients on prolonged courses of antibiotics that may be either unnecessary or suboptimal. We evaluated the use of Oxford Nanopore (ONT) sequencing to rapidly detect microbial species and antibacterial resistance genes present in intraoperative bile aspirates.

Patients undergoing pancreatic head resection for any clinical indication at Mayo Clinic Rochester were recruited from April 2020 – October 2020. Patients received standard care and were monitored for 90 days postoperatively. Intraoperative bile microbial profiles were determined using standard cultures and an optimized ONT sequencing pipeline. Antibiotic recommendations were made using culture and ONT results, and average time-to-results was determined for both methods. Microbial species, antibiotic resistance, antibiotic recommendations, and time-to-result were compared to determine the clinical value of using ONT sequencing to characterize biliary microbes.

In total, 42 patients were recruited, this included 9 patients undergoing total pancreatectomy and 33 patients undergoing pancreaticoduodenectomy. Bile cultures were positive for 55% (n = 23) of patients, of which 4 developed a SSI. ONT sequencing had perfect predictive power for bile culture positivity and generated no false positives. Culture of all samples yielded polymicrobial findings, with typical biliary microbes, including Enterococcus spp., Streptococcus spp., Klebsiella spp., Enterobacter spp., and Candida spp. detected.

Comparison of ONT to culture results revealed that the ONT protocol detected 75% of cultured bacterial species, 76% of cultured fungal species and predicted 81% of antibiotic resistance. Additionally, ONT sequencing improved species identification, increased detection of anaerobic species, and identified significant differences in biliary microbial populations between male and female patients. Comparison of antimicrobial recommendations based on culture and ONT results found correlative recommendations were made for 32% of patients. More critically, in 39% of patients, ONT-based recommendations would have resulted in administration of more narrow-spectrum antibiotics when compared to recommendations based off standard culture results. The average result turnaround time was significantly lower for ONT

sequencing (8 - 14 hours) compared to the time taken for finalize standard culture results (98 hours).

Rapid identification of microbial species and antimicrobial resistance is achievable using ONT sequencing. Following demonstration that it is clinically safe to use ONT sequencing to guide antimicrobial therapy, ONT sequencing has the potential to improve antibiotic stewardship.

Audience Take Away Notes

- This research demonstrates the successful use of Oxford Nanopore Technology to rapidly characterize intraoperative biliary microbes and predict antibiotic resistance within hours. The protocol that we have developed is applicable to any clinical sample type and can be applied to a wide range of infectious diseases. The audience will benefit from learning about a new method of rapidly identifying and characterizing infectious disease. Use of this technique in the clinical setting could significantly reduce diagnostic time for infectious disease, leading to decreased use of broad-spectrum antibiotics and improved antibiotic stewardship

Biography

Dr. Whittle studied Infection and Immunity at the University of Leicester, UK and graduated as MS with distinction in 2016. She then joined the research group of Dr. Tonge at Keele University to research the blood microbiome in relation to atopic disease. She received her PhD degree in 2020 at the same institution, and in March 2020 begin her postdoctoral at Mayo Clinic, Rochester.

Daniel Becker[1]*, Sebastian Ulbert[2], Martin Thoma[3], Ulla König[4], Andrea Traube[5]

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Why low-Energy-Electron irradiation might be a potential game changer for vaccine development, manufacturing, and pandemics prevention

In the ongoing global Covid-19 aftermath, epidemics and pandemics triggered by microbial and viral pathogens remain a significant challenge for global vaccine production and worldwide supply.

The Irradiation of target pathogens with Low-Energy Electrons (LEEI) can reliably and reproducibly inactivate many microbial and viral organisms, regardless of whether these pathogens are related to veterinary or human diseases. KyooBe Tech and their partners present several case studies (Zika virus, Tick-borne encephalitis virus) that show the immunological relevance of ebeam-treated viral vaccines.

Optimized for pharmaceutical process campaigns, KyooBe Tech's upcoming commercial LEEI platform, including either a microfluidic chip module, a stainless steel roller module, or a bag module, can be used as an orthogonal tool for germ reduction (viral clearance) of raw materials (such as sera), treatment of infectious liquid waste, and in vaccine manufacturing. Dead vaccines and live-attenuated vaccines can be addressed with this new technology.

Besides vaccine manufacturing, several irradiation approaches in cell therapy are novel and emerging application fields.

The upcoming LEEI platform can be flexibly integrated within a given process infrastructure and enables batch or continuous process management for users worldwide.

The design of KyooBe Tech's LEEI platform is of additional importance in operation with pathogens of biosafety levels 2-3. The system maps the necessary biocontainment, radiation protection, and a GMP-compliant production environment inside.

The most critical process parameters can be monitored inline and continuously using appropriate state-of-the-art sensors. Overall, LEEI provides a game-changing and promising alternative to standard inactivation processes using chemicals or UV-C or gamma irradiation processes.

in sum, this technology offers promising characteristics for future vaccine applications and pandemic prevention measurements.

Audience Take Away Notes

- This work especially addresses product owners in vaccine R&D and will open new corridors for pathogen inactivation and live attenuation
- KyooBe Tech's approach is relevant for certain fields like raw material and waste treatment, sample treatment and vaccine R&D, and CGT
- KyooBe Tech is open to new discussions and collaboration. We are not limited to vaccine R&D
- KyooBe Tech provides an outlook on its first product and the upcoming market launch

- KyooBe Tech's solutions open new strategies for biocontainment and highly regulated laboratories (such as BSL3). Besides that, we offer vaccine manufacturing in a continuous manner and highly monitored manner

Biography

Daniel Becker studies Industrial Biotechnology with a strong focus on bioprocess technologies and process optimization at the University of Ulm and the Applied University of Biberach, Germany. He graduated with an MS in 2018. He joined the laboratory automation and bioproduction technology department at Fraunhofer IPA in Stuttgart in 2019. Working on different public and industrial projects, he prepared a strategic report for Bausch + Ströbel group, resulting in the spin-off company KyooBe Tech GmbH that he joined as a project lead. Since 2020, Daniel has led a lighthouse project called INACTIVATE to provide next-generation vaccine manufacturing technologies based on electron beams.

Mason Torve*, Hessam Mirgolbabaei
University of Minnesota, United States of America

Low-dimensional analysis of environmental factors mediating norovirus outbreaks from food and water

Introduction: Contaminated oysters are a severe threat to public health in the US, with Norovirus outbreaks being a common concern. To prevent these outbreaks, predicting when they might occur is critical. Fortunately, advanced artificial intelligence models can now forecast contaminated oyster outbreaks up to two weeks in advance. These models account for six environmental factors - water temperature, salinity, solar radiation, rainfall, wind, and gage height. To enhance the accuracy of these predictions, our team is currently conducting a reduced-order manifold, traditionally known as POD or Principal Component Analysis (PCA) on meteorological data. It may be possible to reduce the required input variables for accurate predictions by training an Artificial Neural Network (ANN) using PCs. The potential of such an approach is discussed in the present work.

Methods: Quantitative secondary data from the National Outbreak Reporting System and other state and federal agencies for more than 2 decades are collected from the most popular Oyster harvesting area around the Gulf of Mexico. Pre-processing of the data composed of data cleaning and statistical analysis, including dimensionality reduction, is conducted. ANNs are trained towards the precise prediction of a fraction of the preceding outbreaks in the areas of interest. The training step is followed by predicting the outbreaks from the data that has yet to be presented to the ANN during the training phase.

Results: Based on the preliminary data analysis, it is evident that the proposed method possesses enormous potential in systematically selecting meteorological data for future forecasts.

Conclusion: In summary, training an artificial neural network with principal components could lead to an ANN model capable of forecasting norovirus outbreaks caused by contaminated oysters with fewer environmental predictors than current models. This could allow for predicting norovirus outbreaks in areas with limited meteorological data.

Biography

Mason Torve is a graduate student at the University of Minnesota Duluth, currently working towards a Master of Science degree in Mechanical Engineering. He is a research assistant to Dr. Hessam Kassra Mirgolbabei and is also a member of the UMN-Duluth baseball team. Mason's research interests are focused on data analysis and thermal fluids.

Sabrina Babl*, Julia Seidel, Elisabeth Silberhorn, Sophia Winklbauer, Gernot Längst

Department of Environmental Engineering, Engineering Faculty, Dokuz Eylul University, İzmir Turkey

In vitro characterization of the SARS-CoV-2 nucleocapsid protein

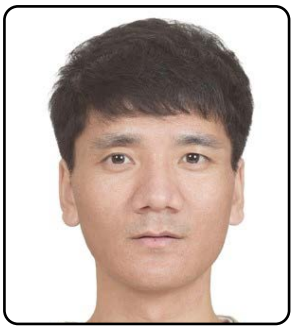
Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is a positive-sense single-stranded RNA virus with a genome size of approximately 30 kilobases. The genome encodes non-structural proteins at its 5' end and structural proteins at its 3' end. Among the structural proteins, the Nucleocapsid (N) protein is crucial for viral genome packaging and is highly expressed in infected cells. The N protein is known to interact with the viral genomic RNA to form a Ribonucleoprotein (RNP) complex that plays a crucial role in viral RNA packaging. The RNP complex is formed by the binding of multiple N protein molecules to the viral RNA, and this complex is then enclosed within the viral envelope to form the infectious virion. In addition to its role in nucleocapsid formation, we demonstrate that SARS-CoV-2 N protein exhibits RNA chaperone activity similar to the SARS-CoV N protein. Our study shows that SARS-CoV-2 full-length N protein enhances RNA hybridization, and its C-terminal domain is sufficient to promote RNA annealing. We also observed that the N protein alters RNA structure, thereby contributing to RNA folding and functionality by displacing RNA chaperone activity. These findings provide insights into the multifunctional roles of SARS-CoV-2 N protein in viral replication and pathogenesis.

Audience Take Away Notes

- Understanding the structure and function of the nucleocapsid protein is critical for developing effective diagnostic and therapeutic tools against SARS-CoV-2 and potential following viruses
- The study demonstrates that SARS-CoV-2 N exhibits RNA chaperone activity, which alters RNA structure and contributes to RNA folding and functionality. This information could be valuable in designing treatments that target the N protein and its effect on RNA function
- We provide new information on the N protein's role in viral genome packaging, which is crucial for the virus' replication and survival, and understanding this process could help develop treatments that disrupt this step in the viral life cycle

Biography

Sabrina Babl studied Biology at the University of Regensburg, Germany and graduated as M.Sc. in 2020. Afterwards she started her PhD in the research group of Prof. Längst at the Institute for Biochemistry III at the Department of Biochemistry, Genetics and Microbiology at the University of Regensburg, working on the SARS-CoV-2 nucleocapsid protein.



Gyaltsen Dakpa[1,4]*, K J Senthil Kumar[2], Nai-Wen Tsao[3], Sheng-Yang Wang[1,2,3,5]

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Effects of the natural compound on Sars-Cov-2 spike protein-mediated metabolic alteration in THP-1 cells explored by the 1H-NMR-based metabolomics approach

A change in metabolism is one of the hallmarks of coronavirus disease 2019 (COVID-19) that cause severity and mortality. The mechanism of SARS-CoV-2 spike protein-mediated perturbations of metabolic pathways and modulation of antcin A, a steroid-like compound isolated from Taiwanofungus camphoratus, are not studied. Here, we investigated the metabolic alteration by SARS-CoV-2 spike protein and the regulatory effect of antcin A on SARS-CoV-2 spike protein-induced metabolic changes in the Phorbol 12-myristate 13-acetate (PMA)-induced human monocytes (THP-1) cells using proton nuclear magnetic resonance (1H-NMR) and MetaboAnalyst 5.0 software. The cytotoxic potential of SARS-CoV2 spike protein, antcin A, and dexamethasone was assessed by MTT assay. The metabolomic perturbations and their relation to human coronaviruses' receptors were evaluated by qPCR. This study indicated that the altered metabolites mediated by SARS-CoV-2 protein, such as methionine, phosphoenolpyruvic acid, canadine, glutamine, ethanolamine, and phenylalanine, were significantly reversed by antcin A. In addition, antcin A significantly inhibited SARS-CoV-2 spike protein-mediated up-regulation of TLR-4 and ACE2 receptors, while GRP78 inhibition was not statistically significant. This is the first study to use 1H-NMR to investigate SARS-CoV-2 spike protein-induced metabolomic changes in PMA-induced THP-1 cells. Antcin A significantly reversed metabolomic alters while dexamethasone failed to fix them. Therefore, antcin A could be a potential candidate for therapeutic agents for viral infections related to a metabolic abnormality.

Keywords: SARS-CoV-2-Spike, 1H-NMR, Metabolomics, Antcin-A, Taiwanofungus Camphoratus.

Audience Take Away Notes

- This study displayed that 1H-NMR is not only solving structure molecules, but it can apply for diagnosis based on metabolomic biomarkers
- Only the SARS-CoV-2 spike altered the metabolomic pathway at the cellular level. Thus, the regulation of metabolic pathways is another clinical therapeutic strategy
- Natural compounds have more potential to rescue from metabolomic alteration via virus infection
- Metabolomic correction is a novel therapeutic approach to tackle virus-mediated metabolomic alteration

Biography

Mr. Gyaltsen Dakpa earned a bachelor's degree in biotechnology from Panjab University (2016), India, and a Master of Science in Biotechnology from Jawaharlal Nehru University (JNU) in 2018. He spent a year teaching at Garden Jang-tse Monastic University, India, collaborating with Emory University, USA. He enrolled as a Ph.D. student at National Chung Hsing and Academia Sinica in 2019 through the Taiwan International graduate program (TIGP). Currently, He is 4th of Ph.D. Candidate and working on the effects of natural compounds on the SARS-CoV-2 Spike protein-mediated metabolomic alteration at the cellular level. Recently his paper has been accepted in Phytotherapy research. He also published a review article in 2022 at Progress in Molecular Biology and Translational Science.

Haoran Ren, Ming Shi*

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Innate receptor PGLYRP2 is a functional sensor and hepatic scavenger for hepatitis B virus

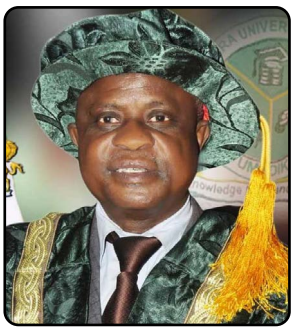
The stealth property of Hepatitis B virus (HBV) has been questioned. The hepatic immunocompetence and effective innate immune responses are necessary for spontaneous clearance of HBV infection, however, the underlying mechanisms remain unclear. Here we observed a negative correlation between the expression level of hepatocyte-specific innate sensor Peptidoglycan Recognition Protein 2 (PGLYRP2) and HBV infection status in HBV-infected human liver tissues ($p<0.001$), and demonstrated that PGLYRP2 with an age-related expression pattern inhibits viral replication by binding to HBV Core/Enhancer II promoter through its PGLYRP2209-377 domain, as well as enhances viral clearance by interacting with HBV capsid. The direct interaction between PGLYRP2 and HBV capsid triggers nucleocytoplasmic translocation of PGLYRP2, and enhances secretion of the capsid-associated PGLYRP2, which subsequently activate immune effector cells. Conversely, loss of PGLYRP2 compromises HBV control in hepatocytes. This study identifies a novel mechanism of interaction between HBV and innate immunity, in which PGLYRP2 exerts its function through direct-acting inhibition of HBV replication, acceleration of HBV core protein-targeting viral clearance, and modulation of hepatic microenvironment, thereby contributing to the recognition and spontaneous HBV clearance.

Audience Take Away Notes

- Despite breakthrough in discovery of NTCP as host cell entry receptor of HBV, the functional HBV sensor and scavenger that related with the pathophysiological mechanism of spontaneous HBV clearance have not been identified
- Most HBV-infected infants cannot achieve spontaneous viral clearance compared to infected adults, indicating that the age-related hepatic immunocompetence and effective immune response contribute to spontaneous HBV clearance
- A better understanding of how immune-competent hepatocytes spontaneously clear HBV infection may present new opportunities to achieve effective control and functional cure of HBV infection
- Hepatic innate sensor PGLYRP2 can achieve spontaneous HBV clearance in combination with its direct-acting antiviral and immunomodulatory activities, which supports that the ability of the innate immunity to sense and react to HBV
- Development of novel strategies for augmenting PGLYRP2-induced antiviral activity may provide an effective therapeutic intervention against chronic HBV infection

Biography

Dr. Shi studied Biomedical engineering at the Harbin Institute of Technology (HIT), Harbin, and entered joint Ph.D. program with Texas A&M Health Science Center, Houston in 2009. He received his PhD degree in 2014. After one and half year's postdoctoral fellowship supervised by Dr. Hao Wu at the Boston Children's Hospital, Harvard Medical School, USA. He obtained the position of an Associate Professor at the HIT. The Shi laboratory of mechanistic immunology focuses on elucidating the molecular and cellular mechanisms that govern the regulation and therapeutic intervention of pattern recognition receptors in innate immunity. Our current research focuses on investigating the mechanisms of inflammation in infectious disease and tumorigenesis, especially the inflammation induced by innate immune signaling.



M. C. O. Ezeibe*, F. I. O. Ezeibe

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Medicinal synthetic aluminum-magnesium silicate {$Al_4 (SiO_4)_3 + 3Mg_2SiO_4 \rightarrow 2Al_2 Mg_3 (SiO_4)_3$} effective for: Viral diseases; Tumors; Antimicrobial resistant infections

Viral diseases, cancers (tumors) and antimicrobial resistant infections are among the world`s biggest health challenges. Literature reveals, that HIV and COVID-19 virus (RNA viruses) are positively charged while DNA viruses and abnormal (tumor/infected) cells are negatively charged. So, electrically charged medicines would mop viruses and tumor-cells by Opposite-charges electrostatic attraction. Infected cells would also be mopped and destroyed (unmasking “hidden infections”). Literature also contains that Molecules of Aluminum-Magnesium Silicate (AMS), a WHO-approved medicine/adjuvant, consist of Nanoparticles which have, negative and positive ends. Ultra-small size of AMS-Nanoparticles (0.96 nm) allows them reach all organs and tissues. As adjuvant, AMS improves antimicrobials-efficacies for effective treatment of secondary infections and as silicate, it enhances immunity. Mopping viruses and abnormal cells, unmasking “hidden infections”, effectively treating secondary infections and enhancing immunity would cure viral diseases and tumors. In addition to antiviral and antitumor efficacies, coexistence of the two charges makes AMS-Nanoparticles hydrate in solutions to form three dimensional colloidal structures. The colloidal structures stabilize other medicines, formulated with AMS. Also, Nanoparticles enhance delivery of drugs to effect-targets and across physiological barriers. When drugs are stabilized, rate of their metabolism reduces, thus prolonging their time of high bioavailability. Prolonging time of high bioavailability and enhancing delivery to targets improve efficacy. With improved efficacy, lower doses achieve desired effects. Use of lower doses for desired effects minimizes side effects so that immune responses enhance. Synergy between improved efficacies and enhanced immunity lead to clearance of infections so that none is left to develop antimicrobial resistance. Infections that are already resistant may be cured by same drugs they resisted. Some countries do not have the solid mineral, AMS [$Al_2Mg_3 (SiO_4)_3$] but they may have Aluminum silicate [AS: $Al_4 (SiO_4)_3$] and Magnesium silicate [MS: Mg_2SiO_4]. So, we, used AS and MS (approved medicines too) to formulate an AMS-brand {$Al_4 (SiO_4)_3 + 3Mg_2SiO_4 \rightarrow 2Al_2 Mg_3 (SiO^4)_3$} and named it, Medicinal synthetic Aluminum-magnesium silicate {MSAMS}. Since AMS, AS and MS are not absorbable, to make MSAMS function systemically, Dextrose monohydrate is incorporated in its formulations, to convey the electrically charged Nanoparticles across mucous membranes (active transportation) into blood-circulation. The MSAMS has proved effective against all viruses, tested, in vitro and/or in vivo, including HIV and COVID-19 virus. It improves efficacy of antimicrobials to make them achieve ≥95 % infection-load reduction (preventing antimicrobial resistance). At 75 %-doses, antimicrobials formulated with MSAMS and supported with antioxidants regain efficacy against resistant infections.

Biography

Maduike Ezeibe holds PhD, from University of Nigeria, Nsukka. He specialized in using animals for medical researches and invented theory of opposite charges electrostatic attraction for treatment of diseases of electrically charged pathogens. Since Aluminum-magnesium silicate (AMS) which has both charges may not exist in every country, he invented a formulation of Aluminum silicate and Magnesium silicate (approved medicines) to get Medicinal Synthetic AMS (MSAMS) and also invented an equation {$Al_4 (SiO_4)_3 + 3Mg_2SiO_4 \rightarrow 2Al_2 Mg_3 (SiO_4)_3$} for the formulation. MSAMS has proved effective against viral/abnormal cell diseases. It also enhances efficacy of other medicines to prevent/cure Antimicrobial Resistant infections.

BOOK OF ABSTRACTS

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VACCINES AND INFECTIOUS DISEASES

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A randomized phase 3 clinical study to evaluate the efficacy and safety of SHR8008 (oteseconazole) vs. fluconazole in subjects with Vulvovaginal Candidiasis (VVC)

Background: VIVJOA® (oteseconazole) is approved in the United States to reduce the incidence of Recurrent Vulvovaginal Candidiasis (RVVC). A Phase 3 study was conducted in China by Jiangsu Hengrui Pharmaceuticals Co. Ltd. to evaluate the efficacy and safety of SHR8008 (oteseconazole) versus fluconazole in subjects with VVC.

Methods: Enrolled subjects presented with a diagnosis of VVC at screening, including a composite signs and symptoms score of ≥ 7, with a positive potassium hydroxide or Gram stain. Subjects meeting all study eligibility criteria were randomized in a 1:1 ratio to received SHR8008 (oteseconazole) capsules (600mg on Day 1, 450mg on Day 2) or the current standard of care, fluconazole (150mg on Day 1, and 150mg on Day 4). Subjects returned to the study site on Day 14 and Day 28.

The primary endpoint evaluated therapeutic cure of VVC, defined as the absence of signs and symptoms of VVC together with a negative culture for Candida species in the mITT population on Day 28. A secondary endpoint also evaluated therapeutic cure on Day 14. The in vitro drug susceptibility and MIC results were also determined.

Results: Baseline demographics and characteristics were similar between treatment groups. A total of 322 subjects were randomized. In the mITT population, therapeutic cure at Day 28 was significantly higher in the SHR8008 (oteseconazole) group than in the fluconazole group (66.88% vs. 45.91%), P = 0.0002. Mycological cure at Day 28 was higher in the SHR8008 (oteseconazole) group than in the fluconazole group (82.50% vs. 59.12%), P < 0.0001.

Susceptibility analysis indicated that MIC's of SHR8008 (oteseconazole) were lower than those of fluconazole when screened against most Candida strains. All collected C. albicans and C. glabrata isolates remained sensitive to SHR8008 (oteseconazole), whereas > 50% of isolates were either resistant or demonstrated dose dependent sensitivity to fluconazole.

No clinically significant treatment-related impact on vital signs, physical examinations, ECG, or laboratory tests were observed.

Conclusion: Data from this Phase 3 clinical study suggests SHR8008 (oteseconazole) is safe and more effective than the current standard-of-care, fluconazole, in treating VVC.

Audience Take Away Notes

- Many women are affected by vaginal fungal infections, also called yeast infections. SHR8008 (oteseconazole) has been developed in clinical studies and may provide an effective treatment option for fungal infections
- Vulvovaginal Candidiasis (VVC) is typically treated with a single dose or short treatments of either

topical or oral azole antifungals. Fluconazole remains the current standard of care, however, drug resistance and safety liabilities are associated with its use. Data from this phase 3 clinical study suggests SHR8008 (oteseconazole) is safe and more effective in treating VVC

- SHR8008 (oteseconazole) has demonstrated greater potency against Candida species, including azole resistant species, than fluconazole

Biography

Dr. Brand is a graduate member of the Institute of Biology (GiBiol) and holds a PhD in Molecular Biology from the School of Medicine, University of Manchester, England. He completed his post-doctoral fellowship at Cold Spring Harbor Laboratory, NY. Dr. Brand currently serves as Chief Development Office at Mycovia Pharmaceuticals, providing strategic direction and technical leadership to the clinical development and medical affairs teams. He is responsible for the overall management and performance of the company's antifungal clinical development programs in women's health and other areas. Dr. Brand most recently served as Vice President, Clinical Development at Viamet Pharmaceuticals where he led cross-functional project teams, resulting in the successful completion of Phase 2b studies in recurrent vulvovaginal candidiasis and onychomycosis. He previously served as President of Agile Sciences and Director at Argos Therapeutics. Dr. Brand has held senior positions in pharmaceutical development at BioStratum, Inc., and Cato Research Ltd.

Nicole Messere*, Whitney Baldwin

Vaccines Business Unit, Takeda Pharmaceuticals, Cambridge, MA, United States of America

Characterization of dengue virus serotype 1 and 2 infection in human dermal fibroblasts

Dengue Virus (DENV) is a mosquito-borne flavivirus with four antigenically distinct serotypes called DENV-1, DENV-2, DENV-3, and DENV-4. Many DENV infections are asymptomatic or lead to mild illness, but occasionally DENV infections can lead to severe disease, characterized by shock, hemorrhagic fever, and even death. Fibroblasts are the main cell type present in skin and release various cytokines and chemokines in response to pathogens. Although dermal fibroblasts likely play an important role in regulating the early response to DENV infection, this role has not been fully characterized yet. In the present study, we characterized DENV infection in human dermal fibroblasts by measuring virus infectivity and assessing markers of innate immune response to DENV. Primary human dermal fibroblasts were infected with DENV-1 or DENV-2 and virus growth kinetics were compared with DENV-1/-2 infected BHK-21 cells, a hamster-derived kidney fibroblast cell line that has been previously shown to be highly susceptible to DENV. The infected primary human dermal fibroblasts were also used to measure innate immune response markers - chemokines and cytokines - released in response to DENV infection using a custom 18-plex analyte Luminex kit. Our results show that, in contrast to BHK-21 cells, infection of human fibroblasts by DENV-1 or DENV-2 at low Multiplicity of Infection (MOI) (0.01 and 0.1) does not induce Cytopathic Effects (CPE), and does not yield infectious DENV at any of the assessed time points post- infection. However, infection at high MOI (5 and 10) induces morphological changes in human fibroblasts by 6 days post-infection for DENV-2 and 10 days post-infection for DENV-1. Cell culture supernatants collected from high MOI infection of fibroblasts with DENV-1 lack measurable infectious virus, while cell culture supernatants collected from DENV-2 infected fibroblasts yield measurable infectious virus. In addition, assessment of the innate immune response of DENV-2 infected fibroblasts (at high MOIs) show expression of several pro-inflammatory cytokines and chemokines (IL-6, IL-8, CCL2, CXCL10, CCL5, CCL7, and CXCL1). These results indicate that infection of human fibroblasts at high MOIs with DENV-2 may be used to characterize the early stages of DENV infection and antagonism of the innate immune response to infection.

Audience Take Away Notes

- From this presentation, the audience will learn new information about the role human dermal fibroblasts play in response to infection by DENV-1 16007 and DENV-2 16681, including the innate immune response of fibroblasts against each serotype. This study furthers dengue research by introducing a novel, reproducible method for assessing infection against dengue viruses and vaccine strains. Lastly, the work to be presented identifies potential dengue virus evasion mechanisms that should be considered by the developers of vaccines and antiviral drugs to control DENV pathogenesis in humans

Biography

Nicole Messere is a Research Associate in the Vaccines Research and Analytics group in Takeda Pharmaceutical's Vaccine Business Unit, specializing in dengue immunology. She received her Master of Biology degree through the Harvard Extension School in May 2023.

Sheeba S Sawant, Ph.D[1]*, Dr. Ayesha Rahman[2], Dr. Timothy Baldwin[3], Dr. Habib Khan[4]

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[3]Reader in Plant Cell Biology, FoSE (Faculty of Science & Engineering), University of Wolverhampton, United Kingdom
[4]SL in Pharmaceutical Microbiology, FoSE (Faculty of Science & Engineering), University of Wolverhampton, Wolverhampton, United Kingdom

Exploring the impact of plectranthus amboinicus L. Extracts on antioxidant system and cell membrane integrity of P. Aeruginosa PA01 and S. Aureus NCTC8325

Plectranthus amboinicus (Indian borage) has been extensively studied for its medicinal properties, which can be exploited to develop new antimicrobial therapeutics. The current study investigated the effect of Plectranthus amboinicus leaf extracts on the catalase activity, reactive oxygen species, lipid peroxidation, cytoplasmic membrane permeability, and efflux pump activity in S. aureus NCTC8325 and P. aeruginosa PA01. As the enzyme catalase protects bacteria against oxidative stress, disruption of its activity creates an imbalance in Reactive Oxygen Species (ROS) levels, which subsequently oxidizes lipid chains, leading to lipid peroxidation. In addition, bacterial cell membranes are a potential target for new antibacterial agents, as efflux pump systems play a crucial role in antimicrobial resistance. Upon exposure of the microorganisms to Indian borage leaf extracts, the observed catalase activity decreased by 60% and 20% in P. aeruginosa and S. aureus, respectively. The generation of ROS can cause oxidation reactions to occur within the polyunsaturated fatty acids of the lipid membranes and induce lipid peroxidation. To investigate these phenomena, the increase in ROS activity in P. aeruginosa and S. aureus was studied using H2DCFDA, which is oxidized to 2′,7′-Dichlorofluorescein (DCF) by ROS. Furthermore, the concentration of lipid peroxidation product (malondialdehyde) was assessed using the Thiobarbituric acid assay and was shown to increase by 42.4% and 42.5% in P. aeruginosa and S. aureus, respectively. The effect of the extracts on the cell membrane permeability was monitored using diSC3-5 dye and it was observed that the cell membrane permeability of P. aeruginosa increased by 58% and of S. aureus by 83%. The effect on efflux pump activity was investigated using Rhodamine-6-uptake assay, which displayed a decrease in efflux activity of 25.5% in P. aeruginosa and 24.2% in S. aureus after treatment with the extracts. This combination of different methods to study various bacterial virulence factors provides a more robust, mechanistic understanding of the effect of P. amboinicus extracts on P. aeruginosa and S. aureus. This study thus represents the first report of the assessment of the effect of Indian borage leaf extracts on bacterial antioxidant systems and bacterial cell membranes and can facilitate the future development of bacterial resistance modifying agents derived from P. amboinicus.

