magnus Group

Joint Event

7th Edition of World Congress on

Infectious Diseases &

4th Edition of International

Vaccines Congress

24-26 October, 2024 | Baltimore, MD, USA

Venue: Best Western Plus Hotel & Conference Center 5625 O'Donnell Street Baltimore, MD 21224 Baltimore, Maryland, USA

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Thank You All. . .

Speakers

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Alaa Abdelmageed Ahmed
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Project HOPE, Ethiopia

Thank You All. . .

Welcome Message

Francis J. Castellino

University of Notre Dame, USA

It is a pleasure to welcome delegates to the 2024 World Conference on Infectious Diseases. We have recently emerged to a large extent from a very costly and deadly viral pand emic, which was brought under some level of control by tireless efforts of a dedicated scientific community. Having personally lived through the pand emics of polio, HIV/AIDS, H3N2 Hong Kong flu, Asian flu and being historically aware of the cholera pand emic, Spanish flu, bubonic plague and Justinian plague afflictions, which in total victimized hundreds of millions worldwide, we can be assured that new infectious threats will emerge and old diseases will reemerge and continue to evolve. New treatment modalities are required since these viruses, bacteria and other virulent microorganisms will mutate and infect more quickly than humans can respond. Only open communication that shares information from many scientific perspectiveswill minimize the cost of human lives and economic burdens. The WCID is one outlet for such information to be transmitted to the community. I wish all a most productive time at this conference.

Welcome Message

Ranjan Ramasamy

ID-FISH Technology, USA

Dear Conference Attendees,

It is an honor and great pleasure to write a welcome note for the seventh World Congress on Infectious Diseases with the theme of **Global Challenges, Unified Solutions: Advancing Infectious Disease Research and Response**. There are many presentations that will address the overarching theme of this Congress. These will highlight new research findings that can be expected to stimulate the interests of early career as well as established scientists, academics and clinicians. The presentations will enhance knowledge, generate new approaches to researchand suggest new solutions for controlling infectious diseases. The Congress alsoprovides an opportunity for participants to develop international networks in order to advance their research, teaching and clinical practice and I hope that everyone will take advantage of this.

Welcome Message

Thomas J. Webster

Interstellar Therapeutics, USA

Dear Conference Attendees,

The statistics are alarming and like nothing we have ever seen: Infectious diseases will be responsible for one death every 3 seconds by 2050 (U. S. Centers for Disease Control). If you thought COVID was bad, stay tuned. Unlike COVID, we can and need to be better prepared. From improving at-home diagnostics to developing quick treatments to understand ing infectious diseases, we can do better than what occured during COVID where our best approach was to tell people to stay home and stop interacting with others. Really? That's the best science could do for COVID?

This conference will help prepare us for what lies on the horizon. It will help you meet new people, not the same old people giving the same old talks at the same old academic conferences receiving the same old awards. New ideas, new people, new concepts. This is what we need to fight infectious diseases. Our old approaches aren't working. Antibiotics and other drug-based therapies? They are part of the problem. Social media and bad actors reporting false news on scientists? That is part of the problem. Let's get back to where science once was – re-install the rigor of in-person scientific debate and discussion. That's where good ideas come from. We are all in this together.

I encourage you all to join our journey. I am looking forward to seeing you here as we pave a path to once and for all reverse the increasing presence of infectious diseases. Come join us and get stimulated to conduct infectious research through infectious diseases!

Welcome Message

Regina Au

BioMarketing Insight, United States

Dear Congress Attendees,

It is my great pleasure and honor to welcome you to the 4th Edition of International Vaccine Congress, 2024. Future vaccine development, adoption and deployment is the hallmark to preventing and managing infectious diseases and you will hear from many experts around the world as infectious disease is a global problem.

Understand ing the disease and then developing a vaccine specifically for that disease is very complex as there are many factors to consider including but not limited to the specific pathway of the disease, the efficacy and safety from a regulatory perspective, the manufacturing process and achieving vaccine acceptance and adoption from the patient, physician, payers etc. Our speakers will cover various aspects of these topics. Please join us for the full conference as it is packed with numerous presentations.