Audience Take Away Notes

- My project revolves around ethnopharmacology and microbiology. In my opinion, my research will help people in gaining a better understanding of the traditional practices of different communities and cultures across the world and thus paving a way for traditional medicines in the field of healthcare. This can surely ignite a new hope in discovery of new drug candidates as these plants are a rich source of phytochemicals and can potentially be developed into new drugs or used in association with other drugs
- My research also promotes sustainability and conservation as these plants are on the verge of extinction due to lack of knowledge. Additionally, they can be used to fight antimicrobial resistance and can be

easily accessible, reduced side effects and cost-effective than other synthetic drugs

- Also, my research is the first report on the various bioactivities of P. amboinicus against Pseudomonas aeruginosa and Staphylococcus aureus. This can help the audience in exploring the different target mechanisms that can be used to destroy these bacteria
- Learning about my research can be relevant and useful for researchers working in various fields such as healthcare, research and development, pharmacology, and microbiology
- For healthcare professionals, my research can help them in providing holistic and culturally sensitive care to people coming from diverse backgrounds and understanding the use of traditional medicines which can complement modern medicine. This can surely help them in identifying the possible interactions between the home remedies and prescribed treatments which can ensure the safety of the patients
- For researchers working in the field of biomedical sciences and microbiology specifically, my work can provide understanding into the different virulence factors of the bacteria and target mechanisms that can be used in drug development. Also, it can help them in exploring different phytochemicals and identifying bioactive compounds from plants as potential new drug candidates. My project is an amalgamation of microbiology, plant biology and biochemistry which opens doors to researchers from different fields to try something innovative with their on-going projects
- Yes absolutely, my research consists of microbiology and plant studies which can be useful for other faculties to expand their research or teaching
- For example, microbiology research can be beneficial for faculties in healthcare, environmental science, life sciences, agriculture, and biotechnology. Healthcare faculties can use microbiology research to better understand infectious diseases, microbes associated with nosocomial infections, develop new treatments with minimum side effects and improve patient outcomes. Environmental science faculties can use my research to understand the role of microorganisms in ecosystems, and presence of endophytes in plants that explains the mutualistic relationship of nature. Similarly, biotechnology faculties can use it to develop new biotechnological applications and sustainable options in drug development to combat AMR
- Similarly, pharmacology faculties can explore my research to identify new drug candidates and natural remedies
- In addition, as my work revolves around microbiology and plant biology research, these topics are very valuable for teaching. Teaching professionals can use my research findings to develop course materials, case studies, and practical applications for students in different fields. They can also use research methods and techniques to teach students about experimental design, data analysis, and scientific communication
- In my opinion, my research can surely improve the efficiency of the design as it aims to provide solutions to an on-going problem such as shortage of new antimicrobials and antibiotic resistance
- My research focuses on identifying antimicrobial properties of compounds obtained from P. amboinicus plant, this will lead to development of natural and new antimicrobial agents that can reduce the need for synthetic agents which have severe side effects on the patients and may develop resistance in the future. This in turn may lead to a more economic and eco-friendly option that designers could incorporate in their designs
- Similarly, in-depth research of these two bacteria will help the designers to develop antimicrobials specifically designed for the bacteria to avoid any form of resistance
- The accuracy of any design does depend on factors such as the quality of the materials, the processing, and designer's skills. My research can provide more information as it is one of the first reports addressing some new innovations that can assist in solving design problems and leading to a more efficient development. My project provides information on the virulence factors and target mechanisms that

help microbes to exhibit AMR, which can be exploited to develop better treatments and avoid mistakes or drawbacks in previous projects or even my research

- In addition, my research can provide new perceptions into the potential risks and benefits associated with phytochemicals and their cytotoxicity. This information could be used to inform the design of safer products, and to help designers make more updated findings about the products they use
- List all other benefits
    - Plectranthus amboinicus also known as Indian borage has been used since ancient times for its antimicrobial activities. Some of the advantages of working with this plant are as follows
    - Natural antimicrobial activities: Indian borage plant is reported to consist of phytochemicals such as thymol, carvacrol, eugenol which display a variety of bioactivities and are known to inhibit a range of microbes. The broad range of activity against fungi, Gram negative and Gram-positive bacteria, makes this plant an ideal candidate for treating infections
    - Low toxicity and side-effects: Indian borage was reported to be safe and non-toxic home remedy for decades and can be an alternative to synthetic drugs which have negative side effects
    - Synergistic effects: Indian borage contains multiple bioactive compounds that could work together with existing antibiotics to provide synergistic effects, potentially increasing its antimicrobial activity

Biography

Sheeba S Sawant completed her bachelor's degree in microbiology at Mumbai University, India in 2016. She subsequently obtained her master's degree in microbiology from St. Xavier's Autonomous College, Mumbai University, India. Currently, she is pursuing her Ph.D. in Pharmaceutical Microbiology at the University of Wolverhampton, United Kingdom. She has published a review article, and a results paper. Evaluation of the effect of leaf development in Plectranthus amboinicus l. on antimicrobial activity and virulence factors of Pseudomonas aeruginosa PA01 and Staphylococcus aureus NCTC8325. Staphylococcus aureus Biofilm: Morphology, Genetics, Pathogenesis and Treatment Strategies.

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The activity of PHMB and other guanidino containing compounds against acanthamoeba

In recent years, a rise in the number of contact lens users in the UK and worldwide coincided with an increased incidence of microbial keratitis. The aim of this study was to investigate the antimicrobial activities of Polyhexamethylene Guanidine (PHMG), Polyaminopropyl Biguanide (PAPB), and guazatine in comparison to the common contact lens disinfectant constituent, Polyhexamethylene Biguanide (PHMB), thereby identifying compounds that show potential for the treatment of microbial keratitis and for the inclusion in Multi-Purpose Solutions (MPS). The study involved at first determining the minimum concentrations of these compounds against Acanthamoeba castellanii and Acanthamoeba polyphaga. Then using these concentrations, the rate of kill for these compounds against each organism was investigated using the time-kill method.

This study demonstrated that PHMG, PAPB, and guazatine are equal in activity to PHMB against Acanthamoeba trophozoites and cysts. All compounds demonstrated significant antimicrobial activity against trophozoites of both Acanthamoeba species resulting in a 2–2.6 log10 reduction in viability in comparison to the control ($p < 0.001$) at 6 h, which is the standard disinfection time for a contact lens solution. However, there was no significant difference between PHMB, PHMG, PAPB, and guazatine at this 6 h time point ($p > 0.05$), which proves and provides insight into the idea of guanidino compounds have similar and yet effective treatment against Acanthamoeba.

Audience Take Away Notes

- Through this research, the audience will become aware of amoebic parasite Acanthamoeba and the impact and correlation the parasite has with contact lenses. The blinding keratitis caused by Acanthamoeba, its incidence and research has been gaining traction through the years with ever growing use of contact lenses around the world. Unfortunately, there is not a standardized therapeutic scheme for the infections cause by Acanthamoeba keratitis. The risk factors being mostly with the use of contact lenses and the disinfection of them, and this research will show how to use compounds with specific chemical structures and whether incorporating them into multi-purpose solutions would be beneficial
- This research demonstrates that guanide containing compound have an effect on an amoebic parasite. For ophthalmologists, clinical researcher, pharmaceutical companies and contact lens companies, this might inspire to revisit the compounds that had had a different purpose at first and to observe if they can be incorporated into multi-purpose solutions (MPS) and affect real change in anti-microbial activity against existing parasitic or even bacterial and fungal eye infections
- Yes, absolutely. The medical faculties could include this research into areas of parasitic infections of Acanthamoeba and similar infectious amoeba, such as the brain eating parasite Naegleria fowleri. The ophthalmology departments could benefit largely from this study's findings, with the use of MPS for

contact lenses being made aware of, and used correctly and safely. Additionally, this research focuses on the guanide or biguanide units of the compounds that were used to screen against Acanthamoeba, therefore could provide interest to Chemistry faculty. There are compounds that could be developed to have one or more biguanide units, such has Chlorhexidine, which has outstanding effectivity against oral bacteria. PHMB, a long standing treatment against Acanthamoeba, has painful side effects in patients. However, there are ample opportunities to find out if such compounds could be created with minimal to no side effects for the purpose of eye infection, considering that the eye is an extremely sensitive part of the body

- Current treatments against Acanthamoeba include association of a biguanide (PHMB or chlorhexidine) with a diamidine (hexamidine or propamidine). This research provides insight into understanding what type of chemical structures have a better effect on parasitic infections, and rather than providing a treatment regime that have painful side effects, this study provides insight as to whether a singular treatment or prevention is possible. Acanthamoeba infections are worldwide, and not specific to regions. These parasites are resilient in nature, and so the need to develop disinfectants or treatment that deals with Acanthamoeba keratitis is urgent
- The chemistry behind the making of contact lens disinfectants can be improved from this study, based on the idea that certain chemical structures or units have an anti- microbial effect. Differently structured compounds with the same units can be created with lesser side effect incorporated into their contact lens disinfectant solutions. Contact lenses have a huge market in which they require a standard combination of drugs in the disinfectant solutions. There is further research being carried within our group, into what other compounds can be used in the disinfectant solutions that also have an anti-microbial effect
- List all other benefits
    - A part from testing against Acanthamoeba, this study also involved screening these drugs against a range of other ocular pathogens, including S. aureus and C. albicans, and we were able to observe a significant affect. Instead of offering a treatment regimen with unpleasant side effects, this research sheds light on what kinds of chemical structures have the most impact on parasitic, bacterial and parasitic infections. It also sheds light on whether a single treatment or prevention is feasible. Infections with Acanthamoeba can occur anywhere. Since these parasites have a tenacious nature, it is vital to create disinfectants or a treatment for Acanthamoeba keratitis. Based on this study's hypothesis that specific chemical structures or units have an anti-microbial impact, the chemistry used to create contact lens disinfectants can be enhanced as a result of this work. Differently structured compounds with the same units can be made and added to contact lens disinfecting solutions with less negative effects

Biography

Dharanga Ratnayake completed her BSc (Hons) in Biomedical Science and simultaneously completed her diploma in Abnormal and Clinical Psychology in the year of 2017. After a few months of lecturing, she then went on to pursue a MSc in Biomedical Science (Medical Microbiology) at the University of Wolverhampton in 2018, with her research largely based on Acanthamoeba disinfection and prevention. Upon successful completion, and with the support of her research supervisor she was able to begin her PhD degree in Biomedical Sciences, which she is in current pursuit. Along with her lab research partner she was able to successfully publish her research titled "The Activity of PHMB and Other Guanidino Containing Compounds against Acanthamoeba and other ocular pathogens". Current research involves developing anti-microbial therapies against Acanthamoeba and further insight and developing models portraying the progression of Acanthamoeba in the human eye.

Haoran Ren*, Zhen Tie, Jin Zhang and Ming Shi

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Innate immune response to hepatitis B virus infection: Recognition and spontaneous viral clearance by hepatic sensor PGLYRP2

Background & Aims: The stealth property of Hepatitis B Virus (HBV) has been challenged. The age-related hepatic immunocompetence and immune response leads to spontaneous clearance of HBV infection, however, the mechanisms underlying spontaneous clearance remain to be clarified. Here we investigate the roles of an innate sensor Peptidoglycan Recognition Protein 2 (PGLYRP2) in HBV infection and demonstrate that crosstalk between PGLYRP2 and HBV exists in hepatocytes and liver microenvironment.

Methods: Biotinylated HBV DNA pull-down assay, size-exclusion chromatography and LC-MS/MS analysis were used to identify HBV-interacting host proteins in human hepatocytes. The functional properties of immune effector cells were analyzed by using PCR array, seahorse metabolic flux assay, flow cytometry and multiplex immunofluorescence staining. Hydrodynamic HBV transfection mouse model utilizing adeno-associated virus vector was established to evaluate the effect of PGLYRP2 on spontaneous viral clearance.

Results: Peptidoglycan Recognition Protein 2 (PGLYRP2), an innate sensor with age-related expression pattern, restricts HBV replication through PGLYRP2209-377 domain binding to Core/Enhancer II promoter, whereas HBV capsid preferably interacting with PGLYRP2PGRP domain facilitates viral evasion. Elevated HBc level-induced nucleocytoplasmic translocation and enhanced secretion of PGLYRP2 in turn contribute to spontaneous HBV clearance. Moreover, the secretion of PGLYRP2/capsid complex enhances functional properties of immune effector cells in microenvironment. Conversely, loss of PGLYRP2 in hepatocytes compromises virus control during HBV infection.

Conclusions: This study identifies a novel interaction mechanism between HBV and innate immunity in which PGLYRP2 is associated with age-related hepatic immunocompetence and spontaneous viral clearance, thus providing a promising target for functional cure of HBV infection.

Audience Take Away Notes

- Innate sensor PGLYRP2 with age-related expression profile restricts HBV replication
- HBV core protein-targeting PGLYRP2 induces spontaneous viral clearance
- PGLYRP2/capsid complex enhances functional properties of immune effectors
- Loss of PGLYRP2 in hepatocytes compromises virus control during HBV infection

Biography

Mr. Ren studied Bioengineering at the Harbin Institute of Technology (HIT), Harbin, and joined the lab of Ming Shi in 2021. His study in the Shi laboratory of mechanistic immunology focuses on elucidating the molecular and cellular mechanisms that govern the regulation and therapeutic intervention of pattern recognition receptors in innate immunity. Current research focuses on investigating the mechanisms of inflammation in infectious disease and tumorigenesis, especially the inflammation induced by innate immune signaling.

Suchada Suphanpayak[1]*, Panuwat Wongkulab[2], Natta Padungwattanachoke[1], Nutcha Leelarthaphin[1], Hathaichanok Haughongthong[1]

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Diagnostic performance of real-time PCR kits for the detection SARS-CoV-2 from fecal swab in COVID-19 patients, Rajavithi Hospital, Thailand

Coronavirus Disease 2019 (COVID-19), caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), is a pandemic disease that can manifest with fever, pneumonia and /or gastrointestinal symptoms with vomiting and diarrhea. Currently, the diagnosis is based on RT-PCR technique in respiratory specimens. Nasopharyngeal swab and throat swab specimens are the gold standard routine method for detection SARS-CoV-2. Some studies reported that the virus can persist for a long time in feces, and it has been proposed to perform SARS-CoV-2 RT-PCR testing on fecal specimen. Thus, the objective of this study was to evaluate the efficacy of real-time PCR kits to identify SARS-CoV-2 in fecal swab. A total of 41 confirmed Covid-19 patients were enrolled in this study from November 2020 to March 2021 at Rajavithi hospital. Real-time PCR results showed that 33/41(80.48%) patients detected for SARS-CoV-2 in nasopharyngeal swab and throat swab, while 16/41 (39.02%) detected in fecal swab. Among the 41 fecal swab samples, we found that 16 samples were detected (16/41), 22 samples were not detected (22/41) and 3 samples were invalid (3/41). Also, we compared with Real- time PCR kits (A, validated by manufacturer) and (B, used in Biomolecular lab, Rajavithi hospital). The sensitivity and Positive Predictive Value (PPV) of real-time PCR kit (B) were 100% and 100%. These results demonstrate that real-time PCR kit was high sensitivity and it can be used for diagnosis of SARS-CoV-2 from fecal swab. Although, we found that detection rate of SARS-CoV-2 in fecal swab was very low but sensitivity of real-time PCR kit was high. Thus, may be fecal swab could be an alternative specimen for the diagnosis of COVID-19 using Real-time PCR kit in some cases.

Keywords: COVID-19, Real-Time PCR Kit, SARS-COV-2, Fecal Swab.

Biography

Suchada Suphanpayak has completed her B.Sc. (Medical Technology) and M.Sc. from Mahidol University. She is the director of Biomolecular Laboratory, Department of Clinical pathology and Medical Technology, Rajavithi Hospital, Thailand.

Esete Assefa[1,2]*, Mesfin Tefera[1], Yoseph HaileMariam[1], Birke Teshome[1], Hiwot Ketema[1], Anjelo Asha[1], Aklog Afework[1], Asefash Getachew[1], Raheal Fikade[1], Berhane Beyene[3], Emmanuael Douk[3], Eshetu Wassei[3], Atetegeb Maru[1], Wubayehu Kasa[1], Yalew Gemechu[1], Habtamu Tilahun[1], Mikiyas Aliyu[1], Kathleen Gallagher[4], Matanock Almea[5], Mesfin Wossen[1]

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Epidemiology of laboratory confirmed measles virus cases under the age of ≤5 in Ethiopia, 2017-2021

Background: Measles is a highly contagious viral infection causing large outbreaks all over the world. Despite the availability of safe and cost effective vaccine, measles remained endemic with persistent periodic outbreaks in the Horn of Africa. The aim of this study is to characterize laboratory confirmed measles cases in the highly affected regions of Ethiopia.

Method: A suspected measles case was defined as any person presenting with fever, maculopapular rash and one or more of the three symptoms cough, coryza or conjunctivitis or a patient in whom a clinician suspects measles. A blood sample was collected for any measles suspected patient with a case based investigation form and specimen transported to the National Measles Laboratory in good condition where it was to be tested for Measles IgM antibody by ELISA technique. Data was entered, finaly merged and analyzed at National Measles laboratory using Epi-Info 3.5.3 software.

Result: A total of 13353 samples were tested for measles IgM over year (2017-2021) and of these 6286 with age ≤5. Of the tested samples, 1338 (21.3 %) were found positive, while 4103 and 134 samples were found to be negative and equivocal (compatible) respectively. Around 711 samples were not tested due to kit shortage Patients with age ≤5 years were the most affected. The most affected region Oromia 616(46%), Amhara 235(17.6%) and Addis Ababa185 (13.8%) sequentially. A seasonal peak was noted in the hot-dry season of the year.

Conclusion: Measles remains to be a public health problem in all Region of Ethiopia, mostly affecting people ≤5 years of age. Measles virus was detected in all zones of the state, reaching its peak in the hot-dry season. To reduce the incidence of measles, it is highly recommended to improve routine immunization, and conduct a wide age group campaign. Additional research to evaluate the knowledge, attitudes and practices of the general population and health care professionals about measles infection and vaccination is important. Genotyping of circulating measles virus strain is recommended.

Key words: Measles, IgM, ELISA, Equivical.

Audience Take Away Notes

- To know the epidemiology of the Measles virus in Ethiopia
- To assess the possible risk factors for the Measles virus
- To conduct genotyping of circulating measles virus strain
- To evaluate sero-convergent of the measles vaccine in a county
- To work with other researches to strength the capacity of the country

Biography

Esete Assefa, was born in Addis Ababa, Ethiopia. After finishing high school at St'Marry catholic school. She performed her Bsc by Medical laboratory in Jimma University. She studied her Msc in clinical laboratory microbiology in AAU. She is working at Ethiopian Public health institute (EPHI) as researcher. She was working also with different responsibility as Bio-safety officer, focal person of Measles and Rubella, supervisor of the laboratory and coordinating the National polio and Measles laboratory at EPHI .And now she is attending her PhD at Jimma university at department of Medical Microbiology.

Huseynov Elchin Mammad
Azerbaijan Medical University, Azerbaijan

Infectious diseases as a medical, social-economic and humanitarian problem

Due to the rapid and widespread distribution, high mortality in the acute period, and persistent residual effects leading to disability and side effects on pregnancy, and the fetus, infectious diseases are always under the close attention of society and all states. In addition, they require substantial economic expenditures for the diagnosis, treatment, and rehabilitation of patients and large-scale prevention. In recent years, threats of the use of pathogens of infectious diseases and their toxins for terrorist purposes among the population and farm animals (bioterrorism) have become more frequent. This could lead to a humanitarian catastrophe, destruction of food stocks, and enormous economic damage.

Keywords: Infectious Diseases, Critical Situations, Intensive Care, Epidemic, Pandemic, Bioterrorism, An Economic and Humanitarian Disaster.

Biography

Elcin Huseynov has completed his PhD at the age of 30 years from Azerbaijan Medical University. He is the director of Lokbatan Medical Center. He has published more than 15 papers in reputed journals.

Anna Kloc, Anais Gardere, Samantha Palermo

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Assessment of parvovirus B19 activation in human heart tissue samples

Myocarditis is the inflammation of the heart muscle (myocardium). The heart's capacity to pump blood may be affected by such inflammation. Chest pain, breathing difficulty, and irregular heartbeat, known as arrhythmia, can all be symptoms of myocarditis. The cardiac muscle may be inflamed as a result of bacterial, viral or parasitic infection, although viruses are thought to be the most common cause. Previously, Parvovirus B19 has been shown to cause acute cases of heart inflammation. This single-stranded DNA virus is associated with the fifth disease, a common childhood illness that causes a number of symptoms including fever, joint pain, rash and anemia. Even though the virus does not directly infect cardiomyocytes, the cardiac damage is thought to occur via infection of endothelial cell of the myocardial vessels and activation of inflammatory cells. The persistence of Parvovirus B19 in cardiac tissue after the initial infection is a well-documented phenomenon that has been associated with atypical angina pectoris and mitochondrial impairment. Because Parvovirus B19 has also been found in the hearts of healthy individuals, it is not known if viral persistence can damage the cardiac tissue over time.

In this study, frozen human heart tissue samples were obtained from patients diagnosed with heart disease, as well as from individuals who had no history of heart related issues (Gill Heart & Vascular Institute-University of Kentucky). A total of 72 heart tissue samples derived from 24 patients contained three different heart layers: epicardium, myocardium, and endocardium. DNA was extracted from these tissues samples using a standard protocol. Primers specific to the Parvovirus B19 genome were used in a PCR reaction, and visualization of the PCR products was performed by gel electrophoresis. We identified the Parvovirus B19 genome in multiple heart tissue samples analyzed to date. The PCR products were verified using Sanger Sequencing, and confirmed as Parvovirus B19. Ongoing studies are focused on the assessment of Parvovirus B19 mRNA transcripts in the human heart tissue, and subsequent comparison of these transcripts in samples derived from patients who suffered from heart disease to negative controls. Such analysis may reveal a potential correlation between the reactivation of Parvovirus B19 and heart damage.

Audience Take Away Notes

- Information about myocarditis and its common causes
- The concept of viral reactivation and its importance for human disease
- Details about Parvovirus B19 infection and its impact on human health

Biography

Anna Kloc completed her PhD degree at Stony Brook University in New York. She performed the post-doctoral research at the Yale University School of Medicine, and at the United States Department of Agriculture – Plum Island Animal Disease Center. Since 2018, she has been an Assistant Professor in the Department of Biology and Environmental Science at the University of New Haven.

magnus Group

23-25 OCT

DAY 02

KEYNOTE FORUM

JOINT EVENT ON

VACCINES AND INFECTIOUS DISEASES

New optical and nanotechnologies for the treatment of infectious diseases

Human infectious diseases are among the most important problems in our healthcare system and today antibiotics are used for the treatment of a variety of diseases and infections. There is, however, increasing awareness and concern about antibiotic resistance, which prevents effective treatment of a large number of infectious diseases, and therefore there is a need for alternative treatments. Especially, for bacteria in the biofilm state that show a high prevalence of resistance to current treatment methods.

In the talk, we report new kinds of antimicrobial methods based on specific wavelength UV light and nanotechnology that lead to both the effective killing of bacterial biofilms and the prevention of bacterial biofilm formation. We discuss how UVA, UVB, and UVC can be used to kill a large number of bacteria including Pseudomonas aeruginosa, Escherichia coli, and Enterococcus faecalis. It will also be discussed how a combination of light and antibiotics can be used to kill bacteria. This synergy between light and antibiotics, called light assisted antibiotics, has been developed by our research group and we show that it can be used to reduce the usage of antibiotics and increase the disinfection effect of antibiotics. In the talk, we also discuss a novel method to fabricate nanostructures directly on a Titanium implant surface.

This technology can reduce bacterial biofilm formation on the implant surfaces and the technology could in the future be important since biofilm formation in human implants leads to a wide range of chronic human infections. Our preliminary work focus on human dental implants where 45% of patients who have dental implants have developed infections within 10 years after implantation.

Audience Take Away Notes

- The audience will learn about bacteria in the biofilm state that show a high prevalence of resistance to current treatment methods
- New antimicrobial methods based on specific wavelength UV light and nanotechnology
- How to reduce the usage of antibiotics and increase the disinfection effect of antibiotics
- How to reduce infections from human implants and especially human dental implants

Yiyu Ou, Paul Michael Petersen*

Technical University of Denmark, Department of Electrical and Photonics Engineering

Biography

Paul Michael Petersen is Full Professor in New Light Sources at the Technical University of Denmark and he is chairman of DOLL – a Photonics Green lab that tests and develops new lighting technology based on LED and diode laser technologies. He has more than 30 years of research experience in laser physics, LED technologies, and optical measuring techniques. He has headed several collaborative research projects within photonics. From 2001 until 2007 he was head of Laser Systems and Optical Materials at Risø National Laboratory. From 2002 to 2011 he was adjunct professor in Optics at the Niels Bohr Institute, Copenhagen University.

Vaccines and monoclonal antibodies in the prolonged treatment of non-small cell lung cancer: 20 years of follow-up

Lung cancer is the first cause of death from cancer in the world and in some countries as the first cause of death for both sexes. Early diagnosis and timely therapy is successful for increasing the survival of these patients, however, the masking with frequent symptoms of other diseases makes it be diagnosed in advanced stages of the disease. It is reported that a group of patients have the probability of being long-term survivors, confirming that with some therapies directed at specific targets, survival increases. For patients with non-small cell lung cancer, survival to the first line of chemotherapy has been extended with some recent immune checkpoint inhibitor therapies up to 24-26 months, but this is not the most frequent. Even this type of therapy is not accessible to all patients at this stage of the disease.

For 20 years, the Center for Molecular Immunology has been conducting clinical trials with products generated at the institution, aimed at tumor antigen therapeutic targets associated with advanced Non-Small Cell Lung Cancer (NSCLC). After analyzing more than 3,900 patients in a database integrated with all the clinical trials conducted in the period from 2002 to 2020 with the Cimavax EGF and Vaxira vaccines and the humanized monoclonal antibody nimotuzumab, it was found that around 20% of the patients had a long survival, greater than 24 months, when they were treated with immunotherapies; but also that a group of patients who were controls in these studies were long survivors.

Seeking to identify the correlation between some significant parameters in patients treated taking into account recipients, immunological inflammation, disease stage, histological type, among others, with long survival, they were analyzed through a covariate classification tree, locating as main variable survival.

Both in the control groups and in those treated with Cuban biotechnology products, it was identified that there is a bimodality in the analyzed populations and that around 7% of the patients have the probability of being long-term survivors. Depending on the product analyzed, predictive parameters of a good response to these treatments were identified, leading to the creation of a therapeutic algorithm to select the appropriate therapy. These parameters are related to the inflammatory level such as the NLR, the PLR and the histological type of the disease.

Mayra Ramos Suzarte

Center of Molecular Immunology, Cuba

Biography

Mayra Ramos Suzarte has completed his PhD at the age of 33 years from Havana Medical University and postdoctoral studies from Modena University, Oncological Medical Center, Italy and Las Condes Hospital Chile. She is the Head of Clinical trials Department at the Center of Molecular Immunology, Cuba since 2009. She has published more than 80 papers, and four books in reputed journals and has been serving as an editorial board member of repute, participated in more than 70 Conferences.

BOOK OF ABSTRACTS

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DAY 02

SPEAKERS

JOINT EVENT ON

VACCINES AND INFECTIOUS DISEASES

Kristen Lee Moriarty M.D[1]*, Pascale Carrel, B.A[1], Emma Kyrzanski[1], Kelsey Manfredi M.D[1], Lucas Godoy[2], Chia-Ling Kuo, Ph.D[2], Andrea Shields M.D[1]

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Nirmatrelvir-Ritonavir counseling and acceptance in pregnancy

The National Institute of Health recommends Nirmatrelvir-Ritonavir (NIR) treatment for pregnant patients with COVID-19. However, little is known about NIR treatment acceptance rates in pregnant patients and what strategies may increase access and acceptance rates of NIR treatment. In April 2022, an NIR access program was started at our institution to offer standardized counseling and access to NIR treatment for all COVID-19-positive pregnant patients who were eligible for treatment. The access program included a standardized workflow with a high-risk nurse triaging and determining eligibility for NIR treatment in COVID-19 positive pregnant patients and a telehealth visit with a Maternal Fetal Medicine subspecialist that same day to review and offer NIR treatment. We observed a 58.3% acceptance rate for NIR treatment in our cohort (n=36). Patients who accepted NIR treatment had lower gravidity and were more likely to have the symptom of myalgia from their COVID-19 infection than those who did not accept NIR treatment. Patients who accepted NIR treatment also were more likely to be SARS-CoV-2 vaccinated although the difference (81% versus 60%) was not statistically significant (p=0.260). We did not observe any significant differences in neonatal outcomes. NIR access programs should be considered to increase access and acceptance of NIR treatment during pregnancy, and future studies with larger sample sizes should explore maternal and neonatal outcomes with NIR access programs in place.

Audience Take Away Notes

- Potential for adverse maternal-fetal outcomes with COVID-19 infection
- Importance of COVID-19 vaccination in pregnancy populations and use of paxlovid
- Increased awareness for provider counseling and instructions with Paxlovid use in pregnant populations
- Formation of formal Paxlovid counseling programs to help standardize patient education and access

Biography

Dr. Moriarty studied Chemistry at La Salle University, Philadelphia and graduated Maxima Cum Laude in 2014. She attended medical school at Drexel University College of Medicine (DUCOM). At DUCOM, she further advanced her teaching skills as a Chemistry and Organic Chemistry tutor, Anatomy Scholar tutor, and multidisciplinary Academic Coach. She completed her Obstetrics and Gynecology Residency at the University of Connecticut Health where she served as Administrative Chief Resident. She has worked on several research projects, presented at various regional meetings, and published one of her projects in a high-impact journal, Placenta. She received the Dr. James Egan Award for Outstanding Obstetric Research Project in 2022.

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A rare case of cerebral phaeohyphomycosis: Tissue biopsy to the rescue

Primary cerebral phaeohyphomycosis is a rare infection caused by brown-black pigmented fungi, namely dematiaceous fungi that can cause infrequent but devastating CNS infection due to their recognised neurotropism. Cladophialophora bantiana is recognised as the most common cause of cerebral phaeohyphomycosis. While intracerebral fungal abscesses have been historically associated with immunocompromised patients, C bantiana has a predilection for immunocompetent hosts. Successful treatment depends on accurate microbiological and histopathological diagnosis and initiation of targeted antifungal treatment.

We hereby report a case of 64 year old male, known hypertensive, chronic smoker, who presented with complaints of bilateral lower limb pain with blackish discoloration of left foot and left foot drop for 1 month. Patient also had breathlessness for 4 days. On examination, He was hemodynamically stable. Dorsalis pedis and posterior tibial pulsations were absent in left lower limb. He was planned for trans femoral embolectomy based on doppler findings which showed thrombotic occlusion of all major vessels. He then developed lower respiratory tract infection due to which the procedure was deferred. On investigations, he was found to have a hemoglobin of 21.1g/dL with PCV of 65.7. Workup for thrombophilia showed JAK-2 mutation positive. Patient underwent phlebotomy for the same. Patient had an episode of dizziness and headache following which MRI brain was done and it showed space occupying lesion in left cerebellum with haemorrhage. PET CT whole body was done which revealed FDG avid pleural based nodular lesion in the left lung along with findings consistent with MRI brain. Biopsy of lung nodule revealed necrotizing granulomatous inflammation and gram stain, KOH, cultures were negative. Anti tubercular treatment was started. Repeated blood cultures were sterile. During course of hospital stay, patient developed sudden onset altered sensorium with involuntary movements of right upper limb and dysphasia following which he was intubated for airway protection. CT brain showed left cerebellar lesion with mass effect for which steroids were added. Patient's sensorium did not improve and MRI brain was repeated which showed increase in size of lesion with multiple cerebellar abscesses in the posterior fossa region, most likely pyogenic or fungal and likely vasculitic subacute infarcts in the left side of the pons and right inferior cerebellar region. Trans Esophageal Echo showed no evidence of vegetation. Steroids/Anti tubercular drugs were discontinued and Amphotericin B was added to the treatment. Autoimmune work up was normal. Brain biopsy was done which showed growth of Cladophilophora bantiana. Echinocandin was added. Despite treatment, patient succumbed to illness after 50 days of treatment.

Audience Take Away Notes

- Phaeohyphomycosis affects immunocompetent individuals
- Brain biopsy is the gold standard for diagnosing of these rare fungal infections
- Early tissue biopsy with aggressive medical and surgical management for the same plays a crucial role

Biography

Dr. Rahul Kumar studied at the University College of Medical Sciences, New Delhi and graduated in 2021. He is currently pursuing DNB Medicine (2nd year) at Sir Ganga Ram Hospital, New Delhi. He has represented his institution at various conferences all over India and presented multiple cases at some of these platforms. He has achieved second prize in Dr. SD Deodhar All India intercollegiate Post Graduate Rheumatology Quiz (2022) and has had an abstract published in the Journals of Association of Physicians of India – APICON 2023 platform, titled "An interesting case of heart failure". He has active participation in academics and passion for teaching.

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Mometasone furoate nasal spray on recovery of long-term olfactory dysfunction due to covid-19: A systematic review and meta-analysis of a randomized controlled trials

PubMed, Cochrane, and Embase databases were searched for RCTs. Data were extracted from published reports, and quality assessment was performed according to PRISMA guidelines. We used a fixed-effect model to calculate the Risk Ratio (RR) and the 95% Confidence Interval (CI). Endpoints of interest were: recovery of olfactory dysfunction, with partial or full response. This review's protocol was registered at PROSPERO, under the number CRD42022382930. Four RCTs studies were included with a total of 340 participants, of whom 146 (42, 9%) were randomized to receive mometasone furoate nasal spray. These participants on average had persistent anosmia or severe microsmia for more than 3 weeks. Completely recovered sense of smell (RR 1.47; CI 95% 1.17-1.84; p = 0.001; I2 = 24%; Figure 1) was significantly higher in patients treated with mometasone furoate nasal spray compared with the control group. Partial or fully recovered from anosmia (RR 1.53; CI 95% 1.19-1.96; p = 0.0009; I2 = 3%; Figure 2) was also significantly increased in the mometasone furoate nasal spray group when compared to the control group. Our meta-analysis suggests that mometasone furoate nasal spray is effective in the recovery of long- term olfactory dysfunction due to COVID-19.