I also invite you to join me in my presentation titled "Why Antimicrobial Resistance is a Global Threat and Its Impact On Everyone". In 2019, antimicrobial resistance was associated with nearly 5 million deaths. The national cost to treat infections caused by six multidrug-resistant germs found in the health care settings was more than $4. 6 billion annually. Combating this threat requires a 5 prong approach to ensure we preserve the effectiveness of existing treatments and our ability to fight infectious diseases in the future. Look forward to seeing everyone in October.

Welcome Message

Albert J Eid

University of Kansas Medical Center, USA

Dear Conference Attendees,

It's my pleasure to welcome you to the World Congress on Infectious Diseases 2024. We are all united by a common goal of understand ing and combating infectious diseases. This conference serves as a testament to our collective commitment to improving global health. As we delve into the latest research, innovative treatments and collaborative strategies, let us keep in mind the profound impact our work has on communities worldwide. The challenges are significant, yet our resolve to overcome them is even stronger. The insights and discoveries we share will provide a path forward. I courage each one of you to engage deeply, share openly and collaborate effectively throughout this conference. Together, we can push the boundaries of science and medicine to create a healthier world for all. Welcome and let us embark on this remarkable journey of discovery and advancement.

Welcome Message

Dr Susanne Surman-Lee

Leegionella Ltd, United Kingdom

Dear Conference Attendees,

It is a real honour to take part in this esteemed event and be able to speak to you today about something which is close to my heart. In the words of Florence Nightingale in her Notes on Hospitals (1863) “The very first requirement in a hospital is that it should do the sick no harm”. Yet over 160 years later we are still harming patients from poorly designed, constructed, commissioned and operated healthcare facilities. The complexity of developing healthcare facilities has obviously increased since Florence was around, but I am sure she would be shocked that putting the patient first and foremost was no longer the prime goal of those developing hospitals today. The National Health Service in England has just developed and published some guidance which is intended to ensure the safety of all types of exposure to water and wastewater taking the susceptibility of patients into account. I look forward to sharing this with you at this conference.

Welcome Message

Ping Xie, PhD

Associate Professor, Department of Cell Biology and Neuroscience
Rutgers, the State University of New Jersey

Dear Conference Attendees,

It is an honor and a great pleasure to welcome you to the session entitled “Infectious and Non-Infectious Diseases”. As you know, infectious diseases are disorders caused by pathogenic microorganisms such as bacteria, viruses, fungi, or parasites, which can spread directly or indirectly from person to person. In contrast, non-infectious diseases are not caused by pathogens and cannot be transmitted from one person to another. These diseases are typically chronic in nature and can result from a variety of factors, including genetic risk factors, lifestyle choices, environmental exposures, or a combination of these factors. Non-infectious diseases encompass a broad range of disorders, including cardiovascular diseases, cancer, diabetes, autoimmune disorders, allergies and neurodegenerative diseases.

Compared to infectious diseases, non-infectious diseases cause a higher mortality rate, accounting for approximately 71% of all deaths globally each year, as well as greater morbidity and a more significant economic burden worldwide. While efforts to control infectious diseases have been relatively successful through vaccination, antibiotics and improved sanitation, managing non-infectious diseases presents greater challenges and requires more comprehensive strategies.

In this session, we will discuss current developments in the understand ing and vaccination for the following: (1) Alzheimer's disease amyloid protein vaccine; (2) Breast cancer vaccine; (3) Ovarian cancer vaccine; (4) Prostate cancer vaccine; and (5) Chronic inflammation. This will be a great opportunity for IVC participants, including both young and senior researchers, scientists and clinicians, to gain knowledge of the latest discoveries and developments in the field.