Audience Take Away Notes

- Several patients have reported persistent olfactory dysfunction after recovering from COVID- 19. We performed a systematic review and meta–analysis of randomized controlled trials (RCTs) to evaluate the efficacy of mometasone furoate nasal spray for long-term olfactory dysfunction due to COVID-19

Biography

Nicole Vieira-Pires is a Science Research Fellow and student Columbia College, Columbia University, NY, pursuing a degree in Neuroscience & Behavior. After two years at Columbia, she has conducted four research projects in the fields of Neuroscience, Endocrinology, and Infectiology. Born and raised in Brazil, her future plans include pursuing an MD-PhD Program in order to continue her scientific career in the United States.

Megha Priyadarshi[1]*, Saurav Sekhar Paul[2], Manish Soneja[3]

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Antibiotic induced bartter syndrome - A systematic review

Background: Bartter syndrome encompasses salt-losing tubulopathies characterized by hypokalemia, hypochloremic metabolic alkalosis, and hyperreninemic hyperaldosteronism with normal blood pressure.

Acquired Bartter or Bartter-Like Syndrome (BLS) is commonly associated with the use of diuretics and antibiotics such as capreomycin, netilmicin, colistin, amphotericin B, cyclosporine, cisplatin. This systematic review was done to understand the time of occurrence of Bartter syndrome post inciting drug and gain knowledge regarding its progression and management.

Methods: A systematic search following the Preferred Reporting Items for Systematic reviews and Meta-Analyses (PRISMA) guidelines was performed in Pubmed, Google Scholar, Embase, medRxiv, and bioRxiv. All case reports, case series, and review articles published in literature from 1986 till March 2022 were screened. Thirty-nine cases were finally included for the review.

Results: Among the 39 cases, the mean age of presentation was 36yrs (SD: 19.8yrs, range 7-92yrs), with a Male: Female ratio of 1:2.7. The most common antimicrobial causing BLS was Aminoglycosides (60%), followed by colistin (32.5%), among the aminoglycosides -Gentamicin was most commonly implicated(62.5%), followed by Streptomycin and capreomycin (12.5% each), Amikacin, netilmicin, and tobramycin(4.1% each). The time of presentation after inciting antibiotic was a median of 8 days (IQR 6-23days).

All cases presented with metabolic alkalosis with a mean pH of 7.49(SD: 0.038, Range: 7.43 – 7.60), and a mean bicarbonate level of 32.9(SD: 4.70). Presenting features of distal tubulopathy was in the form of polyuria, hypokalemia (100%, mean: 2.37meq/L), hypomagnesemia (85%) and hypocalcemia (77.1%), hypercalciuria (51.85%), and urinary potassium loss in the form of raised 24 hr urinary loss or spot potassium/creat ratio or raised Transtubular potassium gradient evident in all the cases (n=39,100%). All the cases were managed with electrolyte supplementation while a few cases with refractory hypokalemia were given spironolactone and NSAID. The median time for resolution of Bartter-like syndrome was 13.5days (IQR: 6-30 days).

Conclusions: Bartter-like syndrome (BLS), although a rare entity should be suspected in patients presenting with features of salt-losing tubulopathy on antimicrobials. The most common drug class implicated is the aminoglycosides (Gentamicin> Streptomycin, Capreomycin). Discontinuation of the inciting drug leads to complete reversal of the state.

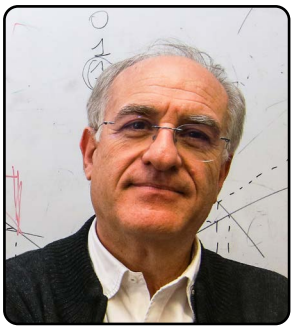
Audience Take Away Notes

- Many antimicrobials may present as Bartter- like syndrome(BLS)
- Most common being the aminoglycoside group followed by polymyxin
- A high index of suspicion for diagnosis in the absence of diuretics with clinical, laboratory, and acid-base features consistent, may lead to suspicion of BLS
- Management is mainly supportive of electrolyte replacement and recovery is seen in all cases after stopping the drug

- If undiagnosed, can lead to significant morbidity and increased hospital stay in these patients

Biography

Dr. Megha Priyadarshi did her commpletd her undergraduation in Medicine at the prestigious Lady Hardinge Medical College in New Delhi. She then joined as a resident in the department of Internal Medicine, Infectious disease super-speciality in All India Medical Sciences, New Delhi. She has keen interest in the fields of antimicrobial resistance, invasive fungal infections. She worked meticulously in the covid pandemic and tended to patients with covid associated mucormycosis and published an article on the risk factors of the same. Apart from academics and research she is a Indian classically trained vocalist, a mountaineerer and a charcoal artist.



Massimo Florio
University of Milan, Italy

Mapping of long-term public and private investments in the development of COVID- 19 vaccines

This study provides a mapping of funds contributed by different actors for the R&D and the expansion of the production capacity of COVID-19 vaccines, with a focus on those authorised in the EU. Nine vaccines are examined. It is found that governments, mainly the US (with some not-for-profit entities) decisively supported corporate investments, either for R&D, manufacturing, or both, by nearly EUR 9 billion, i.e. on average EUR one billion of grants per vaccine, with, however, vast variance across companies. Moreover, almost EUR 21 billion was allocated to companies through Advance Purchase Agreements. While the EU and MS support through Advance Purchase Agreements was key to de-risk the production of vaccines, the role of EU and MS support in directly supporting R&D was marginal compared with the US federal government. The study assesses the necessity for continuing public support to R&D on vaccines for SARS-CoV-2 future variants of concern and possibly other coronaviruses. After highlighting current market failures, new incentive mechanisms in the public interest for vaccine R&D are suggested to grant equity and accessibility, as well as rewards in line with risks.

Biography

Massimo Florio is Full Professor of Public Economics, University of Milan, Italy, and formerly Department Chair, now co-chair of the Jean Monnet Centre of Excellence on European research and innovation policy . His research interest include social cost-benefit analysis, industrial policy, innovation policy and economics of science. Florio is author of over one hundred papers in scholarly journals, his books include " Investing in Science " (the MIT Press, 2019) and " The Privatisation of Knowledge" (Routledge, 2023). He has recently lead an independent study for the European Parliament about the public and private funding of seven COVID - 19 vaccines, leading to policy recommendations adopted by the July 2023 plenary session of the Parliament .

Gangoo Dana[1]*, Gul Zonaira[2]

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Role of infectious disease intervention and medical management in a rare case of aureobasidium pullulans

Introduction: A report on a rare case of fungemia due to Aureobasidium pullulans and the role of Infectious Disease in the evaluation and medical management of this skin condition.

Case presentation: A 42-year-old man with past medical history of Chronic Alcohol Abuse disorder, history of Esophageal esophagitis (treated with Omeprazole, asymptomatic for the past 3 years), and history of Depression (on Paroxetine), presented with skin lesions, initially positive for Methicillin-Susceptible Staphylococcus Aureus. The patient was given Doxycycline for 6 weeks along with Rifampin for 3 days for management of MSSA. The lesions decreased in size with antibiotic treatment, however later returned. Lesions were re-cultured and found to be positive for Pantoea. The patient had completed multiple courses of antibiotic therapy and was referred by Dermatology to Infectious Disease. Infectious Disease workup was completed, patient tested negative for HIV. Infectious Disease referred the patient to Surgery for skin biopsy for fungal cultures with AFPB stain, Gram stain, and routine bacterial cultures. Skin biopsy revealed epidermal thickening, no squamous dysplasia, and no signs of malignancy. Fungal cultures were positive for Aureobasidium pullulans. At which time, Infectious Disease was able to initiate medical management with IV Micafungin for 4 weeks and IV Liposomal Amphotericin B for 4 weeks, with significant improvement of skin lesions.

Conclusion: Identification of Pantoea species with skin biopsy and fungal culture as requested by Infectious disease, lead to effective medical management of fungemia due to Aureobasidium pullulans with IV antibiotic therapy resulting in resolution and improvement of skin lesions.

Biography

My name is Dana Gangoo. I am presently a 4th Year medical student with Saint James School of Medicine, Saint Vincent and the Grenadines. I am also presently a Clinical Assistant for Essen Healthcare. I was born on the Caribbean island of Trinidad and Tobago. My hometown is Plantation, Florida. I attended Vanderbilt University College of Arts and Science for my Undergraduate degree, and earned my Masters in Science from the University of South Florida College of Medicine. I have a passion for patient care, education, and research.

My future career goal is to work as a Hospitalist in an underserved community, with a focus on providing informative transition of care. I hope to be heavily involved in Quality Improvement throughout my career as a physician. I try to leave any environment I have been a part of better than when I entered, be it by uplifting the staff, facilitating effective care, and assisting in any area of need. Hobbies include spending time with my cockatoo, miniature schnauzer, and 3-year old beta; cooking; teaching kids around the world virtually; sightseeing as much as I can; traveling internationally; learning about other cultures, cuisines, and religions; and massage therapy.

Muhiddin Fayazov
Scott Edil Pharmacia, Uzbekistan

Meningococcal infection

Meningococcal infection is an acute respiratory infectious disease disease caused by meningococcal, characterized by a wide range from asymptomatic bacterial carriage to sepsis.

Aetiology: The causative agent is Neisseria meningitides. 12 serogroups, the most common are A, B, C. All but group B have capsules. More than 20 serotypes. Unstable to environmental factors. Produces strong endotoxin.

Epidemiology: The source of infection is a sick person or carrier. The transmission route is airborne. For one generalized form - from 100 to 10000 carriers. Up to 5% of children in DDUs are infected every year. Sources of infection:

- Generalized forms - 1-3%;
- Nasopharyngitis - 10-30%;
- Carriers 70-80%.
- Seasonality - winter-spring.

Pathogenesis: The entrance gate is the mucous membranes of the nasopharynx. Ways of spreading-hematogenous, less often through the ethmoid bone. In children due to immaturity of the blood-brain barrier and of the immune system, generalized forms occur more often. There is discirculation in the cerebral and membrane vessels. Hypersecretion of cerebrospinal fluid and delayed resorption. Overstimulation of the meninges of the brain and nerve roots. Intoxication. Changes in hemocoagulation.

Clinic: The incubation period is from 2 to 10 days.

Classification: Localized forms (carriage of meningococcus, acute nasopharyngitis). Generalized forms (meningococcemia, meningitis, mixed forms). Rare forms (endocarditis, arthritis, pneumonia, iridocyclitis).

Meningococcemia: High degree of intoxication. It occurs acutely, with a rise in temperature, usually against the background full health. A rash appears 8 to 24 hours after the onset of the disease.

Features of the rash with meningoccemia:• Roseolous with a hemorrhagic component in some elements. Star-shaped, spotted, hemorrhagic. Cloudy, common, hemorrhagic. Localized on the lower half of the body, legs, buttocks. Prone to fusion and spread, progresses rapidly.

Complications of meningoccemia: Multiple organ failure, Yoterhouse-Friederiksen syndrome. DV syndrome.

Chryso Th Pallari[1]*, Vasiliki Christodoulou[2], Maria Koliou[3], Alexander N G Kirschel[1]

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First detection of WNV RNA presence in field-collected mosquitoes in cyprus

West Nile Virus (WNV) infections have increased over recent years to the extent that WNV has become one of the most widespread arboviruses in the world, with potential consequences for both human and animal health. While much is known about WNV and the vectors that transmit it from their primary hosts across continental Europe, little is known about the epidemiology of the disease on the island of Cyprus. In this study, the aim was to investigate the prevalence of WNV infection in potential mosquito vectors for the first time in the Republic of Cyprus, using WNV surveillance of mosquitoes. Mosquitoes were collected in 2019, during which an outbreak in humans had occurred, and sampled mosquitoes were then examined for WNV infection by testing them for the presence of WNV RNA. Of 126 mosquito pools tested, one pool, containing Culex pipiens mosquitoes sampled from the Nicosia district, was found to be positive for the presence of WNV RNA. The positive pool found in this study represents the first demonstration of WNV in mosquitoes in Cyprus and confirms that human cases in Cyprus are likely the result of transmission via local Culex mosquitoes.

Biography

Chryso Th. Pallari is a Post-Doctoral Research Fellow at the University of Nicosia Medical School. Dr. Pallari holds a BSc (First-Class Honours degree) in Biological Sciences, and a PhD in Biomedical Sciences from the Department of Biological Sciences at the University of Cyprus. Her research interests are in the fields of epidemiology and infectious diseases. She is particularly interested in the epidemiology and extent of West Nile Virus (WNV) in Cyprus. Furthermore, she has extensive experience in the classification of mosquitoes and her research interests also cover the field of entomology, vector-borne infections, and statistics. She performed her diploma dissertation at the Tumour Viruses and Cancer laboratory, where she investigated the in vivo interaction of the HPV16 oncogenes and telomerase in mouse epithelium. Her PhD Thesis was then performed at the Behavioural Ecology and Evolution laboratory and investigated the epidemiology of WNV in its primary hosts and potential vectors in Cyprus. Her research findings represent the first demonstration of WNV in mosquitoes in Cyprus.

Mayra Ramos-Suzarte*, Tania Crombet-Ramos, Patricia Lorenzo-Luaces, Carlos Hidalgo- Mesa, Yayquier Diaz, Danay Saavedra-Hernandez, Ana Laura Añé Kourí, Mayelin Troche Concepción, Loipa Medel Pérez, Meylan Cepeda Portales, Leticia Cabrera Benítez, Ana Rosa Vals Hung, Milagros Domenecq, Lazara Garcia Fernández, Lizzet Sanchez, Carmen Viada Gonzalez, Yanelda Garcia Vega, Maylen Arencibia Lago, Yanela Santiesteban Gonzalez, Martha María Fors López PhD, Kalet León Monzon

Center of Molecular Immunology, Cuba

Observational study post emergency use authorization of itolizumab in the treatment of COVID-19

Introduction: COVID-19 continues to be a global health problem, it is a multifactorial disease characterized by a process of hyperinflammation. Itolizumab, a humanized anti-CD6 mAb, has the Emergency Use Authorization (UEA) for patients with this disease with signs of hyperinflammation.

Methods: An observational study was conducted to evaluate the safety and efficacy of itolizumab. The study was approved by the MINSAP and the Ethics Committee of the IPK CEI-IPK 63-20(RPCEC00000402; The dose was 1.6 mg/kg, every 72 hours, up to a maximum of four administrations, over a period of six hours, with antihistamine and glucocorticoid premedication to avoid infusion reactions. A retrospective cohort study was conducted using the propensity score.

Results: 249 patients, treated in twelve hospitals from September 2020 to May 2021 were studied. The related SAEs were 0.8% of the total, immunosuppression in those patients was not reported. Lung functions improved 85.9% from the first 48 hours. The ROC curves showed that total leukocytes greater than 6.7, PLR ≥94.37 and NLR >2.21 predict the risk of death. The risk of death in those not treated with Itolizumab was 2.54 (1.18; 5.46) times higher (p=0.007). The Attributable Fraction in Untreated with MAb reveals that 60.7% IC95%: [15.3% ; 81.7%] of the deaths among those not treated could have been avoided had they received itolizumab. The risk of admission to therapy in those not treated was 2.2 (1.45; 3.33) times higher than the risk of admission to therapy in those treated with itolizumab (p =0.000). The population attributable fraction of 0.38 means that, in a prospective scenario, a 38.1% 95% CI: [17.4%; 53.7%] of the deaths in the severe or critical population could be avoided if they were treated with Mab.

Conclusions: Itolizumab is recommended for use in moderate-stage COVID-19 pneumonia with signs of inflammation or severe with inflammatory indices less than the cut-off values of this study.

Biography

Mayra Ramos Suzarte has completed his PhD at the age of 33 years from Havana Medical University and postdoctoral studies from Modena University, Oncological Medical Center, Italy and Las Condes Hospital Chile. She is the Head of Clinical trials Department at the Center of Molecular Immunology, Cuba since 2009. She has published more than 80 papers, and four books in reputed journals and has been serving as an editorial board member of repute, participated in more than 70 Conferences.

Elena Ioniţă[1,2], Aurelian Marcu[3], Mihaela Temelie[1], Diana Savu[1], Mihai Şerbănescu[3,4], Mihai Ciubotaru[1,2]*

[1]Horia Hulubei National Institute for R&D in Physics and Nuclear Engineering, Department of Physics of Life and Environmental Sciences, Măgurele, Ilfov, 077125, Romania

[2]Colentina Clinical Hospital, Department of Immunology, Internal Medicine, 72202, Bucharest, Romania

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Radiofrequency EMF irradiation effects on pre-B lymphocytes undergoing somatic recombination

DNA Double Stranded Breaks (DSBs) occur in lymphocytes exposed to intense Electromagnetic Fields (EMFs). We study developing pre-B lymphocytes following V(D)J recombination at their Immunoglobulin Light chain loci (IgL). Recombination physiologically induces DNA DSBs, and we tested if low doses of EMF irradiation affect this developmental stage. Recombining pre-B cells, were exposed for 48 hours to low intensity EMFs (maximal radiative power density flux S of 9.5 5 □W/cm2 and electric field intensity 3 V/m) from waves of frequencies ranging from 720 to 1224 MHz. Irradiated pre-B cells show decreased levels of recombination, reduction which is dependent upon the power dose and most remarkably upon the frequency of the applied EMF. Although 50% recombination reduction cannot be obtained even for an S of 9.5 □W/cm2 in cells irradiated at 720 MHz, such an effect is reached in cells exposed to only 0.45 □□W/cm2 power with 950 and 1000 MHz waves. A maximal four-fold recombination reduction was measured in cells exposed to1 GHz waves with S from 0.2 to 4.5 □W/cm2 displaying normal levels of □H2AX phosphorylated histone. Our findings show that developing B cells exposure to low intensity EMFs can affect the levels of production and diversity of their antibodies repertoire.

Audience Take Away Notes

- Our data address for the first time how the wireless communication EMF fields impact the repertoires of differentiating B lymphocytes
- We will address in our presentation whether irradiated B cells can elicit an unaltered antibody response in response to antigen challenge, or novel infections
- The methodology used in our study could be extended to investigate the effect on humoral immunity of other exogenous agents (chemicals or biological agents thought to be innocuous), hence it can be of immense benefit for clinicians

Biography

Dr. Ciubotaru studied Medicine at the School of Pharmacy and Medicine "UMF-Carol Davila" Bucharest Romania and graduated as MS in 1992. He then joined in 1997 as a graduate student the research group of Prof. Gerald Koudelka at the University of Buffalo Biological Sciences USA. He received his PhD degree in 2000 at the same institution. After 3 years postdoctoral fellowship supervised by Dr. David G. Schatz at the Immunobiology Department Yale School of Medicine USA he obtained first an Associate Research Scientist position at the same department where he worked until 2012. In 2013 Dr. Ciubotaru returned to Romania as a Principal Investigator Senior Research Scientist at Colentina Clinical Hospital, Department of Immunology, Internal Medicine, Bucharest, Romania, where he currently works leading a team of six trainees (graduate students and postdocs) in Immunobiology. He has published more than 15 research articles in SCI(E) journals, and some of his developed work makes the object of 3 patents.

Mukhayyo Khodjaeva
Scott Edil Pharmacia, Uzbekistan

Emergencies at the clinic of infectious diseases

Shock, Acute respiratory failure, Coma, Swelling-swelling of the brain, Acute hepatic insufficiency, Acute renal failure. Shock is an acutely developing general reflex pathological reaction of the body in response to the action of extreme stimuli with inhibition of all body functions.

Types of shock in the clinic of infectious diseases: Infectious-toxic, Dehydration, Anaphylactic.

Pathogenetic types of shock: Circulatory - an increase in the volume of the circulatory bed with stored circulating blood volume. Hypovolemic - a decrease in the volume of circulating blood with the preserved volume of the circulatory bed.

Infectious-Toxic shock (Tss): An emergency condition that occurs under the influence of a living pathogen and its biologically active substances, which is expressed by a complex of pathological changes in the activity of all physiological systems due to excessive or inadequate compensatory reactions and a violation of vital functions of the body, which are based on heavy disorders of microcirculation, metabolism and tissue hypoxia.

Damaging factors of Tsh: Endotoxins (lipopolysaccharides of the bacterial cell wall). Inflammatory mediators:

- Tumor necrosis factor;
- Interleukin 8;
- Prostaglandins;
- Catecholamines.

Features of Itsh from the pathogen: Gram-negative shock (70% of cases) - activation of the sympathoadrenal system - hypercatecholaminemia (mild agitation, intoxication, spasm of small vessels, cyanotic skin, cold). Gram-positive shock (30% of cases) – early stage – warm dry skin, hypotension (warm shock).

Itsh clinic: Early phase of shock - severe intoxication (shock index - Allgover index - 0.9-1.0), decrease in diuresis (less than 25 ml / hour, 0.35 ml / kgper hour for an adult). Phase of severe shock (heart rate - 120-140 per minute, blood pressure < 90 mm Hg, SHI > 1.5, BH > 30, oliguria: diuresis - less than 15 ml / hour). Late phase of shock - patients in a coma, cold, total cyanosis, hypothermia, a symptom of a "white spot" (more than 2 seconds), blood pressure < 50 mm Hg, shortness of breath, respiratory arrhythmia.

Laboratory criteria for shock severity: Leukocytosis > 10,000 / μl, Thrombocytopenia < 100,000/μl, Fibrinogen < 1.5 g/l, Decompensated acidosis.

Diagnosis criteria: The presence of fever and toxicosis at the onset of the disease. Tachycardia exceeds the level of fever, in the future occurs normalization of body temperature. Lowering blood pressure. The appearance of acrocyanosis, oliguria. Change in cardiac output, minute volume of the heart, CLA. Development of DIC syndrome. Leukocytosis or leukopenia and p / i shift more than 10%. Decreased oxygen volume, high lactate levels, pronounced metabolic acido.

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Applying machine learning and deep learning for multiclass classification of arboviral diseases: A comparative analysis

Motivation: Arboviral diseases, a significant subclass of Neglected Tropical Diseases, impose a considerable health burden globally, particularly in lower-income nations. Dengue, Chikungunya, and Zika trio account for a high proportion of morbidity and mortality in Latin America, South East Asia, and South America. The task of early diagnosis is complex due to symptom similarities and serologic test cross-reactions. Resource limitations, including testing kits, exacerbate the situation in remote locations, hindering timely diagnosis and management. Machine Learning (ML) has recently been employed to aid clinicians in distinguishing these arboviral diseases. However, previous research primarily focused on binary classification using ML algorithms, with scant attention given to multi-class disease classification. To our knowledge, prior studies have yet to explore the application of Deep Learning (DL) algorithms for the multi-classification of arboviral diseases.

Hypothesis: ML and DL algorithms can effectively facilitate multi-class classification of arboviral diseases using clinical and epidemiological data.

Methods and Results: This research uses clinical and socio-demographic data to evaluate the efficacy of diverse ML and DL algorithms for the multi-class classification of Dengue, Chikungunya, and inconclusive cases. The Synthetic Minority Oversampling Technique (SMOTE) was implemented to address imbalanced data. The models were also validated on an external testing dataset. The results reveal that the Random Forest algorithm offered superior performance, achieving an Area Under the Curve of Receiver Operating Characteristic (ROC AUC) of 99% on the validation set and 83% on the external test set. DL models accomplished a ROC AUC of 86% and 87% on the validation and external test sets, respectively.

Conclusion: This study demonstrated the applicability and impressive performance of ML and DL algorithms in the multi-class classification of arboviral diseases using exclusively clinical and epidemiological data. Our models hold promise for supporting clinicians in distinguishing arboviral diseases, especially in resource-constrained environments where laboratory-based diagnoses are not feasible.

Keywords: Arboviral Diseases, Clinical Support System, Deep Learning, Machine Learning, Multi-Class Classification.

Audience Take Away Notes

- Provide an automated clinical decision support system for differentiating diagnosis of dengue and Chikungunya disease
- This research could be applied in other infectious diseases
- This research provide a practical solution to the arboviral diseases diagnosis problem, especially in resource-limited areas

Biography

Thanh Huy Nguyen got a Master degree in Global health and development in 2021, with his expertise in Dengue fever outbreaks and research interest in Machine learning and arboviral diseases. He is now a third-year student of the International Ph.D. program in Medicine at Taipei Medical University, Taiwan.

Ismail Hossain

Department of Quality Assurance, Globe Biotech Ltd, Bangladesh, University Of Asia Pacific, Dhaka, Green Road,1205, Dhaka, Bangladesh

A cross-sectional study to evaluate people's knowledge, attitude and practice towards using disinfectants and sanitizers during COVID-19 pandemic in Bangladesh

The devastating novel coronavirus (COVID-19) pandemic worldwide has become a global health crisis. This disease is highly contagious and caused by the transmission of severe acute respiratory syndrome, coronavirus 2 (SARS-CoV-2). To prevent the transmission of SARS-CoV-2, disinfectants and sanitizers are very effective and readily available preventive agents. In this study, Knowledge, Attitude and Practice (KAP) levels of Bangladeshi people's were assessed regarding the use of disinfectants and sanitizers during the pandemic Situation. An online questionnaire-based survey was conducted among the respondents from February 2021 to December 2021. A total number of 410 respondents participated in this survey. Data were analysed by the Statistical Package for the Social Sciences (SPSS) and interpreted. Results revealed that most of the respondents were knowledgeable, had a positive attitude and engaged in beneficial practice. Among the respondents, a significantly higher knowledge and practice score were observed among females (54.1% and 54.4%, respectively) than their counterpart. Moreover, people living in urban areas (75%) had a better attitude than the rural people (25%). In addition, a medium positive correlation between knowledge and attitude (r = + 0.482), a weak positive association between attitude and practice (r = +0.199), and a weak positive association between knowledge and practice (r = + 0.282) were found. Overall, majority of the respondents had better KAP scores in knowledge and attitude with relatively low scores in practice which indicates some space for betterment.

Key words: COVID-19, KAP, Disinfectants, Sanitizers.

Audience Take Away Notes

- In this study, people's Knowledge, Attitude and Practice (KAP) towards using disinfectants and sanitizers during the COVID-19 pandemic were studied
- One of the major limitations of these study was that being an online based study, it mostly included participants who were habituated and had access to relevant social media and that caused majority of our study participants to be urban young adults which might not be an absolute representative sample of Bangladeshi population
- However, the information from this study can be used as baseline data by the authority to take proper steps in ensuring safer and effective use of disinfectants and sanitizers
- The participants had adequate KAP towards the use of disinfectants. Most of the participants were found knowledgeable, had a significant positive attitude and had better practice regarding disinfectant and sanitizer use
- But relatively low scores in KAP evaluation were found for a considerable number of participants, which indicated some space for betterment
- In addition, inappropriate and/or excessive use of disinfectants could cause serious health hazards. So, more efforts as well as awareness programs are needed on COVID-19 to spread awareness, improve attitude regarding disinfectant use and ensure safe disinfection practices

Biography

Ismail Hossain completed his bachelor's degree in pharmacy in 2010 from The university of Asia pacific, Dhaka, Bangladesh. After passing his Pharmacy degree he joined globe pharmaceutical ltd (globe biotech) as a Quality assurance Executive & expert in QC instrument & regularity department like different types of analytical job & deals with different types of drugs (OTC, Antibiotics, Vaccines etc).

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VACCINES AND INFECTIOUS DISEASES

Rabab Elsadek MD[1]*, Austin Auyeung MD[1], Anuoluwa Oyetoran MD[1], Mohammed F. Ismail MD[1], Sanil Thomas MD[1]

University of Central Florida College of Medicine, Graduate Medical Education / HCA Florida North Florida Hospital, Internal Medicine Residency Program, 6500 W Newberry Rd, Gainesville, FL 32605

Herpes zoster complicated with an asymptomatic irreversible neurogenic bladder and end-stage renal disease case report

Introduction: Herpes zoster (HZ) is a viral condition resulting from Varicella-Zoster Virus (VZV) reactivation. It typically presents with cutaneous symptoms, such as vesicular rash and dermatomal pain. In rare cases, sacral involvement of VZV can lead to a neurogenic bladder, causing bladder and urinary sphincter dysfunction. We report a case of a 36-year-old male who developed an irreversible neurogenic bladder and End-Stage Renal Disease (ESRD) after a herpes zoster infection.

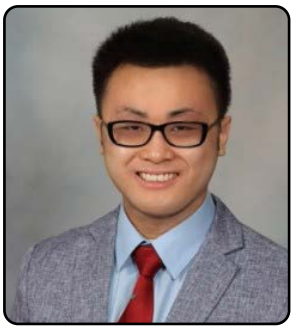
Case Presentation: Our patient is a 36-year-old male with a recent history of right thoracic HZ infection who presented to the hospital for acute kidney injury. Elevated creatinine levels and subsequent evaluations revealed bilateral hydroureter, hydronephrosis, and a severely distended urinary bladder. Despite decompression trials, bladder and kidney functions did not improve for months after presentation, and he was diagnosed with irreversible neurogenic bladder and ESRD. The workup for other possible etiologies was negative, prompting the suspicion that herpes zoster contributed to the neurogenic bladder and subsequent renal failure.

Discussion: Herpes zoster virus can reactivate in immunocompromised or older individuals, affecting various neurological and visceral systems. In this case, inflammation of the sacral nerves is believed to have played a role in the development of the neurogenic bladder and subsequent ESRD. While previously reported VZV-induced bladder dysfunction cases were mostly reversible, this case was asymptomatic, irreversible, and followed by unresolved AKI and subsequent ESRD. Therefore, vigilant monitoring of renal function is crucial in patients with HZ with or without reported urinary voiding dysfunction to identify potential progression to renal failure. Additionally, screening for urinary retention should be considered, especially with thoracic, lumbar, and sacral dermatomal HZ involvement, given the simplicity of the test and the severity of complications if missed.

Conclusion: This case report emphasizes the significance of recognizing HZ as a potential cause of neurogenic bladder and its uncommon yet severe complication leading to ESRD. Timely identification and appropriate management of HZ can potentially prevent irreversible bladder dysfunction and renal failure in affected individuals. Further research is warranted to better understand the underlying mechanisms of VZV-induced neurogenic bladder and its potential progression to ESRD. Also, to determine the importance of urinary retention screening and kidney function monitoring.

Biography

I graduated from Ain Shams University in Egypt in 2020. I am an Internal Medicine resident physician at the University of Central Florida College of Medicine / HCA Florida North Florida Hospital.



Austin B. Auyeung*, Melanie N. Rayan, Xiaolan Tang, Sanil Thomas

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Radiation proctitis with recurrent gastrointestinal bleed complicated by cytomegalovirus: A case report

Cytomegalovirus (CMV) is a well-known DNA virus of the human herpesvirus group that is known to cause a myriad of infections, more commonly in patients who are immunocompromised. Initial infections with this virus are frequently short-lived, presenting in the form a mild mononucleosis-like syndrome, following which this virus remains in a dormant state marked by the presence of antibodies to CMV. However, there are case reports describing CMV colitis in immunocompetent hosts. We present a case of a patient with multiple episodes of life-threatening Gastrointestinal (GI) bleeding secondary to a CMV positive rectal ulcer and CMV colitis after receiving radiation therapy for prostate cancer.

An 81-year-old male who presented with large volume hematochezia had relevant past medical history of paroxysmal atrial fibrillation, mechanical aortic valve replacement on coumadin, prostate cancer status-post radiotherapy and previously diagnosed radiation proctitis. This was complicated by a non-healing rectal ulcer status-post argon plasma coagulation with recurrent large volume hematochezia.

Given our patient's repeated visits with GI bleed and non-healing rectal ulcer, we kept a broad initial differential; including radiation proctitis, rectal malignancy, ischemic colitis, infectious colitis and inflammatory bowel disease. Infectious causes included herpes simplex virus, cytomegalovirus, lymphogranuloma venereum, amebiasis and secondary syphilis.

He had been hospitalized on three prior occasions at our facility over the past 4 months with low hemoglobin, requiring blood transfusions. Flexible sigmoidoscopy during his second hospitalization revealed radiation proctitis and biopsy of a non-healing left-sided rectal ulcer that was positive for CMV, negative for malignancy, and HSV. Follow-up CMV DNA Polymerase Chain Reaction (PCR) was positive with a low viral load and CMV IgM antibody was negative, suggesting that the CMV infection was localized to the ulcer and had not spread systemically.

Initial physical exam revealed temperature of 36.7 degrees Celsius, saturating 96% on room air, blood pressure 180/87 and pulse of 85 beats/min. Frank red blood per rectum was not seen on inspection. Abdomen was soft, non-tender without any guarding, masses or rigidity. Hemoglobin was 7.7g/dL, hematocrit was 24.2% and INR was 2.3. CT abdomen and pelvis revealed an active bleed from the left side of the rectum and proctitis.

The patient had an episode of hematochezia while inpatient and hemoglobin dropped to 6.2, requiring transfusion of 2 units of blood. Embolization of the left middle rectal artery with coil packing was performed the next day by interventional radiology and hemoglobin stabilized. The patient was started on 450mg valganciclovir twice daily as an inpatient to complete a 14-day course for treatment of CMV positive rectal ulcer. Since completion of therapy, there has been no other hospitalization for lower GI bleed.

We present a case of CMV colitis that occurred in a patient diagnosed with prostate cancer, received radiation therapy one year prior, who had neither HIV infection nor medication such as chemotherapy

or corticosteroids that could cause immunosuppression. The CMV colitis was complicated by severe GI bleeding, and required antiviral therapy.

Audience Take Away Notes

- The gastrointestinal manifestations of CMV in immunocompromised patients has already been well established in the literature. However, research regarding its occurrence in otherwise healthy individuals is lacking. The severe, life-threatening complications of CMV disease in immunocompetent patients may not be as rare as previously thought. Antiviral therapy should be taken into consideration as early as possible in patients with severe CMV disease regardless of immune system status. We urge clinicians to consider this diagnosis in patients presenting with symptoms consistent with hemorrhagic enteritis, colitis or overt GI bleeding, with special attention paid to patients with risk factors such as extended hospitalizations, acute severe illness, history of radiation therapy and inflammatory bowel disease

Biography

Austin Auyeung graduated from the Royal College of Surgeons in Ireland in 2022. He is currently an Internal Medicine resident physician at the University of Central Florida College of Medicine, Graduate Medical Education / HCA Florida North Florida Hospital.

Aneta Nitsch-Osuch[1,2]*, Katarzyna Okręglicka[1], Katarzyna Lewtak[1], Krzysztof Kanecki[1], Beata Pawlus[2]

[1]Department of Social Medicine and Public Health, Medical Univeristy of Warsaw, Poland

[2]St Family Hospital, Warsaw, Poland

Antibiotic prescription practices among children with influenza or RSV infection

The important factor in the development of resistance to antibiotics is their overuse, especially for viral respiratory infections. Poland has been for many years a country with a problem of antibiotic overuse on compared to other European countries. The aim of the study was to find out the frequency of the antibiotic therapy administrated to children with influenza or RSV infection in postpandemic season 2022/2023. A total of 218 children younger than 59 months seeking care for the acute respiratory tract infection was enrolled into the study. The enrolled patients had influenza-like symptoms: fever > 38 °C, cough, and sore throat of less than 4 days duration. Nasal and pharyngeal swabs were tested for influenza A and B virus and for RSV infection with rapid antigenic tests and RT-PCR. Forty six cases of influenza were diagnosed: 34 of influenza A (H_3N_2) and 12 of influenza B. The incidence rate of influenza infection was 21 % in the study group. The antibiotic therapy was ordered for 72 % patients with influenza. Antibiotics were given less frequently in the outpatient setting (23 %) compared with the hospitalized patients (91 %) ($p < 0.05$). Fifty two cases of RSV infection were found in a study group (incidence rate 24%). Antibiotic therapy was administrated in 29 patients (25%), antibiotics were more frequently prescribed in ambulatory care patients (33%) compared to hospitalized patients (15%). The most often administrated antibiotics were amoxicillin with clavulanic acid, cefuroxime, and amoxicillin. None of the patients in ambulatory care received oseltamivir while 82% children hospitalized with influenza receiver causative treatment with neuraminidase inhibitor. Conclusions: antibiotics were overused, while antivirals were underused among children with influenza. To improve health care quality, more efforts in the diagnosis of influenza and RSV infections and the appropriate use of antimicrobials and antivirals are required.

Audience Take Away Notes

- Viral respiratory tract infections in young children are very often and should be diagnosed at least with rapid tests to confirm diagnosis
- Antibiotics may be overused in children with influenza and RSV infection which may finally increase the issue of antibiotic resistance
- Antibiotic therapy should be only started when bacterial coinfection or complication is suspected or diagnosed

Biography

Prof. Aneta Nitsch-Osuch is a pediatrician, epidemiologist and specialist in public health, a head of the department of Social Medicine and Public Health and deputy dean of Medical University of Warsaw, Poland. She is a member of Advisory Board of Polish Sanitary Inspection and a member of Scientific Board of the National Influenza Prevention Program, an author and co-author of more than 300 publications in a field of vaccinology, prevention of infectious diseases, epidemiology of infectious diseases and rational antibiotic therapy.

Thea Hein Petersen[1]*, Michael Linde Jakobsen[2], Yiyu Ou[2], Paul Michael Petersen[2], Ravi Kumar Chhetri[1], Hans-Jørgen Albrechtsen[1]

[1]Technical University of Denmark, Department of Environmental and Resource Engineering

[2]Technical University of Denmark, Department of Electrical and Photonics Engineering

Preventing infectious diseases using UV LEDs for water disinfection

Access to safe drinking water is crucial for promoting human health and well-being. Contaminated drinking water represents a significant risk for waterborne infections. Water disinfection using Ultraviolet Light- Emitting Diodes (UV LEDs) is a new method to disinfect water effectively without adding chemicals to the water. Compared to mercury lamps, which are traditionally used for UV water disinfection, UV LEDs offer the advantage of a longer lifespan, compact devices that can be integrated into other systems, and customized wavelengths, which can be used to target different pathogens specifically. Furthermore, UV LEDs do not contain toxic mercury.

The objective of this study was to investigate the inactivation of Escherichia coli (E. coli) and Enterococcus faecalis (E. faecalis) by using 280 nm UVC led light. Our study showed that this wavelength is extremely efficient for water disinfection with log inactivation of more than Log 6 for E.coli and more than Log 5 for E. faecalis when illuminated for less than one minute. Furthermore, a new system based on 395 nm UVA light combined with a solar cell was investigated. The combination of solar cells and UV LEDs creates a self- sustaining system, which is a proposed solution for water disinfection in rural areas, disaster zones, and flooded areas, where access to safe drinking water is crucial. The UV LED disinfection technology offers promising solutions to improve water safety and quality, leading to positive public health outcomes.

Audience Take Away Notes

- The audience will learn about UV LED photoactivated disinfection of bacteria and how the level of disinfection is calculated
- The audience will learn that LED Technology has a huge innovation potential in many companies
- The new LED technology is a hot topic for students in Electronics Engineering at Universities
- The combination of solar panels and UV-LEDs provides a practical solution of how to use the technology in rural areas, disaster zones and flooded areas

Biography

Thea Hein Petersen has a bachelor's degree in General Engineering from the Technical University of Denmark. During her bachelor, she studied for a semester at the University of California Berkeley, where she focused on Technical Entrepreneurship and Innovation. This experience allowed her to gain insight into the process of transforming technical knowledge and ideas into successful companies. She is currently perusing her master's degree in Sustainable Energy at the Technical University of Denmark.

Lev Bladimir Ramírez*, Laura Torres, Laura Salas, Nathalia Suescún, Zarey Torres, Juan David Pardo, Samuel Benitez

Faculty of Medicine, Universidad de La Sabana, Chia, Cundinamarca, Colombia

Association between COVID-19 vaccination and menstrual disturbances: A retrospective cohort analysis

In the wake of the COVID-19 pandemic caused by the Severe Acute Respiratory Syndrome Coronavirus (SARS-CoV-2), the global healthcare landscape has undergone a profound transformation. This transformation has been marked by the rapid development and deployment of COVID-19 vaccines by various pharmaceutical laboratories, including Pfizer-BioNTech, AstraZeneca, Sinovac, Johnson Pharm, and Moderna. While these vaccines have provided a ray of hope in the battle against the virus, they have also been accompanied by a spectrum of adverse reactions, ranging from common side effects like fever and headaches to more severe incidents such as anaphylaxis and myocarditis. However, amid the discussions surrounding these adverse reactions, there has been a lesser-explored topic - menstrual disturbances following COVID-19 vaccination. Despite being less documented in clinical trials, there have been reports of irregular menstruation, prolonged bleeding, intermenstrual bleeding, and menorrhagia in women after receiving the vaccine. To shed light on this intriguing phenomenon, a retrospective cohort study was conducted in Colombia, involving 139 women of reproductive age who reported experiencing menstrual alterations post-vaccination. The study's findings revealed a significant association between COVID-19 vaccination and menstrual disturbances, with amenorrhea and dysmenorrhea being the most frequently reported alterations. Additionally, as the number of vaccine doses increased, the prevalence of menstrual alterations also rose. This presentation delves into the multifaceted impact of COVID-19 on public health, the rapid development of vaccines, and the associated adverse reactions, with a particular focus on the intriguing and relatively understudied domain of menstrual disturbances following vaccination.

Audience Take Away Notes

- Researchers attending the congress can use the presented information as a starting point for further investigation. The data on menstrual disturbances following COVID-19 vaccination, for instance, may inspire additional studies to better understand this phenomenon, leading to improved healthcare recommendations
- In essence, the research presented at the congress can act as a catalyst for further academic exploration, providing valuable insights into a relatively understudied area of vaccine-related health issues. It not only offers opportunities for expanding research agendas but also enriches the educational experiences of students by bringing real-world, contemporary health challenges into the classroom
- In summary, while the research may not provide a direct, ready-made solution to a specific design problem, it offers valuable information that can influence design decisions and approaches, promote adaptability and interdisciplinary collaboration, and underscore the importance of patient-centered and data-driven design. These indirect benefits can ultimately contribute to more efficient and effective design outcomes, especially in healthcare-related contexts

Biography

Lev Bladimir Ramirez, originally from Bogota, Colombia, is currently pursuing a medical degree at Universidad de La Sabana. Lev is actively involved in the "Semillero de Terapia Celular y Metabolismo" under the guidance of Dr. Gustavo Celis. Lev has contributed to the field of research with publications like "Modeling Metabolic Diseases with Organoids: A Review" in the Journal of Biomedical Research & Environmental Sciences and "Doble Aneuploidia 48, XXY, +21 en Células de Líquido Amniótico a las 16 Semanas de Gestación" in Revista Colombiana de Pediatría. Lev also participated in the "VIII Encuentro Institucional de Grupos de Investigación y XI Encuentro Institucional de Semilleros de Investigación,"

Tsedey Damtew
International Clinical Labratories, Ethiopia

Hepatitis B vaccination status and associated factors among health care workers in public health centers in, Addis Ababa, Ethiopia

Background: Hepatitis B infection is the most common and serious liver infection in the world. Health care workers are among the most vulnerable groups to acquire Hepatitis B Virus (HBV) infection; with an estimated risk of four times higher than that of the general population. Vaccination of high-risk groups is a key strategy for the prevention of the infection, therefore Center for disease control and prevention and World Health Organization (WHO) guidelines recommended all health care workers should be vaccinated for hepatitis B virus infection.

Objective: To assess Hepatitis B vaccination status and associated factors among public healthcare workers in, Addis Ababa, Ethiopia, 2023.

Method: Institution based cross-sectional study was conducted in ten public health centers in Addis Ababa JANUARY 2023, a simple random sampling method that was used to select study participants. A structured self-administrated questionnaire was used to collect data. Then the data was entered by Epi data version 3.1 and analyzed by the Statical Package for Social Science (SPSS) version 23. Bivariate and multivariate analysis was carried out to identify the association with the independent variable and outcome. Adjusted odds ratio with 95% confidence interval was used to determine strength and presence of association at P-value of < 0.05 was considered statistically significant.

Result: In this study, a total of 324 health care workers were surveyed. Among the respondents, 74.1 % had received at least one dose of HBV vaccine. The full immunization coverage against HBV was estimated at 57.1 %. Factors associated with full vaccination status were Job experience (AOR 2.445, 95%CI 1.406, 4.252), Availability (AOR 4.591, 95%CI2.764, 7626), and favorable attitude (AOR 2.721, 95%CI 1.283, 4.767).

Conclusion: This study revealed that the vaccination status of Health care workers was low compared with other countries and sub-optimal from WHO estimation of vaccination rate in developing countries. Thus special attention should be given to expanding full coverage of vaccination.

Keywords: Health Care Workers, Hepatitis B Vaccination Status, Associated Factors, Public Health Centers, Addis Ababa.

Audience Take Away Notes

- The study on hepatitis B vaccination status and associated factors among healthcare workers in Addis Ababa, Ethiopia, offers valuable insights for raising awareness, identifying gaps in vaccination coverage, policy formulation, preventing the spread, improving workplace health and safety, and stimulating future collaboration and research. This information can be useful for healthcare professionals, policymakers, and occupational health and safety professionals. The research aims to analyze factors associated with hepatitis B vaccination among healthcare workers, and provide insights for future interventions and policies to increase vaccination rates. The findings can guide designers in designing products, services, or environments considering the needs, safety, and regulatory aspects of healthcare worker vaccination

Biography

My name is Tsedey Damtew, I graduated from Rift Valley University in the year 2016G.c having a BSc degree in public health and presently I am a candidate for a Master of Project Management Evaluation & Analysis in SkillMart International College, Addis Ababa Ethiopia. I do have over 6 years of progressive experience in different research activities especially preventive health care in the primary health care unit also I am capable of different healthcare activities.

Nzolameso Makaya Jennifer
Médecin Généraliste, Democratic Republic of Congo

Management of arterial hypertension and diabetes in elderly people as well as COVID-19 prevention

70% of people over 65 are hypertensive; high blood pressure increases the risk of exposure to cardiovascular disease (myocardial infarction and heart failure) and stroke. This is a public health problem, given the aging of the population.

There are few studies carried out in elderly subjects. This randomized study published in 2008 in the New England Journal of Medicine, compares two groups of patients aged 80 to 105 years. The first group receives antihypertensive treatment with diuretics +/- EIC, while the other group receives the placebo treatment. The results show a significant reduction in mortality, fatal strokes and heart failure (hypertension study in very Elderly trial).

The specific of the elderly subject:

- HTA is mostly systolic
- The blood pressure objectives are different according to age under 80: the objectives are the same as in the general population: <140/90mmhg
- In the over 80s, the objectives are less strict, they tolerate a SBP<150mmhg in the absence of orthostatic hypertension.
- Look for orthostatic hypertension causing falls and loss of autonomy.
- Beware of the white coat effect. Do not hesitate to offer self-measurement of blood pressure or ambulatory measurement of blood pressure (MAPA).

Therapeutic strategies:

- No strict salt-free diet, as it exposes you to a major risk of undernutrition.
- In the event of systolic hypertension, the classes of drugs used in first intention are diuretics, thiazides and calcium channel blockers in monotherapy and progressive increase in dosage.
- In the case of systolic-diastolic hypertension, drugs from the 5 therapeutic classes can be prescribed.
- After 80 years it is better to limit yourself to 3 antihypertensives, in order to limit polymedication and the risk linked to iatrogenic

About the management of diabetes:

- proposed treatment is discussed with the patient's family: basal insulin therapy 1-2*/day
- Teaching on the prevention and treatment of hypoglycaemia.
- Home supervision: nursing visit 2*/day for injection and blood sugar control, meals delivered, blood sugar targets:*10mmol
- Rehabilitation of the treatment on a weekly basis over a month.
- Reassessment of glycemic targets with the patient and his family.
- Monitoring of the overall functional state:

- Geriatric syndrome: with cognitive, nutritional, motor and balance assessment and rehabilitation of treatment one week, one month, three months from the start of treatment

In summary In developed countries, about 12-25% of people over 65 are diabetic. The management of diabetes in the elderly is less well studied than in other age categories. Recently, the diabetology and geartrie companies have taken a position on the priorities and specificities of this care. The adjustment of drug treatment, as well as the glycemic targets adapted to the functional state of the patient must prevent the symptoms of diabetes and delay the onset of geartric syndromes.

The prevention and screening of classic complications of diabetes and geartric syndrome must be integrated into the care of the elderly, in order to optimize their overall health and their quality of life.

Biography

Nzolameso Makaya Jennifer doctor at the general reference hospital of kimbanseke pierre fokom in Kinshasa Biography nzolameso makaya Jennifer is a doctor at the age of 24 at the University of Kinshasa and is training in the management of arterial hypertension and diabetes in 3rd age people In 2016 I created an NGO with a health and maternity center le berger, which takes care of widows and orphans. 2019 I was assigned to the general reference hospital of kimbanseke pierre fokom 2023 poster presentation (in person) on the management of high blood pressure and diabetes in elderly people as well as the prevention and vaccination of covid19 But also the hygieno-dietetic measure of people living with arterial hypertension and diabetes

Artemisia Ntoula[1]*, Maria Babetsa[2], Ilias Apostolakos[2], Maria-Olga Daskalaki[1], Eirini Makridaki[1], Dimosthenis Chochlakis[1], Evridiki Boukouvala[2], Vasilios Sandalakis[1], Anna Psaroulaki[1], Gamal Wareth[3,4]

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Deciphering acidic stress response of brucella melitensis isolates through gene expression analysis

Background: Brucellosis is a widespread zoonotic disease, endemic in the Mediterranean. Brucella can spread to humans through the consumption of raw meat, dairy products, direct contact with an infected animal, or by inhaling infected aerosols. After entering host cells, brucellae fuse with phagosomes, forming Brucella-containing vacuoles which experience transient interactions with lysosomes, leading to their acidification. The intracellular pH increases when they begin to interact with the endoplasmic reticulum, enabling the intracellular replication of the bacterium. Brucella may exploit acidic pH as stimulus for induction of genes essential for altering the biological functions of professional phagocytes and evading their killing mechanisms.

Objective: The aim of this study was to investigate the effect of acidity levels on the expression pattern of genes from the Toxin-Antitoxin, T4 Secretion and Two Component Systems in B. melitensis isolated from humans and animals.

Methods: Brucella isolates (27 from animals and 17 from humans) were cultivated in TSB at pH 7.2 (control), pH 4.4 and 3.4 at time intervals of 1 and 3 hours. We analyzed the expression of seven genes (virb10, cogt, fic, cbb3, otpr, rele, brnt) by RT-qPCR. Primers were designed using Primer3 Software. The integrity of the extracted [NucleoSpin RNA, Mini kit (Macherey-Nagel, Germany)] RNA was tested by agarose gel electrophoresis and the concentration was measured at a Nanodrop. The total RNA was reverse-transcribed (Prime Script RT Reagent Kit; Takara Bio, Japan) into cDNA and tested by real time-PCR (SYBR Select Master Mix; Thermo Fisher Scientific, USA), in duplicate at a Bio-rad CFX96 Real-Time PCR cycler. The expression levels were normalized by 16S rRNA and analyzed using the $2^{-\Delta\Delta CT}$ relative quantification method. All conditions were compared against the control (pH 7.2) by Student's t-test. P-values were corrected for false discovery rate using the Benjamini & Hochberg method.

Results: The genes' expression patterns differentiated among the strains. In most of the strains, the expression levels were higher at pH 3.4 and after 3h of the effect and presented statistically significant differences. Strains exposed to pH 3.4 at both time points exhibited differentiated rates of gene expression compared to pH 4.4. Duration of exposure and different pH levels seem to influence gene expression. Some genes didn't show any specific expression pattern. Interestingly, animal and human isolates didn't steadily follow the same expression patterns.

Conclusion: Although several genes were differentially expressed (over or under expressed) under specific pH and time points it was difficult to distinguish a clear gene-response pattern of the bacteria. Isolates from different hosts didn't always share similar regulation-patterns of gene expression. The induction of certain genes may initiate the expression of others, in order to preserve Brucella's viability.

Acknowledgments: This research has been co-financed by the European Union and Greek national funds through the Operational Program Competitiveness, Entrepreneurship, and Innovation, under the call ERANETs 2021A. Project code: T12EPA5-00064.

Audience Take Away Notes

- Present the effect of acidic stress on B.melitensis field strains
- Discuss the importance of zoonotic diseases
- Make public results that can contribute to the existing research or stimulate new research projects

Biography

Artemisia Ntoula studied Biology at the University of Patras, Greece. She holds a Master Diploma in Medical Genetics. She joined the research group of Prof. Psaroulaki at the laboratory of Clinical Microbiology and Microbial Pathogenesis at the School of Medicine, University of Crete, in 2021. She is expertized in the detection of SARS-CoV-2 in human and wastewater samples by molecular means. She is part of the research group that studies the behavior of Brucella under different stress conditions and the antibiotic susceptibility of novel microorganisms isolated by culturomics.

magnus Group

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SPEAKERS

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VACCINES AND INFECTIOUS DISEASES

Indira Acharya MBBS*, Lanaya W. Smith MD, Chandralekha Banerjee MD, Radhika Vij MD

Medstar, United States of America

Reactive arthritis following mpox (monkey-pox) vaccination

Background: Reactive arthritis after various vaccinations has been previously described but such kind of reaction after mpox vaccination has not been previously reported. Here we present a case of recently diagnosed reactive arthritis following intradermal mpox vaccination (JYNNEOS).

Case Report: A 51-year-old man with a history of HIV on antiretroviral therapy with undetectable viral load, presented with a 2-week history of protracted fever that started few hours after receiving mpox vaccine. He also had severe watery diarrhea and dysuria for a week. Laboratory testing was normal except for elevated acute phase reactants. Cultures, Chest X-ray, and echocardiogram were unremarkable. The diarrhea spontaneously resolved; however, he started having progressively worsening pain and swelling of the left knee and ankle joint. MRI left knee without contrast showed grade 2 tear to the origin of medial collateral ligament with some underlying medial femoral condyle edema and knee effusion. Left knee aspirate yielded 50 cc of clear fluid with slightly elevated WBC count and protein level suggestive of inflammatory arthritis, however ANA, rheumatoid factor and HLAB27 were negative. Joint fluid crystals, cultures and Lyme PCR testing were negative as well. He was started on methylprednisolone for 2 weeks. He subsequently developed migratory arthritis and redness in left eye associated with decreased vision. He was diagnosed with left eye anterior uveitis and treated with prednisone and cyclopentolate eye drops. His symptoms improved while on methylprednisolone, but promptly recurred after completion of steroid course. The patient's presentation with diarrhea, asymmetrical arthritis, dysuria, and uveitis was felt to be due to reactive arthritis. Given the worsening visual field defect along with migratory arthritis unresponsive to NSAIDs, he was re-started on prednisone 20 mg daily for 1 week followed by 10 mg daily in addition to meloxicam 15mg daily. One month after treatment with steroids and NSAIDs, his arthralgias were well controlled and acute phase reactants returned to baseline, however his visual field defect persisted.

Conclusion: The prognosis of reactive arthritis is variable and is largely determined by the genetic predisposition of the patient and the triggering pathogen. Studies regarding long term outcome of reactive arthritis secondary to vaccination are substantial. JYNNEOS is a live, attenuated, non-replicating orthopox virus vaccine, originally formulated for prevention of smallpox and was in approved in 2019 for prevention of mpox. Adverse reactions following JYNNEOS vaccine are anticipated to be very low as it is replication-deficient virus vaccine. Further research is essential for identifying individuals at higher risk of developing an autoimmune reaction to the existent mpox vaccination as well as for the development of safer formulations of vaccinations.

Biography

I am Indira Acharya, a medical professional who completed my medical school and residency specializing in Ear, Nose, and Throat (ENT) in Nepal. Currently, I am pursuing a residency in Internal Medicine at the Medstar Internal Medicine Residency Program in Baltimore, Maryland, USA, and I am set to begin my third year as a resident in July 2023.

Kaydeen Morris-Whyte[1]* MD, Robert Reid MD[2]

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[2]Pediatrics Infectious Disease Specialist, Joe DiMaggio Children's Hospital Hollywood, Florida, United States of America

Encephalopathy: An unusual presentation of MRSA osteomyelitis triad and sepsis

Objectives: Identify encephalopathy as an early presentation of sepsis, Describe systemic approach to making diagnosis of sepsis associated encephalopathy (SAE), Discuss prognosis of SAE, List toxins produced by Methicillin-Resistant Staphylococcus Aureus (MRSA), Describe antimicrobials effective against MRSA.

Introduction: Sepsis Associated Encephalopathy (SAE) is diffuse brain dysfunction that occurs secondary to an infection but not directly in the CNS1-2. We present a case of SAE caused by MRSA osteomyelitis and septic shock.

Case Summary: 15 year old female who is a volley ball player presented with a 2-day history of personality change. She had fatigability which progressed to decreased alertness and monosyllabic speech. History is remarkable for visit to the emergency department and Orthopedic Surgeon within the week prior to presentation for left knee pain. Knee radiograph was normal. She was prescribed Percocet as needed followed by Medrol Dosepak and Flexeril. Current admission, she was febrile to 39.40C and tachycardic at 148 beats/min. Physical examination was significant for obtunded female, GCS 11 and mild edema of left knee. Blood investigations showed: WBC 13000/uL, neutrophils 88%, hemoglobin 8.3 g/dl, platelet 81000/uL, sodium 132 mEq/L, creatinine 0.90 mg/dL, AST 79 U/L, ALT 42 U/L, CPK 1326 mcg/L, C-reactive protein 19 mg/dL, sedimentation rate 87 mm/h and procalcitonin 43ng/mL. Chest radiograph revealed multifocal peripheral areas of patchy nodular infiltrates (Fig. 1) and venous Doppler ultrasound of left lower extremity showed non occlusive thrombus in the left common femoral vein. Cerebrospinal fluid and additional imaging: CT Brain, MRI Brain/Neck, Video EEG and Echocardiogram with bubble study were normal. Blood culture was taken. Patient was started on Lovenox, ceftriaxone and vancomycin. At 15 hours, blood culture resulted positive for gram positive cocci. Antibiotics were switched to ceftaroline and clindamycin on suspicion of MRSA. Due to concern for necrotizing fasciitis, MRI of lower extremity done and revealed left distal femur osteomyelitis with subperiosteal abscess to posterior aspect of distal femur measuring 17.2x3.4x1.5cm (Fig. 2). Specimen from open incision and drainage grew MRSA. Patient managed for septic shock with postulated sepsis associated encephalopathy. She showed clinical improvement but may be exhibiting early signs of cognitive impairment. Inpatient care continues at the time of abstract submission.

Discussion: SAE is a diagnosis of exclusion and requires a thorough evaluation for other etiology of delirium. The pathogenesis is not yet fully understood and data in the literature is limited. Our patient presented with encephalopathy therefore, our work up centered on identifying primary CNS infection, endocarditis, paradoxical embolism, seizure, ingestion as well as Macrophage Activation Syndrome (MAS) given the marked hyper inflammatory state. The prompt to evaluate for other sources of infection came after diagnosed bacteremia in the setting of elevated muscle enzyme. Sepsis is a significant cause of morbidity and mortality, it requires prompt identification in order to tailor antimicrobial treatment. Encephalopathy was the first sign of sepsis in this patient. SAE is an entity that requires further studies to determine risk

factors, prognosis and guide rehabilitation. The case is also unique because patient presented with triad of acute osteomyelitis, deep vein thrombosis and septic pulmonary embolism which is rare in the pediatric population.

Conclusion: SAE though uncommon is the first sign of sepsis in susceptible patients and warrants further studies to determine short and long term sequelae.

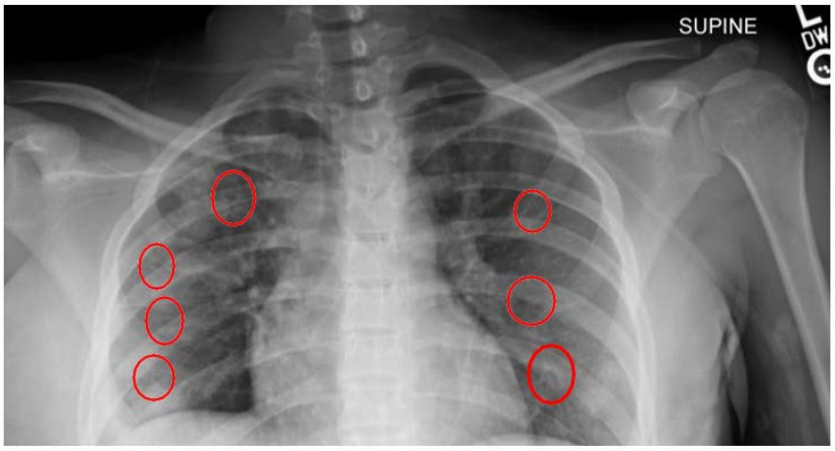


Figure1. Posterior-anterior chest radiograph showing multifocal peripheral areas of patchy nodular infiltrates (red circles).

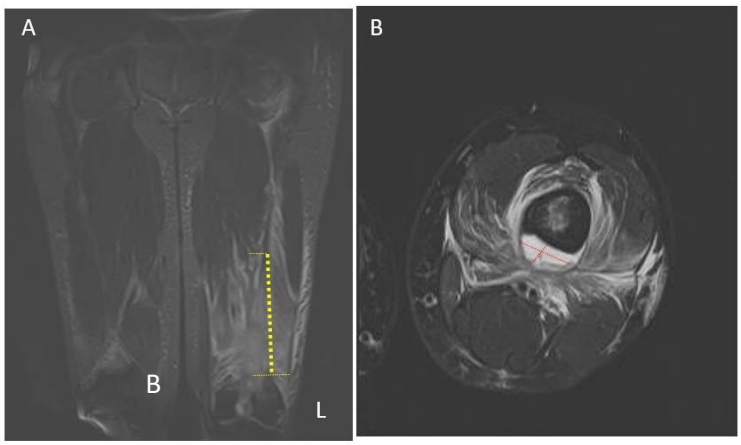
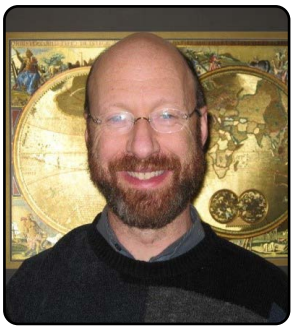


Figure2. Multiplanar multi-sequence non-enhanced MR imaging of the left thigh and femur (A) subperiosteal abscess to posterior aspect of left distal femur measuring 17.2 cm craniocaudal, 3.4cm mediolateral and 1.5cm AP(yellow dashed line). (B) Cross sectional view of left femur subperiosteal abscess measuring 3.4 cm mediolateral, and 1.5 cm AP (red dashed line).

Biography

Dr. Kaydeen Morris-Whyte received her medical education at the University of West Indies in Jamaica and graduated with MB, BS degree in 2016. She worked in the capacity of Pediatrics Junior Resident in Jamaica for 4 years. She is currently a 2nd year Pediatrics Resident at Joe DiMaggio Children's Hospital in Florida with interests in Critical Care and Infectious Disease.



Seema Nair Parvathy PhD[1,2,3], Esfandiar Shojaei MD[2], Kelly Muhsin RN[1], Jeremy Burton PhD[2], Trina Lewis[1], Asifuzzaman Khan MD[2], Saman Maleki PhD[3], Susan Poutanen MD[4], Susy Hota M[4], Michael Silverman MD[1,2,3]*

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[2]Lawson Research Institute, London, Canada
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Efficacy and safety of a canadian Fecal Microbial Transplantation (FMT) rogram for multiply recurrent C. difficile

Background: Options for recurrent C. difficile remain very limited, especially in Canada where bezlotoxumab, REBYOTA™, and VOWST™ are all not yet available. The need for extensive donor testing in order to maintain a stool bank for FMT has been complicated by an increasing number of pathogens for screening, especially since the COVID pandemic further complicated screening protocols. We describe the safety and efficacy of FMT using enema and capsule delivery modes in a single center before and during the COVID pandemic.

Methods: Patients included adults with documented C. difficile infection (Toxin positive or PCR positive with resolution of symptoms while on oral vancomycin or fidaxomicin) with at least 3 episodes within 6 months and failing at least one pulse/taper regimen. After bowel washout with polyethylene glycol, all patients underwent either 2 FMTs one week apart via rectal enema or one administration of oral FMT using capsules. Failure was defined clinically as recurrence of diarrhea and positive C. difficile test in the absence of other contributors within 8 weeks post FMT. Anonymous donor screening was conducted as per Health Canada guidelines including SARS-COV-2 nasal and stool testing.

Results: 111 patients underwent FMT. 9 patients had FMT via Enema and 24 via capsules between Aug 1, 2018 and March 21, 2020. The program was put on hold due to COVID-19 but restarted Aug 1, 2020- May 2023 during which time 18 patients received FMT via enema and 60 via capsules. 8/27 (30%, 95%CI 11-46%) patients failed FMT via enema but 0/84 (0%, 97.5% one sided CI 0.0-4.3%) failed capsule FMT. No clinical infections, including no COVID transmissions related to FMT occurred.

Conclusion: FMT using an anonymous donor stool bank can be safely carried out even in the context of the COVID pandemic. In our center, capsule FMT is extremely effective for recurrent C. difficile.

Goals of Presentation:

- Describe the Clinical Problem of Multiply Recurrent C. difficile.
- Describe the approach to Fecal Microbial Transplantation in an Academic Center.
- Describe the respective efficacy of rectal enema and oral capsule based programs.

Biography

Dr. Silverman received his medical degree and Residency in Internal Medicine at the University of Toronto. He carried out his fellowship in Infectious Diseases at the University of Manitoba in Winnipeg, and an HIV post-doctoral fellowship at the University of California, San Francisco, USA. Dr. Silverman is a pioneer in the field of Fecal Microbial Transplantation for treatment of Clostridium difficile. He was one of the first to perform the procedure in North America and he has established a large clinical and research program associated with this. He has conducted many studies of prevention of infectious complications of injection drug use. He has over 130 peer reviewed publications including recently as a first or senior author in the Annals of Internal Medicine, New England Journal of Medicine, Nature Medicine, JAMA series and Lancet Infectious Diseases. Reviews of his work have been written in Science, Nature and reported in the International mass media including in the New York Times, BBC, CNN, The Times of India etc.

Anju Kaushal (PhD)
Member of New Zealand Organization For Quality, New Zealand

Emerging DNA-sensing mechanism and its therapeutic significance against the infectious and cancer like diseases

Pathogen-associated molecular patterns (PAMPs) and self-DNA in the form of damage-associated molecular patterns (DAMPs) are released from immune cells (Monocytes, Macrophages, and other immune cells) under a stressed condition, that are recognized by pattern recognition receptors (PRRs) already cited in the cytosol, membranes, and other organelles. Various DNA viruses are being detected by the sensors as foreign nucleic acids RNA / or DNA during viral infections like vaccinia virus, HSV-1, and HSV-2, cytomegalovirus, adenoviruses, human papillomavirus, etc. These sensors are denoted as PRRs. Recently discovered a novel enzyme cGAS (cyclic GMP-AMP) catalyses the signals to recognize DNAs while working with adaptor protein the Stimulator of Interferon Genes (STING) helps dissociate PAMPs and DAMPs to trigger the inflammatory / or anti-inflammatory regulations. The final activity of STING is guided by the catalytic form of cGAS, as cGAMP synthase regulates the function of IFN-I. This specific molecular pathway triggers the innate immune response in the cytoplasm and consecutively develops the adaptive immune arm against pathogens. PRR agonists activate the adaptor protein STING to regulate the functionality of CD4+ and CD8+ cells in establishing the sustainable innate and adaptive immune response. cGAS-STING also exerts antitumor effects via activation of p53 and p16 pathways. STING harbors the various properties that could be used in the development of novel therapeutics.

Audience Take Away Notes

- Inflammatory mediators induced during infection or by oncogenes or exposure to pollutants stimulate premature senescence. The diseases like COPD, neurodegenerative diseases, and permanent/ irreversible tissue damage could also start the autonomous process of degeneration in neighboring cells. The inflammatory mediators' pathways e.g., MyD88, STING, p53, p21, and p16 lead to produce phenotype NF-kB at various levels. Therefore, the relationships among these pathways and their balancing effects to regulate the innate response followed by the adaptive arm do provide clues for effective tools in the development of diagnostics and novel therapeutics
- This emerging field of science would provide new opportunities to serve in the field of immunology
- Yes, it is a very useful field to study along with other connected fields in diagnostics and therapeutics
- Yes, this provide a practical solution to a problem that could simplify or make a designer's job more efficient?
- Yes, it will provide new information to design new problems to study these new molecular immunological pathways.
- List all other benefits.
    - It will provide new solutions to how these pathways emerge during the process of inflammation after/ or during viral infection, cancer, or other opportunistic infections or could be exposure to pollutants
    - It will provide clues to develop new diagnostics
    - It will provide better strategies for new therapeutics

Biography

Dr. Anju Kaushal received her MSc. Microbiology from Central Research Institute, Kasuali, India in 1993 and awarded with PhD Microbiology in 2003 from Panjab University, Chandigarh, India in 2003. She worked in various scientific & medical institutes and companies in India and New Zealand. Her expertise is in Science and Technology, R&Ds, Productions and QA/QC in the field of biologicals, diagnostics and academia. She worked on Rabies, Aspergillus, Candida, HIV, enzymes and fermentation technologies. Her area of interest includes vaccines, sera & diagnostics and novel therapeutics. She also attained, more than six years of experience in small Business Management, Brand & Marketing, Communication & Information. She has assisted many scientists in their careers. She has published 12 articles in Scientific Journals and more than 40 articles on LinkedIn.

Van Buynder PG
Griffith University, Southport, Queensland, Australia

Vaccination of older persons: Towards a population approach. Lessons from SARS-CoV-2 in Australia

Immune senescence and inflammaging render older persons more susceptible to severe consequences of infectious diseases and likely to exhibit poorer responses to vaccination. Older persons need influenza, pneumococcal, herpes zoster, pertussis and SARS-CoV-2 vaccines and soon will need RSV vaccines as well. Uptake of these vaccines will depend on older persons understanding of the importance of disease, reassurance about vaccine safety and vaccine effectiveness and access to immunisers and vaccines at an affordable price.

After pursuing “COVID zero” policies via the world’s longest population lockdowns, the opening of borders in Australia, along with poor messaging around vaccine benefit and safety, saw poor uptake of boosters and the world’s second highest Covid-19 mortality rates, almost all of it in older persons. Each day hundreds of aged residential care establishments had COVID clusters. The failure of messaging and lack of clarity on policies for older person vaccination will prevent meaningful uptake of vaccine in this group. Messaging improvement along with legislative support and a curbing of excessive prices for effective vaccines are urgently required.

Biography

Professor Paul Van Buynder is a Public Health Physician and the immediate past Chairman of the Australian Immunisation Coalition. He is a Professor in the School of Medicine at Griffith University in Queensland. He has held senior public health positions in a number of Australian states, in two Canadian jurisdictions and at the Centre for Infections in the United Kingdom. He has held personal appointments on sub-committees of National Immunisation Technical Advisory Committees in three continents. He is a reviewer for over 10 journals and has over 60 refereed book chapters and articles.

Kundoly Velayudhan Suseela

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

Rapid growing mycobacteria infection: An entity in diagnosis?

Nontuberculous mycobacteria includes Rapid Growing (RGM) and slow growing mycobacteria. RGMs like M. abscessus and M. fortuitum- chelonae complex can produce natural chronic infections and the infections of implants. They are usually present in soil and water and get introduced to human body by invasive procedures and by natural means. This presentation describes four cases of M. fortuitum and one case of M. abscessus. Three patients (age group 50-60 yrs) who underwent inguinal hernia repair with mesh had complaints of oozing from wound for several weeks, and one patient for three years. Initially they were investigated for wound infections by culturing the superficial samples for which they had undergone treatment for colonisations like pseudomonas. As the symptoms were persisting, eventually wound explorations were done to grow M. fortuitum and thus they were treated with macrolides and fluoroquinolones.

A 50-year-old male with a history of stent implant in coronary artery presented with Pyrexia of Unknown Origin (PUO) of six months duration. Despite the patient had undergone various antibiotic treatments, his PUO was not relieved. Three blood samples were collected at different time for a detailed evaluation and M. fortuitum was identified. The colonization was possibly associated with stent. Despite a long period of treatment, the patient finally succumbed to disease.

A 3-year-old child was brought with abscess on the front of right ear. Ultrasonogram features were suggestive of tuberculosis. Histopathologiacal examination revealed granulomatous change and there were acid fast bacilli in the drained out pus. The infection was provisionally diagnosed as tuberulosis. But cartridge based nucleic acid amplification test failed to detect M. tuberculosis. Culture of pus on Lowenstein Jensen medium grew M. abscessus which was later identified genotypically as subspecies massiliense. Patient was successfully treated with macrolides and fluoroquinolones. Proper identification prevents the physician from prescribing unnecessary antibiotics and thus reduces the morbidity. This signifies the importance of microbiological diagnosis of situations of menace in infection which could help in all the above cases.

This case series contribute:

- RGM can be cause of infection in implants.
- All granulomatous infections with AFB are not tuberculosis.
- Proper identification of the RGM can prevent unnecessary antibiotic and antituberculous treatments.

Biography

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

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VACCINES AND INFECTIOUS DISEASES

Treatment of Indian kala-azar (Visceral Leishmaniasis) - from one month to one dose

Visceral Leishmaniasis (VL), also known as 'kala azar,' is the most severe form of leishmaniasis, caused by Leishmania donovani in the Indian subcontinent and transmitted by the Phlebotomous sand flies. The disease is almost always fatal if left untreated. The clinical disease of VL is characterized by progressive fever, weakness, anemia, and hepatosplenomegaly. Tests show pancytopenia and hypergammaglobulinemia with hypoalbuminemia.

Treatment of VL - Pentavalent antimonials (Sodium stibogluconate (100 mg/mL) and meglumine antimoniate (85 mg/mL), at the dose of 20 mg/kg body weight for 28–30 days, have been the standard treatment for VL in most parts of the world. However, due to extensive drug resistance to pentavalent antimonials in Bihar, where the cure rate fell to <50%. frequent cardiotoxicity which at times can culminate into occasional fatal life-threatening arrhythmias.

Miltefosine: It is the first oral antileishmanial agent, and India was the first country to register for use in India in 2002 for the treatment of VL after successful clinical trials. It was the chosen the drug for the VL elimination program in the Indian subcontinent. The dose is 50—100 mg for 28 days after meals. Adverse events include frequent vomiting and diarrhea. It has teratogenic potential and entails contraception l5-6 months in women with pregnancy potentials, due to its long half-life. The efficacy of miltefosine appears to be declining in the Indian Subcontinent.

Paromomycin: It is an aminoglycoside antibiotic approved by the Indian Government in 2006 for the treatment of VL after a successful randomised clinical trial. It is used at a dose of 15 mg/kg intramuscular injection daily for 21 days. It has a cure rate of 95% in the Indian subcontinent. The dose in other endemic regions has not been established. The main advantage of the drug is its excellent safety profile and low cost.

Amphotericin B: It is a polyene antibiotic which was used initially for the treatment of antimony-resistant VL and later it was used as first line treatment in Bihar, India,. It has excellent cure rates at doses of 0.75–1.0 mg/kg for 15 doses typically administered on alternate days for one month. Adverse effects are very common include infusion reactions like high fever with rigor and chills, nausea, vomiting, thrombophlebitis occasionally serious and life-threatening adverse events. Lipid formulations of Amphotericin B (AmB) have significantly decreased toxicity. This permits administration of large doses of the drug over a short period. Liposomal AmB [AmBisome®], it is United States Food and Drug Administration (US FDA) approved AmB lipid formulation for VL. In India and Bangladesh, a single dose of 10 mg/kg results in a cure rate of >95%, and is currently the preferred treatments for VL in this region. Its

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[2]Department of Medicine, University of Florida, Jacksonville, Florida, USA

Biography

Prof Shyam Sundar did his MD (Medicine) from Banaras Hindu University in 1981. He later joined the same department and became professor. He focused on research in visceral leishmaniasis (VL). He established a treatment and research center for VL. He developed first oral antileishmanial drug (Miltefosine), he was instrumental in the pivotal RCT on paromomycin, leading to the approval of these two drugs. He developed single dose Liposomal ampho B treatment. This regimen, considered a game changer, was immediately implemented for the Elimination Program of VL, and acclaimed worldwide. He has published more than 500 research articles in pubmed journals.

application in the elimination program led to a drastic decrease in the VL and the case load in the region has diminished from over 44,533 in 2007 to 1,276 cases in 2021. This strategy met with remarkable success in reducing the incidence of VL to target levels in the Indian subcontinent.

Audience Take Away Notes

- This paper explains the developments in treatment for Kala-azar (Visceral Leishmaniasis). Recent advances and current treatment strategies of VL are explicitly discussed

Guidance on MS animal model development: Experimental autoimmune encephalomyelitis models induced by different myelin oligodendrocyte glycoproteins exhibit differentiated pharmacological responses

Up-to-date, experimental autoimmune encephalomyelitis (EAE) represents the most commonly used model for studying autoimmune-mediated myelin degradation in multiple sclerosis (MS). The immunological and neurobiological mechanisms underlying the pathogenesis, progression, and prognosis of MS are complicated. Myelin oligodendrocyte glycoproteins (MOG) 35-55 and MOG1-128 are commonly used peptides for EAE model induction and the selection of MOG is often investigator's preferences. In this presentation, the pharmacologic responses of anti-inflammatory drugs with different mechanisms of actions (MOAs) were evaluated using EAE models induced by either myelin oligodendrocyte glycoprotein MOG35-55 or MOG1-128. The animals with EAE were treated with different anti-MS medications, including three (3) B cell-mediated agents and two (2) T cell-mediated agents, respectively. Clinical symptoms were monitored and scored, and pharmacodynamic markers including cytokine secretion, inflammatory cell infiltration, and demyelination in spinal cord were analyzed. Our results demonstrated that induction of EAE by different myelin antigens resulted in differential pharmacologic responses to drugs with specific MOAs. The MOG35-55-induced EAE model only responded to T cell-modulating drugs, whereas the MOG1-128-induced EAE model exhibited therapeutic sensitivity against both T cell- and B cell-modulating agents. The data suggest the MOG35-55 peptide-induced EAE model is suitable for assessing T cell-modulating agents while MOG1-128-induced model can be employed to evaluate both T cell- and B cell-modulating agents. Due to complex pathogenesis of the disease and interplays between immunological and neurological responses, the finding derived from this work may shed lights on better understanding of disease biology and provide MS animal model preference.

Audience Take Away Notes

- Will help researchers on MS animal model selection and application
- Is this research that other faculty could use to expand their research or teaching? Yes
- Does this provide a practical solution to a problem that could simplify or make a designer's job more efficient? Yes
- Will it improve the accuracy of a design, or provide new information to assist in a design problem? Yes
- Deeper understanding and new insights of MS animal modeling.

WenQing Yang[1]*, Yuxi Yan[2], Quan Zhao[2], Ya Huang[2], Janine Y. Yang[3], Jie Zou[2], Chunxia Ao[2], Xiaojuan Chai[2], Renhong Tang[2]

[1]Chief Scientific Officer and Head of R&D, Clinbridge Biotech Co. Ltd, China

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[3]Massachusetts Eye and Ear, Harvard Medical School, USA

Biography

Dr. Yang completed his Ph.D. on Cell Biology and finished Post-Doctoral training in Cancer Biology at University of Calgary, Alberta, Canada. Dr. Yang has ~30 years of translational and innovative drug development experience on cancer and inflammatory diseases from a range of leading academic institutions or pharmaceutical organizations, including Celgene, Amgen, Crown Biosciences, UCLA, Kosan Biosciences, ImaginAb Inc and Simcere Pharma Group. He has led or crucially contributed to drug discovery programs involving >20 novel targets in the areas of gene therapy, epigenetics, targeted therapy and I/O, which led to 15 INDs or Phase-II/III development. He held several management positions in the biotech industry including Executive

Director, Cancer Biology, Global Scientific Research Innovation Organization, Senior Director of Cancer Pharmacology, Crown Biosciences, Head of Pharmacology at ImaginAb Inc. and Head of Translational Sciences, State Key Laboratory of Translational Medicine and Innovative Drug Development, Simcere Pharma Group. Dr. Yang's expertise focuses on translational medicine and translational research in cancer and inflammatory diseases using innovative drug candidates including small molecules, biologics, nanoparticles or polymeric micelles. Dr. Yang serves as an editorial board member or reviewer/editor for several international scientific journals including Front Imm, Front Onc, Cancer Res J, Cancer Res Cell Ther, J Onco Res Ther, and Int J Mol Onc. He has >100 publications in Journals including J Natl Cancer Inst, Cancer Res, Clin Cancer Res, Gene Therapy, Front Onc and Front Pharm, etc.

Fungal vaccines – Are they important to have

It's not just the bacteria or viruses that most commonly cause life-threatening disease in human, some of them could be fungal pathogens. Since 2013, the Leading International Fungal Education (LIFE) portal has facilitated the estimation of the burden of serious fungal infections country by country for over 5.7 billion people (>80% of the world's population). The substantial morbidity and mortality rates highlight the relevance of developing effective vaccines to control fungal pathogens. Approximately, 80% of this mortality are due to infections caused by opportunistic fungi. Majority of these patients die due to fungal sepsis caused by uncontrolled fungal growth. Additionally, IFIs can impact vital internal organs like lungs, heart, brain, kidneys, and liver leading to end-organ damage.

On October 25, 2022, the World Health Organisation (WHO) released a report that featured the first-ever list of fungal priority pathogens, a list of the 19 fungi that pose the greatest threat to public health, including Cryptococcus neoformans, Candida auris, Aspergillus fumigatus, Candida albicans, and other high- and medium-group pathogens.

Patients with severe illnesses and those who have serious underlying immune system-related problems are frequently affected by these invasive fungal infections. Those with cancer, HIV/AIDS, organ transplants, chronic respiratory diseases, and post-primary tuberculosis infection are among the populations most at risk for invasive fungal infections. A growing body of research suggests that global warming, an increase in international travel, and increased trade are all contributing to a rise in both the prevalence and geographic range of fungal illnesses. The reported incidence of invasive fungal infections among hospitalised patients increased noticeably during the COVID-19 pandemic. Emerging evidence indicates that the incidence and geographic range of fungal diseases are both expanding worldwide due to global warming and the increase of international travel and trade. During the COVID-19 pandemic, the reported incidence of invasive fungal infections increased significantly among hospitalized patients.

Even with the availability of four classes of antifungal drugs, the burden of life-threatening fungal infections is thought to exceed one million deaths annually, although numbers are difficult to estimate due in part to inadequate availability of diagnostic tests and disease reporting. The annual medical cost of fungal diseases is estimated to exceed 7.2 billion dollars in the United States alone. Recurrent vulvovaginal candidiasis (yeast infection) leads to lost productivity of US$14·39 billion annually in high-income countries.

In mouse studies, protection has been achieved with vaccines against such fungal pathogens. Encouraging results have been obtained with vaccines composed of live-attenuated and killed fungal antigens, crude

Sudhakar Bangera

AILEEN Clinical Research Services, Hyderabad, Telangana, India

Biography

Dr. Sudhakar Bangera did his Bachelor of Medicine and Surgery from KIMS, Bangalore, India; MD from KMC Mangalore, India; and Masters Medical Sciences in Clinical Trials Methodology) from The University of Hong Kong. Dr. Bangera is also trained on India Vaccinology Course at CMC Vellore, India and funded by Bill & Melinda Gates Foundation for International Vaccinology Course at International Vaccine Institute, Seoul. He has extensive work experience of 3 decades years in healthcare, of which 27 years are in global and local CRO, ARO, SMO, Medical Imaging, Clinical Bioavailability and Bioequivalence, Public Health, and Pharmaceutical and Vaccine manufacturing companies in various capacities as COO, Country Head, Vice-President, Director, Project Manager in national and international pharmaceutical research organisations. Currently, Dr. Bangera is managing his consulting firm, AILEEN Clinical Research Services, and a medical technology translation advisor to students, faculty and healthcare startup entrepreneurs. Dr. Bangera is an author of two books – "Medical Device – Concept to Commercialisation: India Perspective", and "The CRA".

extracts, recombinant subunit formulations, and nucleic acid vaccines. Novel adjuvants that instruct the immune system to mount the types of protective responses needed to fight mycotic infections are under development. Candidate vaccines include those that target common antigens expressed on multiple genera of fungi thereby protecting against a broad range of mycoses.

However, despite efforts, unfortunately only three vaccines (NDV-3, PEV7 and NXT-3) for Candida have reached human clinical trials. Despite the substantial global burden of human fungal infections, there are no approved vaccines available to prevent and control human invasive fungal infections, especially at-risk individuals.

Audience Take Away Notes

- The burden of serious fungal infections is over 5.7 billion people (>80% of the world's population). Approximately, 80% of this mortality are due to infections caused by opportunistic fungi. Majority of these patients die due to fungal sepsis caused by uncontrolled fungal growth
- Unfortunately, we still do not have any approved prophylactic fungal vaccine
- Formidable challenges remain in developing fungal vaccines

Covid-19 vaccines for optimizing immunity in the upper respiratory tract

Rapid development and deployment of vaccines greatly reduced mortality and morbidity during the COVID-19 pandemic. The most widely used COVID-19 vaccines require intramuscular administration. SARS-CoV-2 initially infects the upper respiratory tract where the infection can be eliminated with little or no symptoms by an effective immune response. Failure to eliminate SARS-CoV-2 in the upper respiratory tract results in lower respiratory tract infections that can lead to severe disease and death. Presently used intramuscularly administered COVID-19 vaccines are effective in reducing severe disease and mortality but are not entirely able to prevent asymptomatic and mild infections as well as person to person transmission of the virus. Individual and population differences also influence susceptibility to infection and the propensity to develop severe disease. I provide a perspective on the nature and the mode of delivery COVID-19 vaccines that can optimize protective immunity in the upper respiratory tract to reduce infections and virus transmission as well as severe disease.

Audience Take Away Notes

- Appreciate mucosal immunity and immunity to SARS-CoV-2
- Assist teaching of public health, immunology and virology
- Help develop research ideas to advance knowledge on vaccines
- Establish and promote collaborative research links in the field
- Improve knowledge of the COVID-19 and help develop measures to mitigate its effects

Ranjan Ramasamy

IDFISH Technology, Milpitas, CA 95035, United States of America

Biography

Ranjan Ramasamy graduated from the University of Cambridge, UK and then obtained a PhD also from the University of Cambridge. He has since 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, Professor of Life Sciences at the Institute of Fundamental Studies in Kandy in Sri Lanka, Professor of Biochemistry in the University of Jaffna in Jaffna Sri Lanka, Professor of Immunology in the University Brunei Darussalam Medical School and held institute appointments at the Babraham Institute in Cambridge in the UK & Scripps Clinic and Research Foundation in La Jolla in the USA. He has more than 280 publications in fields pertaining to Medical Sciences.

Lessons learned for the future of social listening to address vaccine misinformation

Introduction: As the pandemic evolves and nations refocus on routine immunizations and vaccine-preventable outbreaks, it is critical to continue increasing vaccine demand. Misinformation threatens the success of vaccination programs across the world. Since 2017, The Public Good Projects (PGP) has monitored public media data around 15 distinct health topics, most recently related to immunizations and COVID-19 misinformation. PGP has engaged in social listening in dozens of languages and geographic contexts, including all 50 US-states, and 20+ countries across the world. In 2019, PGP began tracking and responding to US-based vaccine misinformation through Project VCTR, which has collected millions of conversations about vaccine misinformation in both English and Spanish. Project VCTR provides weekly misinformation reports to thousands of users, representing health departments, nonprofits, academia, media, and the private sector. This presentation will relay lessons learned from PGP's social listening experience, with commentary on challenges and opportunities, and the future of using social listening to address health misinformation.

Methods: PGP's social listening consolidates online data from social listening platforms with hyperlocal offline data gathered through close relationships with organizations working on the ground. No single social listening platform is responsible for PGP's data; instead PGP has strong relationships with all major social media companies and contracts with multiple competing media monitoring systems. By combining data from these platforms with offline insights from local organizations, data can be triangulated in ways no other social listening system is capable of. Data are used to create programs and messages that speak directly to the way that a health topic is being understood by a specific population. As part of its programs, PGP often provides local partners with customized access to the social listening tools. Providing community-level access to these powerful disease surveillance systems allows local programs to benefit from datasets that categorize a community's understanding of critical health topics. By employing PGP's holistic approach to social listening, communities can benefit from a more nuanced understanding of vaccine misinformation.

Lessons Learned: If utilized effectively, social listening can be a critical tool in helping to bolster global vaccine confidence. Social listening is a nuanced process that involves reviewing multiple social listening platforms, and integrating both on and offline data. Through our work, we have learned the importance of diversifying the resources and tools we use, instead of relying on one platform to make conclusions on overall vaccine misinformation. Yet technology and tools are just one part of the process. Our experiences have highlighted the importance of close partnerships with on the ground stakeholders to monitor and deliver

Joe Smyser, PhD

The Public Good Projects

Biography

Dr. Joe Smyser is the CEO of PGP (The Public good Projects), holds a PhD and masters in global public health, and has worked at the intersection of public health, media, and technology throughout his career. He has designed the core strategies for several of the United States' largest social and behavior change programs; for the US CDC and FDA, Kaiser Permanente, Rockefeller Foundation and CDC Foundation, among others. During Dr. Smyser's tenure, PGP has served as the primary health communications partner for Facebook (Meta), Tumblr, Twitter, and Tik Tok. PGP has, dutifully and often behind the scenes, been among those chiefly responsible for serving the global public accurate and timely health information. Dr. Smyser conducted his postdoctoral training at the US CDC. He is a member of the Education Advisory Board of Rutger's University, and the Forbes Nonprofit Council. He has authored numerous peer-reviewed studies and white papers regarding various aspects of health communications. Dr. Smyser is a highly sought after speaker, participating in forums such as Aspen Ideas, SXSW, World Vaccine Congress, and American Public Health Association. He is a Returned Peace Corps Volunteer, having served in the Kingdom of Eswatini.

information that meets their needs, allowing stakeholders to help PGP lead the way. The creation of cross-sector collaborations is important to identify and operationalize best practices in using big data to directly address vaccine misinformation in ways that are most likely to resonate with specific populations.

Audience Take Away Notes

- After attending this presentation, the audience will be able to:
- Discuss lessons learned around vaccine hesitancy in the U.S., and how those can be applied globally
- Describe the creation and implementation of a media monitoring system to track vaccine opposition
- Apply learnings to improve the implementation of systems to track vaccine opposition
- More effectively leverage media monitoring and social listening tools for programs that improve population health
- Apply practical, hands on advice for organizations that are using social listening to inform their programs

Gram-negative eskape bacteria bloodstream infections in patients during the COVID-19 pandemic in a mexican hospital

Bloodstream infections due to bacteria are a highly consequential nosocomial occurrences and the organisms responsible for them are usually multidrug-resistant. The aims of this study were to describe the incidence of bacteremia caused by Gram-negative ESKAPE bacilli during the COVID-19 pandemic and characterize the clinical and microbiological findings including antimicrobial resistance. A total of 115 Gram-negative ESKAPE isolates were collected from patients with nosocomial bacteremia (18% of the total bacteremias) in a tertiary care center in Mexico City from February 2020 to January 2021. The most frequently isolated bacteria were Acinetobacter baumannii (34%), followed by Klebsiella pneumoniae (28%), Pseudomonas aeruginosa (23%) and Enterobacter spp (16%). A. baumannii showed the highest levels of multidrug-resistance (100%), followed by K. pneumoniae (87%), Enterobacter spp (34%) and P. aeruginosa (20%). The blaCTX-M-15 and blaTEM-1 genes were identified in all beta-lactam- resistant K. pneumoniae (27), while the blaTEM-1 was carried in 84.6% (33/39) of A. baumannii isolates. The carbapenemase gene blaOXA-398 was predominant among carbapenem-resistant A. baumannii (74%, 29/39) and blaOXA-24 was detected in 4 isolates. One P. aeruginosa isolate was blaVIM-2 gene carrier, while two K. pneumoniae and one Enterobacter spp were blaNDM gene carriers. Among colistin-resistant isolates mcr-1 gene was not detected.

Clonal diversity was observed in K. pneumoniae, P. aeruginosa and Enterobacter spp. Two outbreaks caused by A. baumannii ST208 and ST369 were detected, both belonging to the clonal complex CC92 and IC2. A. baumannii was associated with a death rate of 72%, most of them (86%) XDR or PDR isolates, mainly in patients with COVID-19 (86%, 24/28) in the Respiratory Diseases Ward. There was no statistically significant association between the multidrug-resistant profile in Gram-negative ESKAPE bacilli and COVID-19 disease. The results point to the important role of multidrug-resistant Gram-negative ESKAPE bacteria causing bacteremia in nosocomial settings before and during the COVID-19 epidemic. Additionally, we were unable to identify a local impact of the COVID-19 pandemic on antimicrobial resistance rates, at least in the short term.

Audience Take Away Notes

- Audience Microbiologist, Infectious diseases specialists PROTOCOL experience in this hospital during COVID-19 Pandemic time
- Expand their research or teaching and coordination to find microbiological findings including antimicrobial resistance and role of multidrug-resistant Gram-negative ESKAPE bacteria causing bacteremia in nosocomial settings
- Could provide new information to assist in a design problem during this research work

María Dolores Alcántar-Curiel[1], Manuel Huerta-Cedeño[1,2], Ma Dolores Jarillo Quijada[1], Catalina Gayosso Vázquez[1] José Ignacio Santos-Preciado[1], Silvia Giono-Cerezo[2]*

[1]Unidad de Investigación en Medicina Experimental, Facultad de Medicina, Universidad Nacional Autónoma de México. Ciudad de México, México

[2]Laboratorio de Bacteriología Médica, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional. Ciudad de México, México

Biography

Dr. Silvia Giono Cerezo studied PhD at Instituto Politécnico Nacional. ENCB since 1967 and work there as full time Professor. She joined research group of Dr. Alcantar Curiel at 1Unidad de Investigación en Medicina Experimental, Facultad de Medicina, Universidad Nacional Autónoma de México. Ciudad de México, México, to collaborate on Gram-negative ESKAPE bacilli and role of multidrug-resistant consisted in impulse graduate students on Master and PhD to obtain experience on microbiological methods and work together with people with great experience in this area at Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional. Ciudad de México, México. We have several publications.

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Sunita Girish
B. J. Medical College, India

The methylation status of vitamin d genes in correlation with interleukin-6 levels in cytokine storm in severe COVID-19 patients

Background: Cytokine storm in vitamin D deficient covid-19 is characterized by increased production of proinflammatory cytokines, where Vitamin D deficiency increases- the risk of Covid -19 severity. However, the epigenetic contribution of methylation of Vitamin D genes associated with vitamin D metabolism to the inflammatory status is poorly understood.

Method: In our study, we hypothesized that Vitamin D deficiency may be a risk factor for Covid -19, through epigenetic modifications in inflammatory markers. Therefore, we aimed to study the level of proinflammatory cytokines IL6 gene and methylation status of genes related to vitamin D metabolism in severe Covid-19 patients and evaluate their association with serum 25-Hydroxyvitamin D (25(OH)D). We included 48 participants with severe Covid19 patients (RTPCR positive).

Result: We found that the majority of the studied vitamin D genes are hypo-methylated in Covid-19 patients. In addition, serum 25(OH) D was associated with methylation of key vitamin D genes and interleukin (IL) 6 levels in severe Covid-19 patients. Our study suggests a potential correlation between epigenetic regulation of vitamin D affecting further levels of the inflammatory marker, IL6 – in Covid-19 patients, in which 25(OH) D may mediate this risk.

Conclusion: Therefore, vitamin D could affect the epigenetic status of IL6, which can be considered for additional preventive strategies in Covid -19 patients.

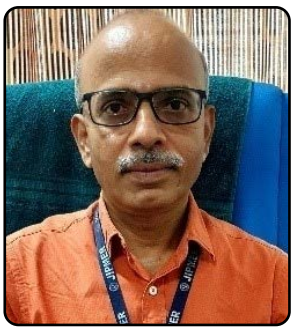
Biography

Dr. Sunita Girish holds a Ph.D. in Medical Biochemistry from Pune University, which was awarded in 2005. The topic of their research was the antioxidant status in Leprosy. They currently hold the position of Associate Professor in the Department of Biochemistry at B.J.G.M.C. in Pune. In 2014, Dr. Sunita Girish was a BJGMC-JHU HIV-TB Fogarty fellow. Their research interests include studying the molecular mechanisms of TB latency, developing rapid molecular diagnostic methods for the detection of TB and drug resistance, and expanding laboratory capacity for the isolation and characterization of TB. Dr. Sunita Girish is also pursuing a Ph.D. in Genetics, specifically studying the Vitamin D methylation status in Covid patients.

Abduh Abdullah Abdulwahab Murshed
Guangdong Medical University, China

Highly selective titanium (IV)-immobilized O-phospho-Ltyrosine modifi ed magnetic nanoparticles for the enrichment of intact phosphoproteins

Phosphorylation is one of the most important protein post-translational modifications, which possesses dramatic regulatory effects on the function of proteins. In consideration of the low abundance and low stoichiometry of phosphorylation and non-specific signal suppression, efficient capture of the phosphoproteins from complex biological samples is critical to meet the need of protein profiling. In this work, a facile preparation of titanium (IV)-immobilized O-Phospho-L-tyrosine modified magnetic nanoparticles were developed for the enrichment of intact phosphoproteins. The prepared magnetic nanoparticles were characterized by various instruments and had a spherical shape with an average diameter of 300 nm. The adsorption isotherms were investigated and the maximum capacity for β-casein was calculated to be 961.5 mg/g. Standard protein mixtures and biological samples (non-fat milk and human serum) were selected to test the enrichment performance. Sodium dodecyl sulfatepoly acrylamide gel electrophoresis analysis demonstrated the excellent enrichment performance with high selectivity. With the superparamagnetic property, titanium (IV)-immobilized O-Phospho-L-tyrosine modified magnetic nanoparticles were convenient for the practical application and clinical promotion, thus having a promising prospect in the field of phosphoprotein research.



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Role of fine needle aspiration cytology in the diagnosis of leprotic lesions

This study is a compilation of some interesting leprotic lesions diagnosed by simple Fine Needle Aspiration Cytology (FNAC). A series of patients with palpable leprotic lesions, including polar tuberculoid and lepromatous neuritic leprosies, Erythema Nodosum Leprosum (ENL), leprous osteitis, and histoid leprosy, will be presented.

Key Words:

- Our study would enable physicians and dermatologists coming across such lesions to make effective use of the simple FNA procedure.
- It would also help improve awareness of the utility of this simple, cost-effective procedure in the diagnosis and management of patients with various leprotic lesions.
- Leprosy is not yet totally eradicated from the world, and hence there is scope for further epidemiological research.
- The FNAC procedure is a practical solution in these relatively rare clinical scenarios.
- Overall benefits: FNAC is a simple, minimally invasive, cost-effective screening tool as well as a diagnostic procedure that is highly useful in the clinical management of patients with a variety of leprotic lesions, including neuritic and reactionary leprosies.

Biography

Dr. Siddaraju completed his postgraduate studies at Mysore Medical College, Mysore (Karnataka), India, in 1991. Currently, he is a senior professor in the department of pathology at the Jawaharlal Institute of Postgraduate Medical Education and Research (JIPMER), Puducherry, India. His field of interest is cytopathology. He is a postgraduate teacher and a Ph.D. guide. He has participated in various national and international conferences and published more than 130 scientific papers and a book chapter. He has been a reviewer for various peer-reviewed journals, and currently he is also an Editorial Board Member of the Journal of Cytology.

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Mortality from HIV infection in Russia before and during the COVID-19 pandemic

Purpose of the study: To study the dynamics of mortality from HIV infection in Russia before and during the Covid-19 pandemic.

Materials and methods: Rosstat data on the number and causes of death of contingents with HIV infection for 2012-2021. For the analysis, the StatTech program (developed by Stattech Ltd, Russia) was used.

Results: In Russia, before the pandemic in 2012-2019 mortality from HIV infection increased by 2.2 times and in 2019 was 12.7 per 100 000 of the population (in 2012 - 5.8 per 100 000 of the population). The overall growth rate was high at 119%. Starting from 2019, mortality from HIV infection in Russia began to decline, and this trend continued during the pandemic (2020-2021): in 2021, its values decreased by 1.2 times compared to 2019 and amounted to 10.7 per 100 000 of the population, while the rate of decline was 15.7%.

Before the pandemic in 2017 and 2019 in Russia, for the first time, a decrease in the number of contingents who died from HIV infection was recorded: in 2019, their number was 26869 people (in 2017 - 25981 people). During the pandemic (2020-2021), this trend continued and the number of deaths of contingents with HIV infection decreased by 4.2% and 8.3% compared to 2019 and amounted to 25750 and 24634 people respectively. Among patients whose cause of death was HIV infection (ICD-10 B20-B24), there was a gradual decrease in the proportion of patients with TB associated HIV infection (TB/HIV) before and during the pandemic. The largest proportion of TB/HIV patients among patients who died from HIV infection, which was 47.6%, was registered in 2014, when almost every second case of death from HIV infection was observed among TB/HIV patients.

Starting from 2015, the proportion of TB/HIV patients began to gradually decrease and in 2019 its value reached 37.9%. Although this trend continued during the pandemic and in 2020 the proportion of TB/HIV patients among patients who died from HIV infection decreased to 34.8%, it was still high, i.e. in 2020 Every 3rd patient whose cause of death was HIV infection was a TB/HIV patient.

The main factor that had a positive impact on the dynamics of mortality from HIV infection in Russia in recent years was an increase in the coverage of contingents with HIV infection with Antiretroviral Therapy (ARVT), whose share in 2020-2021 increased to 82.2% and 83.3% (in 2017 - 50.1%). As a result, the life expectancy of contingents with HIV infection has increased: in 2021 to 13 years (in 2019 - 8.5 years) and their number, which in 2021 was 749227 people. (in 2019 - 662208 people).

Conclusion: In Russia, a year before the start of the pandemic and during it, a decrease in mortality from HIV infection was observed due to a significant increase in the coverage of contingents with HIV infection with antiretroviral therapy. At the same time, the persistence of a high proportion of TB/HIV patients in the structure of the death rate from HIV infection will have a negative impact on the decrease in the values of this indicator, slowing down the pace of its decline.

Biography

Dr. Tsybikova Erzheny defended her PhD thesis at the Scientific Center of Surgery of the Russian Academy of Sciences in 1992. In 2013, she defended her doctoral dissertation on public health at the Federal Research Institute of Organization and Informatization of the Ministry of Health of Russia. Currently, she is the chief researcher of this institute. She has published 70 scientific papers on various public health issues, including morbidity and mortality from TB and HIV infection. Annually participates with scientific reports in international and Russian scientific conferences devoted to various problems of public health.

Delia Teresa Sponza

Environmental Engineering Department, Engineering Faculty, Dokuz Eylül University, İzmir, Buca Kaynaklae Campus, Turkey

Removals of some protozoan, coliphage, viruses and bacteria from the drinking water via reverse osmosis: Effects operating parameters

Impacts of the main operating parameters on permeate flux and pollutants rejection of the RO process, as well as fouling on the membrane surface, were examined for removing the significant ionic concentration and remaining natural organic and dissolved organic matter load of the System. The effects of permeate fluxes (20, 30, 40 and 60 L/m2·h), pressure (8, 22, 30 and 40 bar) temperature (15, 20 and 26 Oc) and ph (6, 7 and 8) on the rejections of the RO process, on the pollutants and removals of Escherichia coli, Pseudomonas aeruginosa, and Klebsiella pneumoniae. Giardia, Cryptosporidium MS-2 coliphage and Corona Virus -19. The maximum TOC, NOM, dissolved COD and TDS yields were around 99% and 99,90% at a permeate flux of 40 L/m2·h, at a pressure of 30 bar at a 20 Oc temperature and at a Ph=7. The Escherichia coli, Pseudomonas aeruginosa, and Klebsiella pneumoniae. Giardia, Cryptosporidium MS-2 coliphage and Corona Virus -19 removals varied between 4.2 and 6, 2 log 10.

Audience Take Away Notes

- Yes, this research that other faculty could use to expand their research or teaching
- Yes, it improve the accuracy of a design, or provide new information to assist in a design problem

Biography

Prof. Dr. Delia Teresa Sponza is currently working as a professor at Dokuz Eylül University, Department of Environmental Engineering. Scientific study topics are; Environmental engineering microbiology, Environmental engineering ecology, Treatment of fluidized bed and activated sludge systems, Nutrient removal, Activated sludge microbiology, Environmental health, Industrial toxicity and toxicity studies, The effect of heavy metals on microorganisms, Treatment of toxic compounds by anaerobic / aerobic sequential processes, Anaerobic treatment of organic chemicals that cause industrial toxicity and wastewater containing them, Anaerobic treatability of wastewater containing dyes, Treatment of antibiotics with anaerobic and aerobic sequential systems, Anaerobic and aerobic treatment of domestic organic wastes with different industrial treatment sludges, Treatment of polyaromatic compounds with bio-surfactants in anaerobic and aerobic environments, Treatment of petrochemical, Textile and olive processing industry wastewater by sonication, Treatment of olive processing industry wastewater with nanoparticles and the toxicity of nanoparticles. She has many international publications.

Nozethu Mjokane*, Maphori Maliehe, Olufemi S Folorunso, Adepemi O Ogundeji, Onele MN Gcilitshana, Jacobus Albertyn, Carolina H Pohl, Olihile M Sebolai

Department of Microbiology and Biochemistry, University of the Free State, Bloemfontein, State, South Africa

Activation of SARS-CoV-2 spike protein by a fungal protease(s)

SARS-CoV-2 is the causative agent of the novel corona virus disease of 2019 (COVID-19). It first emerged in the city of Wuhan, China in December 2019 and has resulted in millions of infections and deaths worldwide. To invade a cell, this enveloped virus targets cells that display ACE-2 receptors and relies on host serine protease(s) such as furin for the initial priming of the spike protein. Importantly, COVID-19 may also manifest in persons with underlying microbial infections. Some of these microbes like Cryptococcus neoformans secrete microbial protease(s) to breach the epithelial barriers for purposes of dissemination. It is in this context that microbial protease(s) may also activate the spike protein of SARS-CoV-2.

To investigate the latter, a fluorogenic peptide mimetic of the spike protein with a furin cleavage site was used. Thereafter, the biochemical efficiency of cryptococcal protease(s) to mediate cleavage of a potential furin site (underlined, SPRRAR↓S) at the interface between the S1 and S2 subunit was compared to that of a recombinant furin.

We observed that cryptococcal protease(s) processes this site in a manner comparable to the efficiency of furin ($p > 0.581$). In general, this preliminary work suggests cryptococcal protease(s) have the potential to activate S protein of SARS-CoV-2 leading to host invasion.

Audience Take Away Notes

- The audience will understand the impact of coexistence of Cryptococcus neoformans and SARS-CoV-2 in a host
- They could use some of the experimental procedures in their related projects
- Yes, the potential manifestation of COVID-19 in the context of an underlying cryptococcal infection could result in the synergistic activation of SARS-CoV-2 spike protein by cryptococcal proteases. This would help to establish sufficient merit to clear any underlying microbial infection
- It would improve the vaccine response

Biography

Miss Nozethu Mjokane studied Microbiology at University of Fort Hare, South Africa and graduated for honours degree in 2019. She joined the Pathogenic yeast research group of Prof Sebolai, Department of Microbiology and Biochemistry at the University of the Free State in. She received Master's degree with distinction in 2021 at the same institution. Currently working on her PhD and has published 4 articles.

Whegang Youdom Solange
Department of public health/Faculty of Medicine and Pharmaceutical Sciences/ University of Dschang/Dschang/Cameroon

Missed opportunities for vaccination among children aged 0 to 23 months in Cameroon

Complete childhood vaccination remains poor in Sub-Saharan African countries. Although Missed Opportunity for Vaccination (MOV) was found responsible for low coverage, median time-to-corrected is useful to assess delay in vaccination. MOV also reflects quality of immunization service. We aim to assess its burden and associated factors, knowledge of caregivers and health personnel on MOV; reasons why MOV occurs and possible solutions to reduce it in order to increase vaccination coverage.

We first used existing survey datasets to explore its burden, incomplete vaccination coverage, describe characteristics of children who experienced corrected MOV for all antigens, and estimate median survival time. Secondly, a cross-sectional survey with mixed methods was conducted to provide insights on strategies to reduce MOV. We thoroughly used survival Kaplan-Meier analysis to estimate median time-to-corrected MOV for each vaccine. Multiple Correspondence Analysis (MCA) was called to describe characteristics of children with corrected MOV and incomplete vaccination. We analyzed focus group discussion and highlight possible implementation solutions.

Second birth order children experienced more MOV than first born children. Children born to non-educated/primary level mothers had increased odds of experiencing a MOV than those born to educated mothers. Children from poorest households were at high risk of experiencing MOV for any vaccine than richest households. Identified solutions were : strengthening parents' knowledge on vaccination, encourage health workers to systematically assessing children's vaccination status, promoting service integration for identification of eligible children. There is an urgent need to use implementation research to reducing MOV, and increase vaccination coverage.

Audience Take Away Notes

- The work provides methodology for going through survey dataset and exploring secondary indicators that are useful for the control of vaccination coverage
- It also provide knowledges on methods that be taught to Students, as well as how to present results
- Of course because, the work aims to show how results can be turn to implementation research strategies that are more suited in filling gaps in infectious disease outcomes

Biography

Dr. Solange Whegang Youdom studied Mathematics and applied statistics at the University of Yaounde I-Cameroon and University of Paris Descartes-France. She joined the Department of Public Health and Epidemiology at the University of Dschang (Cameroon), Faculty of Medicine and Pharmaceutical Science where, she is currently a Senior Lecturer in Statistics. She is interested in public health and epidemiology, Biostatistics, modelling and analysis of complex sampling survey. She has published several research articles.

Dr. Abu Sayed Md. Mosaddek[1,2]*, Dr. Md. Siddiqul Islam[3], Dr. Salma Parvin[4], Dr. Mohammad Mahbubur Rahman[5]

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Effect of ABCB1, ABCC4, and GSTP1 gene polymorphisms on the response and toxicities of antiretroviral therapy in Bangladeshi AIDS patients

Background: Antiretroviral therapy was reported to show varying degree of responses and toxicities. The inter-individual variation of the therapy outcomes is due to different factors including biological factors. Genetic factors are one of the leading causes of this variation. Therefore, it is warranted to investigate the influence of genetic factors that leads to variation of the therapy outcomes.

Objective: Our objectives were to evaluate the role of genetic polymorphisms in ABCB1, ABCC4 and GSTP1 on the drug response and toxicities of antiretroviral therapy in AIDS patients and to identify molecular (genetic) marker for selecting better treatment regimen and reducing toxicities.

Methodology: A total 414 AIDS patients were recruited from Infectious Diseases Hospital (IDH: 208) & (BSMMU: 206) of Bangladesh receiving Lamivudine-300 mg+ Tenofovir-300mg + Efavirenz-400mg (for 6 months). PCR-RFLP had been applied to determine the genetic polymorphisms. Viral load and regimen change and drug induced toxicities have been evaluated from recorded hospital data of the patients as well as it was matched with the data obtained from interview of the patients with the help of structured questionnaire.

Result: ABCB1 gene was associated with the high viral load such as for CT (p= 0.0095, OR=0.49), TT (p=0.0068, OR=0.40), and for CT+TT (p= 0.0018, OR=0.45) as well as regimen change (drug resistance) like for CT (p= 0.0091, OR=0.50), TT (p= 0. 0.0017, OR=0.36), and for CT+TT (p= 0.0009, OR=0.45). On the other hand, GSTP1 gene was linked with drug induced toxicities like drug allergy (hypersensitivity) such as for AG (p= 0.048, OR=1.99), GG (p= 0.04, OR= 2.39), and for AG+GG (p= 0.016, OR=2.2), nausea and vomiting: for GG (p= 0.017, OR= 2.96), and for AG+GG (p= 0.025, OR=1.9), hyperacidity: for GG (p= 0.023, OR= 2.96), and for AG+GG (p= 0.026, OR=2.16), diarrhea: GG (p= 0.031, OR= 2.98), and for AG+GG (p= 0.03, OR=2.22) and insomnia: for AG+GG (p= 0.039, OR=2.1). No other significant association was observed for ABCB1, ABCC4 and GSTP1.

Conclusion: ABCB1 gene was associated with viral load and drug resistance. On the other hand, GSTP1 gene was related with drug induced toxicity in AIDS patients.

Audience Take Away Notes

- The role of genetic polymorphisms in ABCB1, ABCC4 and GSTP1 on the drug response and toxicities of antiretroviral therapy in HIV patients will be learned
- Molecular (genetic) marker for selecting better treatment regimen and reducing toxicities will be identified

Biography

Current faculty at the Department of Pharmacology, Uttara Adhunik Medical College, Bangladesh and working as an examiner of undergraduate and post-graduate medical academic courses. Also working as Director, Clinical trials Affairs of Quest Bangladesh. Also involved as Principal Investigator in clinical trials of drugs among patients with different diseases (diarrhea, UTI, Cervical Cancer, Autism, malnutrition) over five years and basic research activities in human genetic research and rationale use of medicine especially antimicrobial agents. Familiar to deliver scientific talk in domestic and international settings. Fluent in English and Bangla. Have published 50 articles in different journals in home and abroad.

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Unraveling potential early diagnostic biomarkers of opisthorchis viverrini infection through comparative immunoproteomics of the sera of infected mice and hamsters

Opisthorchiasis, caused by Opisthorchis viverrini, continues to pose a significant public health challenge, particularly in the Lower Mekong Basin of Southeast Asia, necessitating urgent attention and intervention. Research on O. viverrini has primarily focused on proteomic and transcriptomic analyses of adult worms, neglecting the study of Newly Excysted Juveniles (NEJ) and immature worms, representing crucial stages of the parasite's lifecycle. We employed Sodium Dodecyl Sulfate-Polyacrylamide Gel Electrophoresis (SDS-PAGE) and western blotting techniques to investigate the kinetics of host immune responses targeting worm proteins during an early stage of infection. These methods assessed antibody responses in two animal species, hamsters and mice, following infection with O. viverrini at different intervals. The results demonstrated the propensity of mice to effectively eliminate Ov-infection, accompanied by a robust antibody reaction towards an approximately 100-kDa component of NEJ somatic extract. Conversely, hamsters displayed a notable depression in antibody response during the early stage of O. viverrini infection. Expanding on these initial findings, we aimed to identify a set of immunoreactive proteins in the tegument and somatic extract obtained from NEJ, immature and mature adult worms on Days 1, 7, 14 and 28 post-infection, respectively, in both hosts. The comparative analysis of serum samples from hamsters and mice may provide insights into the specific protein(s) targeted by mice early, leading to the successful elimination of the infection. The discovery of early diagnostic biomarker may also be potential therapeutic target against O. viverrini.

Keywords: Opisthorchis Viverrini, Newly Excysted Juvenile (NEJ), Immunoproteomics, Biomarker.

Audience Take Away Notes

- Researchers can validate the biomarker candidates in dead-end hosts to develop rapid early diagnostics for infection
- Clinicians can eventually use the resulting diagnostic tests to identify and treat infections earlier, leading to better patient outcomes
- Epidemiologists can leverage potential diagnostics to improve disease surveillance in high incidence areas and inform control strategies
- Parasitologists can take a similar comparative immunoproteomics approach to uncover biomarkers for other neglected tropical diseases
- Sharing these methods and findings helps advance the broader field of biomarker discovery and diagnostic test development
- Identifying infective stages early provides key insights for those developing vaccines, therapeutics, and interventions

Biography

After obtaining his MS in Microbiology from Mahidol University, Mr. Alok Kafle pursued doctoral research on the carcinogenic parasite Opisthorchis Viverrini (Ov) at Khon Kaen University's WHO-collaborating Center, motivated by the parasite's association with high liver cancer rates in the region. Undertaking his PhD in one of the Neglected Tropical Diseases (NTDs) in the highest incidence areas, he's determined to find biomarker and therapeutic targets for Ov-associated cholangiocarcinoma. His research addresses major health burdens, making good impact and significant contributions despite being early in his career.

Majda Bouraddane[1]*, Karima Warda[1], Sara Amari[1], Aboubacar Sidiki Sidibé[3], Youssef El Kamouni[1,2], Lamiae Arsalane[1,2], Karam Harou[3], Abderraouf Soumani[3] and Said Zouhair[1,2]

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[2]Laboratory of Bacteriology-Virology, Avicenne Military Hospital, Marrakesh, Morocco
[3]Gyneco-obstetric departement, Mohammed VI University Hospital, Marrakesh, Morocco

Immunological status of antibodies of human parvovirus B19 among pregnant women with spontaneous abortion, fetal mortality and non immune hydrops fetalis in Marrakesh, Morocco

Background: Human parvovirus B19 (B19V) is a small DNA virus. Acute B19V infection is a risk for pregnant women. After vertical transmission the infected may develop Non-Immune Hydrops Fetalis (NIHF), Intrauterine Fetal Death (IUFD), Intra Uterine Growth Restriction (IUGR) and spontaneous abortion.

Objective: The aim of this study was to determine the seroprevalence of anti parvovirus B19V IgG and IgM among pregnant women with spontaneous abortion, NIHF, IUFD and study the relation with other risk factors such as age, having children, gravidity.

Study design: In this present study, 91 serum samples of pregnant women with spontaneous abortion (69), IUFD (3), IUGR (4) and NIHF (15) are collected during the period January to July 2023. Patients were recruited in Gynecology-obstetrics department of the University Hospital Mohammed VI of Marrakesh, Morocco.

Serologic tests were carried out by searching for IgM and IgG antibodies using recombinant capsid protein VP2 as antigen via the Parvovirus Virclia® Chemiluminescence monotest kits (Vircell Microbiologist, Granada, Spain) at the Bacteriology-Virology laboratory of the Avicenna Military Hospital in Marrakesh, Morocco.

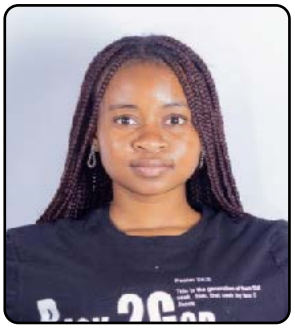
Results: Among study the mean age is 30.7 years of case group of spontaneous abortion and 29.6 years of the others group cases IUFD, IUGR and NIHF. The seropositivity of IgM was 2.89 (2/69) for two cases of pregnancy women with spontaneous abortion. However, any case of primary B19 infection was detected for the other case groups. In addition, the B19V IgG seroconversion was founded to be 60.86 % of spontaneous abortion, 46.66% of IUFD, 75% of IUGR and 33, 33% of NIHF. Multiples variables regarding incidence of B19V specific antibodies IgM and IgG was evaluated. In effect, the results of logistic regression, showed significant association between duration of pregnancy, anemia and IgG seropositivity in pregnant women with abortion. The IgM seropositivity in this group is affected by the gravidity and having children under six years ($X2=3.862$, $P=0.048$). The maternel age, gravidity, gestational age and having children are the significant association with IgG seropositivity in NIHF case group ($X2=3.000$, $P = 0.000$). Residence area and social class are a significant association with IgG seropositivity in IUGR.

Conclusion: The prevalence of B19V infection in spontaneous abortion cases is important. The results of this present study showed that the pregnant women have a high susceptibility to B19V infection. However, more studies are needed to prove the absolute role of B19V in these abortions.

Keywords: Immunological status, parvovirus B19, pregnant women, spontaneous abortion, hydrops fetalis, intrauterine fetal death and Intra Uterine Growth restriction.

Biography

Majda BOURADDANE is a doctoral researcher at the Laboratory of Microbiology, Virology at the Faculty of Medicine and Pharmacy of Marrakech at the Cadi Ayyad University in Morocco. Graduated with a Master's degree in Biomedical Analysis in 2007 and a Master's degree in Microbiology and Engineering of Bio Industry in 2009 from the Faculty of Sciences and Techniques in Morocco and also with a university degree in Advanced Immunology. She is a PhD student researcher from the CLAUDE BERNARD University of Lyon-1 2012-2016 in allergology immunology. His research has focused on: allergy to olive pollen in Marrakech, Morocco, prevalence of E. coli in the Mediterranean marine environment and biochemical and molecular characteristics of pathogenic strains, research by PCR and RT-PCR of Enterovirus in shellfish samples. And currently his research is focused on the seroprevalence of Parvovirus B19 in pregnant women for his national doctorate. She is currently in charge of initial and continuing training at a research and innovation centre at the Marrakech Faculty of Medicine and of practical immunology and microbiology work in the same faculty. its publications are: IgE d1 and d 2: are they both necessary for the exploration of allergy to mites, published in 2017 in the French journal of allergology and parvovirus B19 and pregnant women: a bibliographic journal published in 2021 in the open journal of obstetrics and gynecology.



N.A Maswanganyi[1], R.M. Lekalakala-Mokaba[1,2], and I. Rukasha[1,2]

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Diagnostic Accuracy of Rapid Assays for Diagnosis of Bloodstream Infections And Antimicrobial Profiling of Pathogens That Causes Bloodstream Infections At a Tertiary Hospital In Polokwane, Limpopo Province, South Africa

Background: Antimicrobial resistance is a cause of high morbidity and mortality in South African hospitals. Turnaround time for diagnosis of bloodstream infections is long, rendering results clinically irrelevant. Thus, there is a need for a faster and more accurate diagnosis platform for diagnosis of BSI. The aim of this study was to evaluate the performance of the BioFire Film Array BCID2 machine for rapid identification (ID) compared with the standard of VITEK 2 workflow for Identification and antimicrobial susceptibility testing (AST).

Methods: We conducted a prospective cross-sectional study in patients suspected of having Bloodstream infections at Pietersburg Hospital, Polokwane, South Africa from January to May 2023. The blood cultures were incubated in the BD Bactec machine. The positive blood cultures were run on the VITEK 2 and BioFire Film Array BCID2 machines, to identify the pathogens, their AMR genes, as well as their antimicrobial susceptibility patterns. The results were loaded on excel and analysed using Statistics and Data (STATA) latest version.

Results: Of the pathogens that were isolated from the positive blood cultures, most of them were Gram-negative bacilli. The most common organisms isolated were Acinetobacter baumannii complex constituting 30%, followed by Enterobacter cloacae complex with 24%, Klebsiella pneumoniae group with 18%, Escherichia coli with 15%, and Pseudomonas aeruginosa with 12%. The AMR genes identified were mecA/C gene (33%), CTX-M (33%), NDM (18%), OXA-48 Like (12%), and VIM (3%). Of all the antimicrobials tested, ampicillin (82%), cefotaxime (77%), and trimethoprim-sulfamethoxazole (76%), showed the highest level of resistance. Most pathogens were isolated from male patients (48%), and from children between 0 to 5 years (48%).

Conclusion: The BCID2 provides a faster and more accurate diagnosis of BSI as compared to the traditional culture methods and VITEK2. The BioFire FilmArray BCID2 allowed species ID and carbapenemase detection within around 1 h after blood culture positivity, which is a significant reduction in the turnaround time of the PBC workflow. There is a significant rise in the statistics of Carbapenem-resistant organisms. The impact of multidrug-resistant organisms may be reduced in the future with the use of novel antimicrobial methods, modified usage of antimicrobial agents, public health measures, and the use of more rapid molecular assays.

Keywords: Bloodstream Infections, Diagnostic Accuracy, Antimicrobial Profiling

What will audience learn from your presentation?

- Learning molecular assays that are more rapid and accurate for the diagnosis of bloodstream infections,

which will then help to improve patient clinical outcomes and reduction of mortality that is caused by BSI.

- The most common pathogens isolated in blood cultures and the most common resistant genes of these pathogens and which antimicrobials are these pathogens mostly resistant to in South Africa.
- Ways to minimize bloodstream infections and mortality rates that are caused by bloodstream infections.
- Ways to minimize resistance to antimicrobials.

Biography

Ms Nhlayiso Atalia Maswanganyi studied BSc. In Medical Sciences at the University of Limpopo, which is situated in Polokwane, Limpopo province, South Africa. I am currently doing MSc in Medical Sciences, specializing in Medical Microbiology.

Nsana Sjelin Nardiouf
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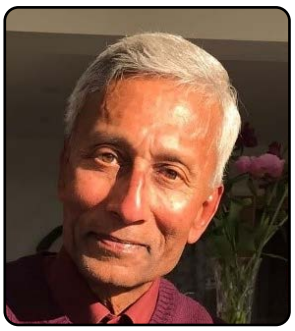
Impact of the long-acting insecticide-treated mosquitonet in the strategy to combat malaria vectors in the republic of Congo from 2012-2017

The insecticide-treated mosquito net is one of the preventive tools in the fight against malaria vectors in the Republic of Congo. The general objective of this study was to assess the impact of the use of long-acting insecticide-treated mosquito nets in the strategy for the control of malaria vectors in the Republic of Congo from 2012-2017.This is a cross-sectional analytical study with a retrospective aim, carried out from January to June 2022 in 13 localities located in the North and South of Congo-Brazzaville. It focused on a sample of 1405 participants.

The type of sampling was probability based on a convenience sample. The data was collected using a tested and validated questionnaire administered to participants during the period of 2012-2017.The data collected was stored on the Excel spreadsheet and analyzed on SPSS. At the end of its analyses, 48.75% of the participants are men and 51.24% are women. Most of the respondents are young people aged 1-15, that is 73.38%. The LLIN utilization rate is 68.25% in its 13 localities in Congo. The correlation between the use of the LLIN and the examination of the rapid diagnostic test, showed a significant association (OR= 5.18 and p= 0.00), the analysis carried out using a regression logistics showed a link between the use or not of LLINs and chemoprophylaxis (OR= 1.7646 with the 95% CI (1.2159; 2.5608), p= 0.0028) and also, in favor of sex (OR= 0.0144 with 95% CI (0.0084; 0.0246), p= 0.0000).

The impact of the use of the MII by the populations of its localities is effective, however, this rate remains below that recommended by the WHO. Free mass campaigns using insecticidetreated nets should be done from time to time to ensure good coverage.

Key Words: Impact- LLIN- Vectors of malaria- Republic of Congo.



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Recombinant protein immunoblots supporting clinical diagnosis and differentiation of babesia microti and babesia duncani infections

Babesiosis is a worldwide tick-borne disease with an increasing incidence in North America. Several species of apicomplexan Babesia parasites, including B. microti and B. duncani, cause human babesiosis. Babesiosis exhibits many non-specific clinical manifestations. Direct and indirect laboratory diagnostic tests therefore have an important role in diagnosing babesiosis. Light microscopic examination of Giemsa-stained blood smears, PCR and Fluorescent in Situ Hybridization (FISH) are useful direct diagnostic methods in acute babesiosis. Immunofluorescence Assay (IFA) that detects antibodies in patient sera is a common indirect diagnostic method. Recombinant proteins used in Line Immunoblot (IB) tests previously described for detecting antibodies in Lyme disease, Tick-borne relapsing fever and COVID-19 have now been applied to detect antibodies against Babesia parasites in patients. Recombinant Babesia proteins were prepared by cloning hybrid gene constructs or portions of the selected genes into pET23 vectors, and expressing the encoded proteins in Escherichia coli. The proteins were purified by metal affinity chromatography and gel filtration to >95% purity. Seventy-two patient sera, positive for babesiosis by IFA or FISH, and 24 control sera including nine from patients with other tick-borne diseases, were tested in Babesiosis IBs for IgM and IgG antibodies. All 24 control sera were negative in the Babesiosis IBs indicating 100% specificity. The estimated sensitivity for detecting either IgM or IgG antibodies in the Babesiosis IBs was 87.5% (63/72) for the genus Babesia. Additionally, 25/72 and 20/72 of patient sera contained antibodies reacting respectively only with B. microti and B. duncani specific-antigens in the IBs.

Audience Take Away Notes

- Appreciate the complex immunodiagnostic needs in Babesiosis and other tick-borne diseases
- Assist teaching of immunodiagnostics and clinical immunology
- Improve application of immunodiagnostic tests for tick-borne and other infectious diseases
- Advance understanding of immune responses in Babesiosis
- Help develop better immunoassays for clinical and veterinary diagnostic purposes

Biography

Ranjan Ramasamy graduated from the University of Cambridge, UK and then obtained a PhD also from the University of Cambridge. He has since held academic appointments in the UK, Australia, Sri Lanka and the USA. He was the Chairman of the National Science Foundation of Sri Lanka, Professor of Life Sciences at the Institute of Fundamental Studies in Kandy in Sri Lanka, Professor of Biochemistry in the University of Jaffna in Jaffna Sri Lanka, Professor of Immunology in the University Brunei Darussalam Medical School and held institute appointments at the Babraham Institute in Cambridge, UK and the Scripps Clinic and Research Foundation in La Jolla, USA. He has more 250 publications in fields pertaining to Medical and Biological Sciences. He was on the Committee on Scientific Planning and Review of the International Council for Science, and the Board of Governors of the International Centre for Genetic Engineering and Biotechnology.

Brandon Lucke-Wold MD, PhD, MCTS
Baylor University, United States of America

NLR as a diagnostic and prognostic marker for neonatal sepsis: A systemic review

Neonatal sepsis is a bloodstream infection that affects newborn infants under the age of 28 days and is a leading cause of morbidity and mortality in these children 1,2. There is little information on the prevalence of newborn sepsis, however Fleischmann-Struzek et al. estimate that there are around 2,200 instances of neonatal sepsis per 100,000 live births, with a death rate of 11 to 19 percent 3. Early-Onset Sepsis (EOS) and Late-Onset Sepsis (LOS) are two types of neonatal sepsis based on when symptoms appear after birth (LOS). Sepsis in neonates that occurs before 72 hours of life (some experts use seven days) is referred to as EOS, while sepsis that occurs after 72 hours of life is referred to as LOS 4.

The spread of infections from the female genitourinary system to the infant or fetus is the most common cause of Early-Onset Sepsis (EOS) 1,2,4–6. These infections can contaminate the amniotic fluid or may ascend the vaginal canal, cervix, and uterus. As they pass through the vaginal canal in pregnancy or upon delivery, neonates can become contaminated. Group B Streptoccoci (GBS), E. coli, coagulase-negative Staphylococcus, Hemophilus influenzae, and Listeria monocytogenes are common bacterial infections associated with EOS1,2. Chorioamnionitis, GBS infection, birth before 37 weeks (premature newborns), and protracted rupture of membranes longer than 18 hours are all maternal variables that enhance the risk of neonatal sepsis 2. Prematurity and delayed treatment of newborn sepsis are linked to a variety of negative outcomes, including persistent lung illness and neurodevelopmental concerns such hearing and vision loss, cerebral palsy, and poor psychomotor and mental development 2,7. Overuse of antibiotics, for prophylactic treatment in sepsis prevention, on the other hand, can raise the risk of severe candidiasis and multidrug-resistant organisms1,2,4,5.

In contrast, Late-Onset Sepsis (LOS) usually occurs via the transmission of pathogens from the surrounding environment after delivery, such as contact from healthcare workers or caregivers2–4. A percentage of LOS may also be caused by a late manifestation of vertically transmitted infection. Infants requiring intravascular catheter insertion, or other invasive procedures that disrupt the mucosa, are at increased risk for developing LOS1–3. Preterm neonates are at higher risk for sepsis/infection than term neonates. Mortality rates are inversely proportional to gestational age, such that preterm or younger neonates have higher mortality rates than do term neonates 2,5. E. coli has also been found to be associated with a higher mortality rate when compared with GBS - this can be attributed to the introduction of GBS intrapartum antibiotic prophylaxis which has decreased mortality rates5,8. The treatment of clinically suspected neonates with negative cultures has also significantly decreased mortality rates8.

The immature immune system is the primary cause of increased neonatal sepsis susceptibility 2,6,8–10. Polymorphonuclear neutrophils, macrophages, and T lymphocytes are unable to carry out a complete inflammatory response in newborns due to their immature function. Furthermore, newborns have a restricted quantity of immunoglobulins at birth and are unable to mount an appropriate quantitative and/or qualitative response to pathogens 1,2,6,8,10,11. The premature infant's limited time in the uterus reduces the transfer of immune globulins to the fetus. When compared to term infants, preterm infants have a substantially higher risk of sepsis due to immunoglobulin deficiency 1,2,6.

Neonatal sepsis can manifest itself clinically in a variety of ways, including feeding intolerance, temperature instability, tachycardia, pneumonia, and respiratory distress 2,5,7–10. Because these symptoms are similar to those of noninfectious diseases, newborn sepsis is difficult to identify clinically. Some neonates with bacteremia might even have no symptoms and present with a normal physical examination2,5,6. This emphasizes the importance of decisive tests with quantitative measures for diagnosing sepsis. Blood culture as a diagnostic marker is currently the gold standard for diagnosing sepsis in neonates, although it has drawbacks such as a long waiting period and the risk of contamination 2. CBC with differential and C-reactive protein (CRP) are additional crucial lab tests to get and are routinely collected on a serial basis, however these indices are weak at diagnosing newborn sepsis and are better suited for ruling it out 2. These flaws have emphasized the necessity for a neonatal sepsis marker that can be tested rapidly and easily. As a measure of newborn sepsis, neutropenia has a higher specificity than neutrophilia 2,12. An elevated immature to total neutrophil (I/T) ratio of more than 0.27 has a very high negative predictive accuracy (99%) but a poor positive predictive value (25%) because it can be elevated in up to 50% of uninfected infants 2,13. These counts can be erroneously raised, especially after a baby is born. However, several clinical investigations have recently established the efficacy of the neutrophil to lymphocyte ratio (NLR) in predicting newborn sepsis and showed it to be a more accurate diagnostic tool with high specificity for predicting patient prognosis 13. NLR has been shown to be a good predictor of deadly outcome in newborns with sepsis by Djordjevic et al 12. Liu et al. whose findings indicate the positive relationship between NLR levels and mortality in septic newborns, observing NLR as having power for predicting bad outcome, as suggested by an area under the curve of 0.695 0.036 14. This paper provides a systematic review of studies that evaluated the NLR as a marker for diagnosis and prognosis of neonatal sepsis.

Biography

Brandon Lucke-Wold was born and raised in Colorado Springs, CO. He graduated magna cum laude with a BS in Neuroscience and distinction in honors from Baylor University. He completed his MD/PhD, Master's in Clinical and Translational Research, and the Global Health Track at West Virginia University School of Medicine. His research focus was on traumatic brain injury, neurosurgical simulation, and stroke. At West Virginia University, he also served as a health coach for the Diabetes Prevention and Management program in Morgantown and Charleston, WV, which significantly improved health outcomes for participants. In addition to his research and public health projects, he is a co-founder of the biotechnology company Wright-Wold Scientific, the pharmaceutical company CTE cure, and was a science advocate on Capitol Hill through the Washington Fellow's program. He has also served as president of the WVU chapters for the American Association of Pharmaceutical Scientists, Neurosurgery Interest group, and Erlenmeyer Initiative Entrepreneur group. In addition, he has served as vice president for the graduate student neuroscience interest group, Nu Rho Psi Honor Society, and medical students for global health. He was an active member of the Gold Humanism Honor Society and Alpha Omega Alpha Honor Society. He is currently a member of the UF House Staff Council, Positive Culture Committee, Quality Improvement Committee, Board of Directors Alachua County Medical Society, and Accreditation Requirements Review Committee. He is married to Noelle Lucke-Wold and has two children. As a family, they enjoy running with their dogs, rock climbing, and traveling. In his spare time, Brandon frequently runs half marathons and 10ks together with is wife. Brandon also enjoys reading, playing piano, discussing philosophy, and playing chess. He is currently a Pgy5 neurosurgery resident at University of Florida with pursuing endovascular enfolded training and was awarded the Dempsey Cerebrovascular Research Fellowship.

Bethan Hussey[1]*, Pamela Proud[1], Daniel Knott[1], Mark Manak[2], Luc Gagnon[2], Steven Phay-Tran[2], Philipa.Levesque-Damphousse[2], Aymeric Fabie[2], Matthieu Daugan[3], Ali Azizi[2], Valentina Bernasconi[2], Sue Charlton[1], Bassam Hallis[1]

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Developing a network: Supporting SARS-CoV-2 assays vaccine clinical trials through the CEPI centralized laboratory network

The UK Health Security Agency (UKHSA) has longstanding expertise in the technological support of vaccine development through a vast array of immunological assays. In early 2020, using this valuable knowledge, scientists within UKHSA were able to rapidly develop a live virus microneutralisation assay (WT-MNA) that could be used in a high throughput setting to support the development of the SARS-CoV-2 vaccines. At the same time, the Coalition for Epidemic Preparedness Innovations (CEPI) issued a call to establish a global network of well-qualified laboratories to centralize immunological laboratory assessment of vaccine candidates. The UKHSA partnered with CEPI and other laboratories, such as Q2 Nexelis, to form the CEPI Centralized Laboratory Network (CLN). The CLN shares assays for quantitation of anti-COVID-19 activity including antibody binding and neutralization, pseudo virus neutralization and cell mediated immunity to eight participating laboratories around the world, with additional laboratories coming online in 2023. The CEPI Centralized Laboratory Network (CLN) is the first and largest global group launched to harmonize the assessment of COVID-19 vaccines for support of preclinical and clinical trials.

The CEPI CLN program has successfully provided clinical trial support to over 50 developers and tested over 70,000 samples to date. This coordinated laboratory analysis for the assessment of immune responses to vaccines provides a blueprint for how the network can support the CEPI 100-day mission to develop a vaccine and prepare for Disease Z. Critical evaluation of the successes and challenges in forming the CEPI CLN will aid in preparedness for the next pandemic.

Audience Take Away Notes

- Understand the role of the UKHSA in the development of the CEPI Centralized Laboratory Network.
- Demonstration of the power of the network in supporting the development of vaccines during the COVID-19 pandemic and beyond
- A look to the future with what lessons can be learnt from this pandemic to the next, how these can be addressed and used to be prepared for Disease Z

Biography

Dr. Hussey studies Human Biology at Loughborough University, UK and graduated with a BSc in 2014. She joined the research group of Dr. Mastana and Lindley on the Anti-Inflammatory Modulation mini-Centre for Doctoral Training Studentship and received her PhD degree in 2018. Dr. Hussey moved to the Wellcome Sanger Institute where she worked supporting the Cellular Genetics Programme, led by Dr. Teichmann, and provided operational support to the Programme. Following this, Dr. Hussey joined the UK Health Security Agency where she manages the clinical testing for COVID-19 vaccines and the tech transfer of the microneutralisation assay to CEPI partner labs.

Sushmita Koley[1]*, Andrew Kocot[2], Michael J. Betenbaugh[3], Andrew Pekosz[4], Steven M. Cramer[2]

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Purification process development of COVID antigens to identify sera needed for plasma therapy

One of the crucial steps in deploying plasma therapy for COVID-19 has been the development of critical assays to detect SARS-CoV-2 antibodies and evaluate their potential suitability. Unfortunately, assays that assess neutralizing antibodies involve use of live SARS-CoV-2 virus in a high containment facility (BSL3) which can take up to a week to complete. The assay cost, time for completion, and requirement for PPE make it a weak link in the pipeline for the rapid identification of plasma donors. Also, the commercial assays lack the precise quantitation of protective antibody levels desired in sourcing plasma. Therefore, the goal of the project was to rapidly biomanufacture purified COVID antigens for scaling up a quantitative ELISA assay for characterizing plasma needed for treatment and prophylaxis. In this project, we developed purification processes to generate high quality purified SARS-CoV spike (S) protein and the SARS-CoV-2 S Protein Receptor Binding Domain (S-RBD) to be incorporated into these quantitative ELISA assay. The presence of an extremely sensitive and robust assay technique using multiple antigens helped specify the highest binding and protective antibodies (and their targets) from a pool of volunteers and recipients. This presentation will focus on the purification process development of Spike and Spike-RBD antigens as well as other COVID variant antigens and how the workflow helped understand the intricacies of the human immune response after vaccination.

Biography

Dr. Koley studied Bioprocess Technology at the Institute of Chemical Technology, India and graduated as MTech in 2013. She then joined the research group of Prof. Lali at the same institution and received her PhD (Tech) degree in Bioprocess Technology in the year 2018. Later, she joined Prof. Cramer's Lab at Rensselaer Polytechnic Institute (RPI, New York) where she worked as a Postdoctoral Research Associate for 3 years and gained experience in diverse research areas including gene therapy, multimodal adsorbent characterization, and public health response to COVID pandemic. Currently, Dr. Koley holds a Senior Scientist position at Bio-Rad Laboratories, California in the Process Chromatography Application Laboratory.

Amulya Prakash
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Oncogenic potential of SARS-CoV-2: A trouble in the future?

Coronavirus disease 2019 (COVID-19) emerged as a pandemic caused by the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) with high mortality worldwide. COVID-19 infection can be asymptomatic or can cause multi-system disease of varying severity. The long-term effects of COVID-19, such as fatigue, loss of smell, dyspnea, etc., are still being studied. Through this discussion, we will try to explore the oncogenic potential of SARS-CoV-2.

Cancer is the world's second leading cause of death. The association between viral infections and the risk of developing cancer is well established. It is estimated that 15.4% of all cancer cases can be attributed to carcinogenic infections, for which viruses are the main risk factor [1]. The connection between various cancers and viruses such as Human Papillomavirus (HPVs), Hepatitis Viruses B and C (HBV and HCV), human gamma herpes viruses (HHV4/Epstein-Barr Virus, EBV), HHV8/Kaposi's sarcoma-Associated Herpesvirus (KSHV), Merkel Cell Polyomavirus (MCPyV), and human T-cell leukemia virus I (HTLV-1) have already been established. On the other hand, SARS-CoV-2 is a new player and is still being researched. There are growing concerns that SARS-CoV-2 can increase the incidence of lung, colorectal, breast, pancreatic, and oral cancer.

SARS-CoV-2 may induce the expression of nsp15, which causes proteasomal digestion of tumor suppressor PRB and can downregulate p53 gene, disrupting apoptotic pathways. It can also interact with epigenetic modifiers or chromatin and epigenetic changes that are known to be important for both viral infection and cancer progression. Another proposed mechanism is through inducing inflammatory pathways. SARS-CoV-2 is known to cause cytokine storm-generating free radicals, NF-κB activation via TNF-α, etc., which can damage DNA and evoke tumorigenic processes. Chronic inflammatory diseases such as lung fibrosis and interstitial lung disease are complications of SARS-CoV-2 infection and are known to be precursors of cancers. During SARS-CoV-2 infection, the virus binds to ACE2 receptors to enter the cell and then downregulates AT1R, which leads to dysregulation of the RAAS system. This process can cause inflammation, vasoconstriction, fibrosis, oxidation, and capillary permeability, contributing to cancer progression and development.

There are various hypotheses, but the exact mechanism is still unknown and remains a hot topic for research. Future research into cellular mechanisms, long-term observational studies, and analyses are needed to reveal the truth.

Audience Take Away Notes

- The audience will learn about the long-term complications of COVID-19 infections
- To increase awareness among clinicians of this potential complication, which can improve patient outcomes through screening and early diagnosis
- To motivate peers for additional research in this field
- In the long term, we can develop new guidelines for screening and treating such patient population

Biography

Dr. Prakash completed his medical school training at Patna Medical College, India, and then moved to the United States in 2018. He finished his residency in Internal Medicine in 2021 at Monmouth Medical Center, affiliated with The Rutgers University, New Jersey. Currently, he serves as Chair of Medicine, clinical faculty, and a hospitalist at Haywood Regional Medical Center, NC. He is involved in medical student education and research. His primary area of interest and research is hematology and oncology. He has more than 20 article publications, abstracts, and poster presentations.

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From crisis to resilience: Rethinking pandemic response strategies

The outbreak of the COVID-19 pandemic has underscored the importance of effective pandemic crisis management. This research article explores the need for comprehensive pandemic crisis management strategies and the lessons learned from the COVID-19 crisis. It discusses the key components of successful crisis management, the role of government, public health organizations, and the private sector in pandemic response, and the importance of international cooperation. Furthermore, it delves into the importance of preparedness, communication, and flexibility in managing pandemics and highlights the potential long-term impacts of effective crisis management.

Biography

Chital Naresh is a Research Scholar in the School of Health System Studies, Centre for Public Health, TISS, Mumbai, Maharashtra, India. She is a qualified patient safety and quality healthcare professional. She has an experience of 19 years in the field of patient safety and quality in healthcare.

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Khursheed Ul Islam*, Saleem Anwar, Dr. Jawed Iqbal
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Multifaceted role of lipid species in hepatitis C virus replication, assembly, and host antiviral response

Hepatitis C Virus (HCV) is a leading cause of liver diseases. Like other RNA viruses, HCV has also been known to alter cellular lipidome for its survival. There are evidences regarding involvement of lipid and Lipid Droplets (LDs) in HCV replication and assembly in the literature. LDs also have protein-mediated antiviral properties that are activated during HCV infection. Studies have shown that HCV replicates well in cholesterol and sphingolipid-rich membranes, but the ways in which HCV alters host cell lipid dynamics are not known yet. In this study, we performed a kinetic study to check the enrichment of LDs at different time points of HCV infection. Based on the LD enrichment, we selected early and later time points of HCV infection for global lipidomic study. Early infection represents the window period for HCV genome sensing followed by host immune response while later infection represents the establishment of viral RNA replication, virion assembly, and egress. We identified the dynamic profile of lipid species at early and later time points of HCV infection by global lipidomic study using UPLC-ESI- MS. At early HCV infection, Phosphatidylinositol Phospholipids (PIPs), Lysophosphatidic Acid (LPA), Triacyl Glycerols (TAG), Phosphatidylcholine (PC), and trihexosylceramides (Hex3Cer) were observed to be enriched. Similarly, Free Fatty Acids (FFA), Phosphatidylethanolamine (PE), N- Acylphosphatidylethanolamines (NAPE), and tri acylglycerols were enriched at later time points of HCV infection. Lipids enriched at early time of infection may have role in HCV genome sensing, viral attachment, and immune response as LPA and PIPs are important for immune response and viral attachment, respectively. Moreover, lipid species observed at later infection may contribute to HCV replication and virion assembly as PE, FFA, and triacylglycerols are known for the similar function. In conclusion, we identified lipid species that exhibited dynamic profile across early and later time points of HCV infection compared to uninfected Huh7 (mock) cells, which could be therapeutically relevant in the design of more specific and effective anti- viral therapies.

Audience Take Away Notes

- Our research has revealed important lipid species at early and later HCV infection
- The pathways that regulate the identified lipid species can be further explored for novel drug targets against HCV
- Lipid droplets can be explored for their role in innate immune response pathways

Biography

Mr. Khursheed Ul Islam is a Ph.D. scholar at Multidisciplinary Center for Advanced Research and Studies (MCARS) Jamia Millia Islamia New Delhi India. He is studying hepatitis caused by hepatitis C Virus in Dr. Jawed's virology lab. He has expertise in virus culture, mammalian cell culture and molecular biology.

Dr. Harshavardhini Kommavarapu[1]*, Dr. Tony Oliver[2]

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Ulceroglandular tularemia following arthropod bite - A case report

Introduction: Tularemia is an uncommon disease. An average of 173 cases per year were reported in the US for the past 20 years.(1) A low minimal-infective-dose, high rate of dissemination and the possible mortality make tularemia a potential weapon for bioterrorism.(2) This report summarizes the presentation of the ulceroglandular form - the most common among the six major classified forms of Tularemia.

Case: A 68-year-old male with a past medical history of deep vein thrombosis presented to the local hospital with concerns of left ankle pain, swelling and redness, two days after what he suspected was a spider bite over his left ankle. He was prescribed oral clindamycin for suspected cellulitis. However, he returned five days later, for worsening of his leg symptoms. He was afebrile but hypotensive with systolic blood pressure in the 80s. He was fluid resuscitated, treated with vancomycin and transferred to our institution for worsening cellulitis and suspected septic ankle joint.

On arrival, he rated the lower limb pain as 9/10. Upon further questioning, he recalled having two tick bites - one on the chest, another on the left leg. He also reported having subjective fevers, chills and anorexia for the past few days. On examination, he was hemodynamically stable, his left lower limb was warm to touch and had an ulcer. Edema and erythema could be demarcated from the surrounding skin. He had palpable pedal pulses and intact sensations. There was left groin lymphadenopathy. Rest of the examination was unremarkable. Labs were significant for elevated CRP (41.9mg/L), ESR (72mm/hr) with normal WBC (6.9k/uL). He was started on cefepime and vancomycin empirically.

Over the course of hospitalization, the ulcer progressed and turned into an eschar. Blood cultures and joint fluid aspirate were negative. Meanwhile, wound cultures grew Francisella tularensis. He was diagnosed with ulceroglandular tularemia. The antibiotics were switched to Ciprofloxacin 750 mg twice daily for 10 days and the patient made a good recovery.

Discussion: This case report re-emphasises the importance of detailed history-taking. All patients presenting with dermatologic lesions should be questioned about any recent history of outdoor exposure or exposure to animals or insects. Tularemia is a rare zoonotic disease and could be transmitted by various modes, the most common being through insect bites, particularly tick bites.(3) It should be included in the differential diagnosis involving refractory/worsening dermatologic lesions with lymphadenitis especially following an insect bite and/or when accompanied by fever. The best way to confirm is through blood and wound cultures along with serological assays. Effective antibiotic treatment options include Streptomycin, Gentamicin, Doxycycline or Ciprofloxacin depending on the severity of the disease.

Biography

Dr. Harshavardhini Kommavarapu is an international medical graduate from Osmania Medical college, India. She underwent her externship at Sanford USD Medical center affiliated with the University of South Dakota. Her other US clinical experiences include medical rotations at Mayo Clinic Health System (Minnesota), Texas Tech University of Health sciences (Texas) and at Center for Hypertension and Internal Medicine (Texas). She is working on several case reports and clinical studies concerning primary care as well as speciality care. She aspires to pursue her Internal medicine residency in the United States.

Dr. Diego Tomassone M.D. Ph.D

Department of Biomedicine and Biophysics, “Holos Medica” Clinical and Research, Turin, Italy

Will host genetics influence the response and risk of adverse reactions to SARS-CoV-2 vaccines? Historical precedents

Recent advances in genomic and bioinformatic technologies have enabled the emergence of the field of immunogenomics. This intersection of immunology and genetics has expanded our understanding of how the immune system responds to infection and vaccination. While the immunogenetic basis of the enormous clinical variability in response to severe acute respiratory syndrome coronavirus 2 (SARS-CoV- 2) infection is now widely studied (including by our research group), the host genetic determinants of SARS-CoV-2 vaccines remain largely unknown. Previous reports have shown that vaccines may not protect all populations or individuals equally, leading to even severe adverse reactions in predisposed individuals, due to multiple host- and vaccine-specific factors. Several studies of vaccine response to measles, rubella, hepatitis B, smallpox, and influenza have highlighted the contribution of genetic mutations or polymorphisms in modulating innate and adaptive immunity after vaccination. Specifically, genetic variants in genes encoding viral receptors, antigen presentation, cytokine production, or related to immune cell activation and differentiation could influence how an individual responds to vaccination. Although such knowledge can be used to generate personalized vaccine strategies to optimize vaccine response, studies in this field are still scarce. Here we aim to briefly summarize the scientific literature related to the immunogenetic determinants of vaccine-induced immunity, highlighting the possible role of host genetics also in response to SARS-CoV-2 vaccines.

Keywords: SARS-CoV-2, COVID-19, Vaccines, SNPs, Host Genetics, Adverse Effects.

Audience Take Away Notes

- From this presentation, it will be possible to learn how important immunogenetics is in the development and research of increasingly personalized, therefore more effective and safer vaccines
- In fact, knowing more and more about individual response to vaccinations will increase the benefits while minimizing the risks of this important but sometimes dangerous and ineffective practice

Biography

Diego Tomassone received master's degrees in Medicine, Chemistry and Physics, a bachelor's degree in Mathematics and a Ph.D. in Infectious Diseases, Microbiology and Public Health. He directs the medical center "Holos Medica” clinical and research, working as a clinical physician and researcher, also dealing with research in physics and chemistry. He has published about 20 papers on Covid-19 disease alone, co-author of Chapter 12 of the scientific paper: "COVID-19 infection as a chronic disease: Factors and pharmacological perspectives". He is also FoPRC (Foundation of Physics Research Center) researcher, reviewer and editorial board member of several international scientific journals.

Joana Kira Besecke*, S. Schopf, D. Ullrich, U. König

Medical & Biotechnological Applications, Fraunhofer Institute for Organic Electronics, Electron Beam and Plasma Technology FEP, Dresden, Saxony, Germany

Novel dosimeters for process control of next-generation production of vaccines and immune-therapeutics

The use of Low-Energy Electron Irradiation (LEEI) is a novel and highly efficient method for manufacturing vaccines and other pharmaceutical products. This technology provides advantages against conventional methods for virus inactivation, as the process is faster, does not require toxic chemicals and minor radiation shielding is needed in comparison to the use of gamma irradiation. 1 However, the performance of processes using LEEI such as virus inactivation and cell modifications for immune therapeutics is correlated to a certain dose, which must be monitored by a suitable liquid dosimetry system. While vaccine production by virus inactivation needs a high dose, i.e. the Tick-Borne Encephalitis virus or Zika virus around 20 kGy1,[2], blood irradiation for immune therapy should not be higher 300 Gy3.

This study established different chemical dosimeters with calibration functions for different dose ranges. Their absorbance spectra were measured and the storage stability prior to irradiation was determined.

The samples were irradiated in small volumes in an LEEI plant with a built-in blending system using 200 kV acceleration voltage. Dose rates from 20 kGy/h to 125 kGy/h were applied. Each liquid dosimeter was studied at different pH levels and concentrations. Not harmful dyes such as 1,9-Dimethyl-Methylen Blue (MTB), resazurin, and tartrazine Harmless dyes such as 1,9-Dimethyl-Methylene Blue (MTB), resazurin and tartrazine were suitable as chemical dosimeters between 100 Gy and 4 kGy. These solutions bleach gradually and dose-dependently when exposed to the electron beam. As a result, aqueous solutions of 0.2 mM MTB and 0.2 mM resazurin at pH 10 were suited dosimeters for the low dose range. The MTB showed a dose-dependent decolorization from 150 Gy up to 1.5 kGy and excellent stability within 35 days. The absorbance of resazurin was fitted with a second-order polynomial function at 63 Gy to 1040 Gy and the initial absorbance spectrum showed excellent stability within 7 days. A 0.5 mM tartrazine solution at pH 4 was appropriate for dose measurement in the mid-dose range. Its absorbance decreased gradually over a dose range of 24 Gy to 4.18 kGy and was stable for two days with a percentage change of 7.7 %. Another chemical dosimeter based on the colorization of a solution of 2,3,5-Triphenyl-Tetrazolium Chloride (TTC), which has already been established for virus inactivation[2], made it possible to measure high dose rates from 6.5 to 40 kGy.

In conclusion, this study provided novel solutions for process control and monitoring of LEEI for the production of vaccines and immune therapeutics, which is a next-generation technology providing many benefits against traditional pharmaceutical methods.

Audience Take Away Notes

- Overview of Low-Energy Electron Irradiation (LEEI) for virus inactivation and generation of immune therapeutics
- Advantages of LEEI in comparison to traditional methods of vaccine production
- Solutions for process monitoring and control by liquid dosimetry
- Introducing different potential and novel liquid dosimeters for different dose ranges developed for LEEI

Biography

Ms. Besecke studied Biomedical Engineering at the Technical University of Denmark and graduated as M.Sc. in 2021. As a doctoral candidate, she is joining the research group of Dr. Schopf at Fraunhofer Institute for Organic Electronics, Electron Beam and Plasma Technology FEP, Germany. In her work, she is developing liquid dosimetry systems for low-energy electron irradiation to monitor biotechnological processes.

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A case report of leptospirosis in cattle in Sicily (South Italy)

Bovine leptospirosis is a zoonosis causing economic losses in livestock. This work reports an outbreak of Leptospira interrogans serogroup Sejroe serovar Hardjo in a cattle farm in province of Enna (Sicily). The farm was officially free from Brucellosis, Tuberculosis and Enzootic Bovine Leucosis. In February 2022, serum samples were collected from 2 cows, showing full-term abortion without placental retention, eight days after the first abortion signs (T0). Three additional samplings were carried out on these two animals as well as in the other animals of the farms 1 month (T_1), 2 months (T_2), 8 months (T_3) and 12 months (T_4), after the antibiotic treatment.

Blood, milk and stool samples were also collected at T_2. Research of antibodies against pathogenic Leptospira species was carried out by Micro Agglutination Test (MAT). Antibodies against the main abortion agents (Chlamydia abortus, Coxiella burnetii, Neospora caninum) were searched by ELISA.

Blood, milk and drinking water samples were subjected to Real Time-PCR to detect DNA of Leptospira pathogenic species. The main abortion agents (Chlamydia abortus, Coxiella burnetii, Neospora caninum, Coronavirus, Cryptosporidium spp., Escherichia coli K99, Rotavirus) were also investigated.

No animals resulted positive at differential diagnosis except for two ones seropositive for N. canimun and C. burnetii, without showing signs of abortion. At T0 one of the two sera resulted positive to L. interrogans serogroup Sejroe serovar Hardjo at MAT. At the other sampling times, the following results were obtained at MAT: 30 positive samples/40 total samples (75%) at T_1, 25/25 (100%) at T_2, 22/54 (41%) at T_3, 19/59 (32%) at T_4.

This study describes clinical manifestations, diagnostic implications and epidemiological characteristics of an outbreak in cattle due to L. interrogans serogroup Sejroe serovar Hardjo, confirming that L. interrogans plays a role in determining leptospirosis infection in cattle reared in Sicily.

Audience Take Away Notes

- The study provides new insights into the epidemiology of this infection
- The control of zoonotic pathogens such as Leptospira spp. contributes to reduce animal and human infections and to limit the related economic losses to the farms
- The results improve occupational awareness of the exposure-related health risks to the farmers

Biography

Dr. Francesca Grippi studied Biological Sciences at the University of Palermo (Italy) and obtained her Master's Degree in 2000. Until 2008 she worked for Co.Ri.Bi.A. a Public Institution who deals with Applied Research. In 2006 she obtained the Post-Graduate Specialization at the University of Palermo and obtained the title of Clinical Pathologist. In 2009 she won the position of Biologist Laboratory Head at the Istituto Zooprofilattico Sperimentale della Sicilia, Palermo (Italy). Today she has the position of Laboratory Manager and Deputy Area Director.

Valeria Blanda*, Ilenia Giacchino, Rosalia D'Agostino, Marilena Alfano, Sergio Migliore, Santina Di Bella, Roberto Puleio, Domenico Vicari, Vincenza Cannella, Francesca Grippi

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Phylogenetic relationship of toxoplasma gondii in dolphins stranded in Sicily (South Italy)

Toxoplasma gondii, a protozoan pathogen causing zoonosis, represents a serious threat for aquatic mammals including dolphins, as it causes severe brain lesions in dolphins leading them to stranding and death.

This study aimed to investigate T. gondii DNA presence in organs collected from dolphins stranded along Sicilian coasts and to carry out sequence analysis based on gra6 gene.

From 2021 to 2023, n.16 dolphins were analysed, found stranded along the coast of Sicily. The animals belonged to different species, including Stenenella coeruleoalba, Delphinus delphis and Tursiops truncatus. Different organs were collected, including brain, spleen, liver, lung, lymph node, muscle and heart, for a total of 87 examined organs. One gram of tissue sample, diluted in 9 mL of saline solution, was homogenized in the Stomacher. Genomic DNA was extracted from the homogenate using a commercial kit. T. gondii DNA was amplified by both a nested PCR targeting the B1 gene and a TaqMan Real Time PCR targeting the 529 bp repeat element. A fragment of 773 bp of the gra6 gene was amplified in positive samples by nested PCRs and sequenced. Obtained sequences were analysed using BioEdit and MEGA version 7.0. Phylogenetic analyses were performed by neighbour-joining using the Maximum Composite Likelihood method. Phylogenetic tree was constructed with several valid type I (RH), II (Beverley and ME49) and III (NED, TONT and C56) T. gondii strains.

Two dolphins resulted positive for T. gondii DNA. The nucleotide sequences of gra6 fragment was obtained from all the different organs of one of them, a S. coeruleoalba found in the Western coast of Sicily and all the examined organs of this animal (brain, lymph nodes, spleen, hearth, liver and muscle) were positive, including those of choice for this pathogen. Gra6 sequence revealed high percentage of sequence similarity with the published sequences of T. gondii gra6, thereby establishing its specificity.

In silico analysis of the consensus obtained sequence of gra6, its subsequent phylogenetic analysis and pairwise distance calculations revealed the closest genetic relationship of the T. gondii strain from Sicilian stranded dolphin with that of type III strains (NED, TONT and C56).

T. gondii Type II lineage as well as a Type II-atypical isolate have been previously characterized from dolphins stranded along the northern coasts of Italy. Further studies will be addressed to the phylogenetic characterization of T.gondii detected in the second dolphin.

The positive animal belonged to cetacean species living in the open sea, making interesting better understanding the transmission routes of T. gondii for such animals in this area. Further studies are necessary to better characterize the genetic configuration of the strain and to clarify its possible origin and transmission routes in aquatic mammals.

Audience Take Away Notes

- The study provides new insights into the spread of T. gondii infection in dolphins
- Phylogenetic analysis revealed the closest genetic relationship of the obtained T. gondii strain with that of type III strains
- The study provide information to better understand the transmission routes of T. gondii in aquatic mammals in Sicilian sea

Biography

Valeria Blanda obtained a Master's Degree in Cellular and Molecular Biology, University of Palermo (Italy) in 2006. She is Specialist in Clinical Pathology and Clinical Biochemistry, University of Naples "Federico II" (Italy) and PhD in Cell Biology, University of Palermo. She is researcher at the Istituto Zooprofilattico Sperimentale della Sicilia (Italy) since 2009 and expert of Babesiosis for the World Organization for Animal Health – WOAH since 2021. In 2015 and 2019, she was appointed as expert in the Belgian evaluation program for Human Microbiology National Reference Centers assignment. Her research areas include zoonotic agents, tick borne pathogens, diagnostic technique development.

Catherine Lawton[1]* Jacob Boudreaux[2] MD

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Staphylococcus pettenkoferi: A first case report on abscess formation

Coagulase-Negative Staphylococci (CoNS) remain some of the commonest causes of nosocomial bacteremia, and as genomic identification become more precise, new infectious organisms are reported as the causative agent of bacteremia. Here we report the first published case of Staphylococcus pettenkoferi in Louisiana, the first known infection to form an abscess, and a patient's clinical course for an emerging opportunistic infection in the United States. Poorly understood, S. pettenkoferi is a commensal bacterium of rising clinical importance.

A 44-year-old woman with class III obesity presented to hospital for evaluation of fever and abdominal pain for three days associated with dyspnea, palpitations, nausea, and frequent emesis. Upon arrival, she was tachycardiac with abominable distention, erythema, abdominal mass, and tenderness to palpation in the umbilical region.

The patient was started on vancomycin and piperacillin/tazobactam and admitted for further management. Abominable/pelvic CT demonstrated a large ventral defect with extensive soft tissue inflammation without fluid collections. Plastic surgery was consulted, who deemed surgery to perform a panniculectomy too risky. Blood cultures resulted in Gram-positive cocci, and piperacillin/tazobactam was discontinued. Infectious disease specialists recommended cefepime which was started. The following day, drainage was noted from the patient's prior hernia scars, and a CT was repeated which demonstrated a fistula connecting an abscess measuring 10.2 x 4.9 x 13.3 cm in the anterior abdominal wall to colon. Interventional radiology and general surgery were consulted for possible intervention of the abscess. Due to body habitus both procedures were contraindicated. CeDAR score showed a 99% chance of a major complication if surgery were to be undertaken. Repeat blood cultures taken on day three of hospitalization resulted as negative.

The patient remained in hospital on antibiotics for 11 days then transferred to a Long-Term Care Facility (LTAC) in stable condition. Piperacillin/tazobactam was changed to vancomycin for MRSA coverage and then to doxycycline and amoxicillin/clavulanic acid. Two-month follow up demonstrated lingering though smaller abscess presence and continued fistula drainage while the patient remained on oral antibiotics.

Multiple opportunistic infections can cause serious harm once given the chance to infect, yet the ability of S. pettenkoferi remains poorly understood. Here we report of the first known instance of S. pettenkoferi in the state of Louisiana and the first known to cause abscess. Current published literature conflicts the status of S. pettenkoferi as possible of causing true bacteremia versus it being a benign contaminant. As microbial analysis and identification becomes more precise, S. pettenkoferi may reveal to be the underlying agent in increasing numbers of CoNS infections.

Audience Take Away Notes

- Identification of S. pettenkoferi as a commensal bacterium capable of causing disease
- S. pettenkoferi can form intrabdominal abscess
- Further research into S. pettenkoferi is needed to classify infectious potential
- Antibiotic resistance of a S. pettenkoferi culture taken in Louisianna

Biography

Catherine is a fourth year medical student at the University of Queensland/Ochsner Clinical School. Through this university she completed the first two years of medical school in Brisbane, QLD and is currently doing clinical rotations in New Orleans, LA. Catherine received a Bachelor of Science from the University of Michigan in 2019 where she majored in Biopsychology, Cognition and Neuroscience with a minor in Biochemistry. She recently published an article regarding traumatic cardiac arrest patients in The Journal of Emergency Medicine Australasia.

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Isolated renal failure without respiratory failure: Severe rhabdomyolysis as a rare presentation of COVID-19, a case series

Introduction: The SARS-Cov-2 virus is classically associated with respiratory tract infections. Here we present two rare cases of isolated renal failure resulting from severe rhabdomyolysis due to COVID-19, in the absence of respiratory symptoms.

Case 1: A 40-year-old African American male with no past medical history presented after he noticed "purple" urine, decreased urine output, and leg edema. This was preceded by 3 days of myalgia and chills. The patient was unvaccinated for COVID-19 and admission COVID-19 viral PCR was positive. He had a negative Chest X-Ray (CXR) and no respiratory symptoms. Labs revealed BUN 111, Creatinine >28 and Creatinine Kinase (CK) >144,000. The patient became anuric and developed worsening hyperkalemia despite fluid resuscitation requiring initiation of Renal Replacement Therapy (RRT) on hospital day 2. After 16 days of hemodialysis, his CK improved, and he started making urine. The patient was liberated from hemodialysis and was discharged with creatinine at a nadir of 4.4.

Case 2: A 28-year-old African American male, unvaccinated for COVID-19, with no past medical history presented with 4 days of myalgia after developing "red" urine. He was positive for COVID-19 on viral PCR, with negative CXR. Initial labs revealed BUN 42, Creatinine 4.5 and CK >144,000, with oliguria. On hospital day 4, his urine output remained <0.1 cc/kg/hour and he developed hyperkalemia despite aggressive fluid resuscitation. Hemodialysis was initiated. He then underwent a quadriceps muscle biopsy, which revealed scattered necrotic myofibers without lymphocytic infiltration, consistent with necrotizing myopathy. He continued hemodialysis and symptomatically improved without pharmacologic intervention. Ultimately was discharged on hospital day 12 with plans for hemodialysis weaning as an outpatient.

Discussion: COVID-19 frequently results in respiratory infections; however, as cases have accumulated, reports of alternative primary organ involvement have emerged. Current literature reports a prevalence of rhabdomyolysis between 2-17% in patients hospitalized with COVID-19. The vast majority of reported cases occurred concurrently with respiratory failure or were attributable to medication toxicity, with very rare reports of rhabdomyolysis severe enough to necessitate RRT. Both of our cases are unique due to the severity of rhabdomyolysis, with elevations in CK to >144,000, as compared to the average CK of 3000-6000 reported in current literature. These cases are made even rarer by renal failure requiring RRT and the absence of respiratory findings. How COVID-19 causes rhabdomyolysis is poorly understood, but may be attributed myositis from direct viral toxicity or from immune-mediated cytokines. Although not performed in our first case, our second patient underwent muscle biopsy revealing necrotizing myopathy, consistent with biopsies in other reported cases of COVID-19 induced myopathy. Notably, in both our cases, the patients were unvaccinated at the time of presentation, potentially contributing to the severity of their presentation. Both patients received hemodialysis with no other intervention and clinically improved, with one patient even liberated from RRT before discharge.

Though rare, rhabdomyolysis should be considered in all patients with COVID-19 presenting with myalgia,

dark colored urine, or unexplained changes in renal function. We recommend routinely screening these patients with CK and urinalysis.

Audience Take Away Notes

- They will learn of the rarely documented and rarely reported presentation of COVID-19, isolated rhabdomyolysis and renal failure. This should be considered in all patients with COVID-19, as it could exist, even underlying existing respiratory symptoms
- They will learn the expected pathologic findings on muscle biopsy, when suspecting COVID-19 myositis
- They will learn when to suspect this presentation, and how to screen and diagnose rhabdomyolysis
- They will learn how to treat COVID-19 associated rhabdomyolysis and associated renal failure

Biography

Rahul Gomez, DO is a Chief Medical Resident for the 2023-2024 academic year in the Internal Medicine Residency at Scripps Mercy Hospital, in San Diego, CA. He graduated with a BS in Kinesiology from the University of Miami, and attained is Doctorate is Osteopathic Medicine at Western University of Health Sciences before attending Residency in Internal Medicine at Scripps Mercy Hospital. He has presented 6 works of original research and case reports at various conferences, and is currently pending multiple publications, in pursuit of fellowship in pulmonary and critical care medicine.

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A mysterious tale of two joints and two bacteria

Introduction: Acinetobacter Radioresistens (AR), as resistant as the name sounds, is a Gram-negative, aerobic bacillus that survives desiccation, hydrogen peroxide, and UV irradiation and thrives in the hospital environment. It evades detection in the laboratory, adding vile to its name. To date, only 9 cases of AR bacteremia have been described worldwide.1 Here we describe a case of bacteremia caused by this rare organism which kept us guessing its source.

Case presentation: A 68-year-old man with obstructive sleep apnea, asthma, hypertension, atrial fibrillation, benign prostatic hyperplasia, and severe osteoarthritis of both knees presented to the emergency department with chills for 10 days and diarrhea for 3 days. Clinically, he was in septic shock requiring vasopressors. His initial work up revealed leukocytosis, acute kidney injury, metabolic acidosis, pyuria, and prostatitis on CT abdomen. Due to increasing encephalopathy and vasopressor requirements, he was placed on mechanical ventilation. He was started on broad spectrum antibiotics vancomycin and piperacillin-tazobactam.

Examination of knee joints revealed warmth and effusion without obvious erythema. Upon further questioning his wife, the patient received corticosteroid injections into both knees 2 weeks ago for longstanding severe osteoarthritis. Arthrocentesis of both knees revealed frank pus. Synovial fluid culture from both knees and blood cultures grew heavy colonies of Methicillin-Sensitive Staphylococcus Aureus (MSSA). While the patient was treated for high-grade MSSA bacteremia with cefazolin, one subsequent blood culture from an aerobic bottle demonstrated Acinetobacter radioresistens. Antibiotic coverage was broadened to meropenem, ampicillin-sulbactam, and minocycline in view of persistent fevers and elevated white cell counts. The patient was placed on strict contact isolation. Source control was achieved by arthroscopic lavage of both knees. The patient's clinical condition progressively improved and he was discharged home.

Discussion: Staphylococcus aureus septic arthritis and secondary bacteremia are well-reported in the literature. However, a thorough evaluation failed to reveal the source of Acinetobacter bacteremia. AR is a normal inhabitant of human skin mostly in moist areas, still a rare agent for human disease. In our case, even though the portal of entry was possible via joint injection, AR was not cultured in synovial fluid. Additionally, its detection only in the subsequent blood cultures makes a nosocomial origin likely. Identification of AR is quite challenging due to its ability to retain crystal violet, and resist decolorization misleading it as Gram-positive cocci, which may underestimate the true prevalence of AR bacteremia.

Conclusion: Identification of Acinetobacter radioresistens has important implications. AR has been reported to cause profound bacteremia leading to death.2,3 It has been reported to be a source of class D OXA-23 carbapenemase which confers carbapenem resistance. Prompt identification of this organism and starting appropriate antibiotics can improve patient outcomes as well as potentially prevent the spread of the organism in the hospital and prevent carbapenem resistance.

Audience Take Away Notes

- Our case highlights important facts about Acinetobacter radioresistens that could prove useful for physicians treating infectious diseases
- When Acinetobacter radioresistens infection is proven, it is important to treat it to prevent carbapenem resistance in Acinetobacter baumani. Also implementing strict contact prevention can help prevent the spread of this highly resistant organism
- Since this is a rarely reported organism, with unknown true incidence or prevalence due to the challenges in identification, more vigilant identification and reporting in different settings can improve our understanding of this organism to better control it

Biography

Dr. Kodishala graduated from Medical School in 2010 from Bangalore Medical College and Research Institute, India. He trained in Internal Medicine and subsequently in Rheumatology in India. He has worked at the Mayo Clinic, Rochester, Minnesota as a research fellow in rheumatology, identifying the risk factors for cognitive dysfunction in patients with rheumatoid arthritis. He is currently working as Internal Medicine resident at Canton Medical Education Foundation, Canton, Ohio, USA.

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3D- Vaxlock technology stabilizes the prefusion conformation of the RSV F protein resulting in a highly potent and stable subunit vaccine candidate

Viral fusion proteins enable cellular infection by fusing viral and cellular membranes accompanied by their transition from the pre-fusion to the post-fusion conformation during viral entry. Fusion proteins in their prefusion conformation elicit high neutralizing antibodies, but they are metastable and readily transition to postfusion irreversibly when used as subunit vaccines. Therefore, conformational stabilization is required to maintain the more potent prefusion state. In order to achieve this, we have developed a proprietary engineering technology, 3D-Vaxlock, that introduces Dityrosine (DT) crosslinks between Tyr residues in proximal side chains in the protein structure to stabilize protein conformations. Dityrosine crosslinks form naturally in proteins like elastin, collagen, and resilin where they provide structural rigidity and high stability. We have leveraged these specificities to stabilize the spring-loaded prefusion conformation of the RSV F protein in order to elicit the most potent neutralizing Antibodies (nAbs), resulting in a better subunit vaccine immunogen. We engineered tyrosine crosslinks in the soluble RSV F glycoprotein trimer by structure-based design that lock the prefusion conformation by stabilizing two potent antigenic sites (Ø and the IV/V interface). These crosslinks preserve epitopes recognized by potent prefusion-specific mAbs resulting in improvements to stability and potency. Dityrosine crosslinked prefusion F protein (DT-preF) maintained the prefusion conformation for 5 weeks at 4 °C and improved shelf life in an immunogenicity experiment compared to DS-Cav1 (a traditionally stabilized prefusion F protein). DT-preF also demonstrated 9-fold higher nAbs as compared to DS-Cav1 in a mouse immunogenicity study, complete protection in cotton rats, and overcame immunosenescence in aged mice with a high dose formulation on alum.

Biography

Devarshi Brahmbhatt, M.S, B.Pharm is a Principal Scientist at Calder Biosciences Inc. He graduated from Gujarat Technological University, with a Bachelor's of Pharmacy degree and started working as a Pharmacist in India. He obtained a Master of Science in Pharmaceutical Sciences from Temple University, in Philadelphia and initially worked in a biologics manufacturing facility at Janssen Pharmaceuticals, Malvern, PA. With a deep passion for research, he joined Calder Biosciences Inc. in 2019. Calder Biosciences is a next generation vaccine research and development company using its proprietary "3D-Vaxlock" platform technology that provides conformational stability and generates immunogens that elicit more protective responses. Currently, he is working on RSV and Universal flu vaccine projects under the leadership of Drs. Christopher Marshall and Mark Yondola. He has accumulated extensive experience in vaccine research, development, and manufacturing.

Sonal graduated from Mumbai University with a Bachelor's of Science degree in 2012, majoring in Biotechnology and Chemistry. She later obtained her Master's of Science in Biotechnology with a focus on Molecular Biotechnology, graduating in 2014 from Northeastern University. Sonal performed molecular biology experiments and upstream & downstream development activities at the Walz Lab at Harvard Medical School and at the DNA Enzymes Research Dept. at New England Biolabs Inc. prior to joining Calder Biosciences Inc.. She has been working at Calder on Subunit Vaccine Design & Development since 2015 where she is integrally involved in all aspects of Calder's bioprocess and development. Presently, she is leading Analytics Design & Development where she utilizes the unique, intrinsic properties of dityrosine bond formation to develop fluorescent and separation-based quantitative assays to characterize Calder's target immunogens.

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Food microbes influenced horizontal transfer of β-lactam resistance genes in the mouse gut

Ingestion of Antibiotic-Resistant (AR) bacteria may lead to transmission of AR genes in the gut microbiota and cause AR bacterial infection, a significant public health concern. However, it is not clear if and how microbes from the food matrix (food microbes) may influence resistance transmission. Thus, we assessed the colonization of a β-lactam resistant Salmonella Heidelberg strain (donor) and a β-lactam susceptible S. Typhimurium strain (recipient) and the transfer of the resistance genes in the mouse gut in the presence or absence of food microbes that were derived from washing freshly-harvested carrots. Mice were pre-treated with streptomycin and then inoculated with both donor and recipient bacteria in the presence or absence of food microbes. Donor, recipient and potential transconjugant bacteria were enumerated in fecal samples using selective culture techniques. Transfer of AR genes was confirmed by whole genome sequencing. Gut microbial composition was determined by 16s rRNA amplicon sequencing. Significantly lower numbers of donor and recipient were shed from mice that were inoculated with food microbes compared to those without food microbe inoculation. S. Typhimurium transconjugants were only recovered from mice without inoculation of food microbes. However, non-Salmonella transconjugatns, including Escherichia coli, Enterobacter, Citrobacter and Proteus were detected from mice with inoculation of food microbes. The results suggest that the food microbes may modulate AR gene transfer through changing the gut microbiome compositions.

Biography

Jiewen Guan received her Bachelor (1994) and Master (1997) degree in Biochemical Engineering, in the South China University of Technology in Guangdong, China, and her PhD (2002) in Food Microbiology, in the University of Massachusetts – Amherst in Massachusetts, the United States of America. She joined the Canadian Food Inspection Agency (CFIA) in 2002 and since then she has been working as a research scientist in the CFIA at the Ottawa Laboratory (Fallowfield) in Ottawa, Canada. Her early career focused on safe disposal of animal carcasses and disinfection of animal premises for control of infectious animal disease outbreaks. Later on, she developed research interest in airborne transmission of avian influenza viruses. More recently, her research interest expands to understanding the mechanisms of horizontal transfer of antimicrobial resistance in the gut microbiome.

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Assessing political sorting in response to COVID-19 vaccine mandates: A preliminary analysis

Introduction: In recent years, politics and business have become increasingly intertwined, with employees increasingly seeking workplaces that align with their political views (Stuckatz, 2020). The COVID-19 pandemic response introduced public health regulations that became contentious in the political sphere, and issues such as vaccine mandates began to divide communities and workplaces. Prior research has identified a phenomenon described as political sorting, wherein employees seek environments that match their political ideology (Bermiss and McDonald, 2018). Departure is more likely for employees whose personal ideology is more conservative than their workplace, and these employees tend to relocate to organizations that are more aligned with their political beliefs (Bermiss and McDonald, 2018, Brown et. al, 2020). This preliminary study examines the extent to which mandatory COVID-19 vaccination in healthcare workplaces impacted employee turnover and political sorting.

Methods: We gathered data from three sources - employee turnover data from Revelio, COVID-19 vaccine mandate dates from hand-collected research and news articles, and employee political orientation from federal filings stored and made public by the FEC. From Revelio, we aggregated employee counts and turnover rates to the firm-state-year-quarter level. From the FEC we collapsed data to firm-state level observations, tracking the number and total dollar amount of donations to Republican and Democratic committees to assess overall political alignment. We then regressed employee turnover rates on the presence of a vaccine mandate, as well as a set of controls.

Results: Data was collected from 31 healthcare firms split into 263 firm-state groups. Average turnover rates were around 15% prior to vaccine mandates and increased to 26% in the quarter after vaccine mandates were implemented. Among the 31 firms, 7 firm-metropolitan statistical area combinations were found in the quarter after the vaccine mandate was introduced. The raw correlation between vaccine mandates and turnover rates is positive. However, this association becomes economically smaller, though still meaningful, and is no longer statistically significant (p-value of 0.19) once industry-fixed effects are included. When firm fixed effects are included, the coefficient on the vaccine mandate becomes negative, economically meaningful, and statistically significant. The firms that showed increased turnover were largely liberal-leaning with limited data found on conservative-aligned firms.

Discussion: While we analyze the coefficients on vaccine mandates in this study, we note that these results are speculative, as we currently do not have the power to find statistically significant effects due to limited data on employee turnover post-vaccine mandate. This preliminary study indicated that there may be a relationship between vaccine mandates and employee turnover, which suggests the presence of political sorting within the healthcare industry. Due to the potential implications of political polarization on healthcare delivery, further research should be done to include more firms and understand the impact of sorting on health outcomes.

Audience Take Away Notes

- How COVID-19 vaccine mandates appear to impact employee turnover and potential implications, including political polarization within the workplace
- Why there is a need for more research on the impact of political sorting within healthcare firms
- How political alignment within a firm can dictate employee retention and satisfaction
- Why future vaccine-related policies should account for political sorting and its economic impact

Biography

Olivia studied neuroscience Northwestern University and played Division I volleyball before beginning medical school at Dell Medical School at UT Austin. Her interest in leadership and advocacy led her to roles as a student senator and representative to the Undergraduate Medical Education Healthcare Delivery Subcommittee. Olivia's desire to understand the health business ecosystem and to unite her passions for leadership and healthcare led her to pursue her MBA through McCombs School of Business during her third year of medical school. Following completion of her MD/MBA, she intends to apply to residency for pediatric neurology.

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Environmental surveillance of enteric viruses: Evaluation of urban wastewaters contamination in sicily (Southern Italy)

Enteric viruses are responsible for sporadic or epidemic-related infections. They are typically transmitted via the fecal-oral route through person-to-person contact or through the consumption of contaminated food (shellfish, vegetables, etc.) or water. Their main health effect is gastroenteritis, but they can also cause hepatitis, conjunctivitis, respiratory symptoms, meningitis and chronic diseases. Among the enteric viruses we find: Noroviruses (NoV), considered the main etiological agents responsible for sporadic cases and epidemics of Acute Gastroenteritis (AGE) in all age groups, Hepatitis A Virus (HAV), Hepatitis E (HEV). Data on enteric virus contamination of wastewater in Sicily are not well known. The aim of this study was to investigate the prevalence of enteric viruses in Sicilian wastewater and shellfish.

Since January 2022, the genomes of NoV, HAV and HEV have been searched for in urban sewage, collected by the Experimental Zooprophylactic Institute of Sicily (IZSSi) from three purification plants in the province of Trapani, during the systematic surveillance of SARS-CoV infection - 2 and its variants in wastewater, according to EU Recommendation 2021/472. Sewage samples were concentrated, following the method of Wu and co-workers, RNA was extracted from silica beads and subsequently purified. NoV GI, NoV GII, and HAV were searched by a One-Step real-time RT-PCR assay for the well-conserved region at the 5' end of ORF2. HEV was tested using a One-Step Real-Time RT-PCR assay for the ORF3 region. 109 wastewater samples collected from January 4, 2022 to August 23, 2022 during monitoring programs were analyzed. A total of 76 fresh and frozen shellfish were also collected between January and August 2022, sampled by local public health inspectors in the framework of the national official monitoring activities.

NoV GI and NoV GII RNA was detected in all (100%) urban sewages collected from January to August 2022 from Marsala (39), Mazara del Vallo (31) and Trapani (39). Of the 109 wastewater samples, 5 (4.59%, 95% CI 0.66-8.51%) were positive for HEV. No sample was found HAV positive. Only sewages collected From January to March 2022 from Trapani were contaminated by HEV. Only 3 Mytilus galloprovincialis of 76 shellfish samples (3.95%; CI95% -0.43%-8.32%) collected from March to August 2022 were positive NoV genome, one for NoV GI and two for NoV GII. No shellfish was found HAV or HEV positive.

Molecular surveillance of wastewater has clearly demonstrated that Noroviruses are widely present in environments. Residential wastewater can be a source of various types of contaminants, including a wide range of enteric viruses, HAV, NoV, and HEV selected for this study due to their epidemiological role as food- and waterborne pathogens.

Wastewater monitoring, more than shellfish, is therefore an important epidemiological tool for assessing the spread of viruses and represents an effective method for implementing environmental surveillance.

Audience Take Away Notes

- The study provides new information on the spread of enteric viruses in Southern Italy
- The study indicates that residential wastewater can be a source of viral contaminants

- Wastewater monitoring is an important epidemiological tool to detect viruses circulation at the community level

Biography

Francesca Gucciardi studied at the University of Palermo and graduated in 2012. She is Sspecialist in Microbiology and Virology at the Department of Health Promotion, Mother and Child Care, Internal Medicine and Medical Specialties “G. D'Alessandro”, University of Palermo (Italy). She is researcher at the Istituto Zooprofilattico Sperimentale della Sicilia (Italy) and her research areas include zoonotic agents, vector-borne pathogens, development of methods for serological and molecular diagnosis.

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A biomolecular survey on the presence of zoonotic bacteria in troglophile bats in sicily (Southern Italy)

Bats are mammals of the order Chiroptera that exhibit distinctive characteristics such as the ability to fly, a wide distribution, a long lifespan and diverse feeding strategies. They are important members of the ecosystem but also are natural reservoirs and carriers of numerous zoonotic bacteria and viruses, being immune to many of them. Humans are often in contact with bats in particular due to the anthropogenic alteration of their natural habitat which forces them to seek alternative sites and, consequently, to interact with other animals including domestic animals and humans. From this perspective, it is therefore essential for public health to know the pathogens carried by the bats.

In the present study, the results of a panel of biomolecular tests for bacterial agents Bartonella henselae, Borrelia spp., Coxiella burnetii, Leptospira spp., Chlamydia spp., Rickettsia spp. and Anaplasma phagocythopilum are shown. The analysis were carried out on oral swabs, oculoconjunctival swabs, urine and feces of insectivorous bats from 4 caves in the province of Ragusa and Syracuse (Sicily, Italy). The aim of the study was to evaluate the presence of potential zoonotic bacteria in different body habitats.

From December 2020 to April 2023, samples from 149 bats of 6 species, 4 guano samples and 16 bat ectoparasites were collected. Three oral swabs and 1 oculoconjunctival swab were positive for Bartonella henselae; 1 oral swab tested positive for Leptospira; 4 urine, 1 feces, 1 guano, 1 oral swab and 1 oculoconjunctival swab tested positive for Chlamydia spp. None of the tested samples showed positivity for Borrelia spp., Coxiella burnetii, Rickettsia spp. and Anaplasma phagocytophilum. The insects tested negative for all biomolecular test carried out.

Zoonotic bacteria of which bats can be a reservoir were identified in the samples examined, in particular Chlamydia spp., Leptospira spp. and Bartonella henselae. Chlamydia was found in all body habitats, but more prominently in feces and urine than in oculoconjunctival and oral swabs. Concomitant detection of Chlamydia in multiple body habitats of the same individual could correspond to an acute infection. Zoonotic bacteria such as Bartonella henselae have also been detected in saliva. Although transmission of Bartonella in bats is usually associated with arthropod vectors and droppings, these bacteria have also been found in the saliva of dogs and cats, suggesting that Bartonella may also be transmitted within bat populations through behaviours that result in transmission of saliva, such as biting and grooming.

In conclusion, the results of the study provide a broader view of the bacterial species excreted within a throglophile bat community, highlight that bats can be reservoir of pathogens and furthermore show that, in addition to the examination of fecal samples, also saliva, ocular secretions and urine, due to the different microbiota, are useful for evaluating the potential role of bats as vectors of zoonotic infectious agents.

Audience Take Away Notes

- The study provides new information on the role of bats in the spread of potentially pathogenic bacteria to humans

- The results suggest future studies on the bacterial community composition of different bat body habitats to evaluate potential transmission routes such as saliva, urine, eye secretions
- Given the role of bats as potential carriers of zoonotic pathogens, the analysis of the interaction between microbiota and infection dynamics represents an important challenge

Biography

Santina Di Bella obtained a Master's Degree in Biology, University of Palermo (Italy) in 2004. She is Specialist in Microbiology and Virology, University of Palermo (Italy). She received her PhD in experimental Oncobiology in 2014 at the same institution. She is researcher at the Istituto Zooprofilattico Sperimentale della Sicilia (Italy) since 2005. Her research areas include zoonotic agents, virology, cell culture, tick borne pathogens, diagnostic technique development. She has published more than 40 research articles.

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VACCINES AND INFECTIOUS DISEASES

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Serological aspects of the specific immune response in patients with measles of different ages in a territory with a high incidence

Relevance: Not only children are involved in the epidemic process, but also adults, whose encounter with the measles virus is accompanied by the synthesis of antibodies according to the primary or secondary type of immune response. The diagnosis of measles infection in previously vaccinated individuals is a difficult task, since the results depend not only on the format of the diagnostic kits, but also on the qualitative and quantitative indicators of the immune response.

Target: Assessment of the significance of humoral immune response indicators in measles patients of different ages in a territory with a high incidence.

Materials and methods: To confirm the primary and secondary immune response in 1832 measles patients of different ages in a territory with a high incidence rate (6.3 per 100 thousands of population), qualitative and quantitative indicators of IgM and IgG were determined using specific kits of different formats: VectoMeasles-IgM, (Vector-Best, Russia, capture format), Anti-Measles Virus NP ELISA IgM (Euroimmun, Germany, indirect format). Detection of IgG and determination of the degree of avidity of class G antibodies were performed using commercial test systems Anti-Measles Viruses ELISA (IgG) and Avidity Anti-Measles Viruses ELISA IgG, (Euroimmun, Germany). The basis for laboratory confirmation of the diagnosis of measles with a primary immune response in the patient was a positive result for IgM, the presence of class G antibodies with a low degree of avidity; with a secondary immune response - positive for IgM, high concentration (>5 IU / ml) of highly avidity IgG in sera obtained on days 4-7 of the onset of the rash.

Results: As a result of testing 1832 blood serum samples for the content of specific IgM, it was found that measles was laboratory confirmed in 100% of cases using the VectoMeasles-IgM capture variant test systems and 88.33% using the Anti-Measles Virus NP ELISA IgM indirect format. In the sera of 75.05% of patients with a primary immune response, low-avid IgG was detected at a concentration of 0.83±0.9 IU/ml; in sera with a secondary immune response - highly avidity antibodies of class G at a concentration of 24.2 ± 5.4 IU / ml, which was 29.2 times higher than in the group with a primary immune response (0.83 ± 0.9 IU / ml) ($p<0.05$). Age-specific analysis showed that in the group with a primary immune response, the number of children under 14 years old and adults 18-70 years old was almost the same: 49.6% and 47.56%, respectively, and children and adult patients with a secondary immune response - 1.31 % and 97.16%, respectively ($p<0.05$).

Conclusion: a) a significant difference was found in the detection of IgM using test systems of different formats: 100% in the VectoMeasles-IgM "capture" kit and 88.33% in Anti-Measles Virus NP ELISA IgM indirect format (Euroimmun) ($p<0.05$);

b) qualitative and quantitative indicators of specific IgG antibodies were determined in the primary immune response - low avidity (18.8±14.8%) at a concentration of 0.83±0.9 IU/ml and in the secondary - high avidity (95.5±6, 5%) at a concentration of 24.2±5.4 IU/ml;

c) data have been obtained to assess both the composition of the “participants in the epidemic process” and the “gaps” in the organization of the measles immunization program.

Biography

Dr. Tamara Mamaeva studied biology and chemistry at Moscow University in Russia. Received PhD in Biology 1987. Leading scientific staff Laboratory of Applied Immunochemistry Gabrichevsky Moscow Research Institute of Epidemiology and Microbiology. She completed an internship at CDC (Atlanta 2003) under the guidance of Dr. W.Bellini and Dr. P.Rota in virology and immunology. In 2008 she completed an internship in Hôpital Paul-Brousse (Paris) under the guidance of prof. L.Keros. Since 2003 she has been the coordinator at the reference laboratory (Moscow) for the CIS laboratory network, which is under the EURO/WHO Dr. M.C.Ben Mamou (Copenhagen) and WHO Dr. M.Mulders (Geneva).

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Notes

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