Welcome Message

Vijay Prabha

Department of Microbiology, Panjab University, Chandigarh, India

Dear conference attendees, it is with great honor and pleasure that I extend a cordial welcome for the session on 'Bacterial Infectious Diseases,' acknowledging the collective expertise gathered in pursuit of advancing our understanding in this critical domain. The antibiotic era may have fostered an illusion that bacterial infections were subdued, yet bacterial adaptability, notably through biofilm formation, challenges this perception. Additionally, escalating prevalence of acquired antibiotic resistance compels us to acknowledge that we are far from controlling the development of bacterial infections. This session serves as a pivotal platform for the exchange of insights, the presentation of groundbreaking research, and the fostering of collaborative discussions, covering prevalent bacterial diseases such as Meningitis, Pneumonia, Tuberculosis, as well as addressing other significant challenges like Sexually Transmitted Infections (STIs), Urinary Tract Infections (UTIs), and zoonotic diseases. As we navigate through the nuances of bacterial infectious diseases, I encourage each of you to actively engage in the discourse. Your presence and contributions are integral to the success of this session, and I am confident that our collective efforts will lead to meaningful advancements in the understanding, diagnosis, and treatment of bacterial infectious diseases.

ABOUT
MAGNUS GROUP

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

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

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

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KEYNOTE FORUM

Neutralizing antibodies response to SARS-COV-2 XBB1.5 mRNA vaccine in nephrology patients on dialysis against different viral variants

Background: Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) has caused millions of deaths and substantial morbidity worldwide, particularly in fragile subjects including dialysis patients. The continuous evolution of SARS-CoV-2 alters its pathogenicity and infectivity in human hosts, thus vaccines need to be continuously updated. XBB.1.5 mRNA vaccines are updated vaccine approved in September 2023 to help protect against the evolving threat of COVID-19.

Methods: In the present study we have performed the analyses of the IgG neutralization titers against 10 different viral variants in dialysis patients and healthy controls vaccinated with XBB 1.5 containing mRNA vaccine. 84 patients receiving maintenance dialysis and 10 healthy controls were enrolled. The nephrology patients had been vaccinated with 4 doses the original mRNA-based vaccines and in November 2023-January 2024 they received the 5th dose with the XBB1.5 updated vaccine. Healthy controls received 3 doses of the original vaccine, and at the end of 2023 received an additional dose of XBB 1.5 updated vaccine. Serum samples were taken before the vaccination and 1 to 1.5 months later. The surrogate IgG SARS-CoV-2 neutralization test, developed by Lausanne University Hospital researchers was used to evaluate the response to the vaccination and its potentials to neutralize 10 SARS-CoV-2 viral variants.

Results: Dialysis patients mount significant response to the vaccination in terms of the production of neutralizing antibodies. Those who were vaccinated and received up to 4th doses responded strongly with the production of neutralizing IgG, especially against Wild Type (WT) and Delta Sars-CoV-2 variants but not for other variants. 5th dose of new, XBB 1.5 vaccine, gave significant boost and augmented the neutralizing IgG titers not only against WT and Delta variant, but significant increased protection against XBB, XBB.1.5, BQ.1, BA.1, BA.2.86, BA.4, GK.1, and EG5.1 variants. The levels of the IgG neutralizing titers of patients were not significantly different from those of healthy controls.

Conclusions: Dialysis patients respond to SARS-COV-2 XBB1.5 updated vaccine similarly to healthy controls. This vaccine generated high IgG titers that can neutralize new SARS-CoV-2 variants. These data support the vaccination of fragile nephrological subjects with the updated vaccine to protect them from severe diseases and extend protection against new variants.

Audience Take Away Notes

- Both primary care physician and nephrologist will acquire valuable information on SARS-COV-2 vaccine efficacy in dialysis patients

Agostino Riva[1]*, Giuseppe Lipari[3], Celine Pellaton[2], Craig Fenwick[2], Rony Gingis[4], Vincenzo Fattizzo[3], Nicoletta Landriani[3], Cristina Airaghi[3], Sara Khemara[3], Arianna Gabrieli[1], Giuseppe Pantaleo[2], Maurizio Gallieni[1], Maciej Tarkowski[1]

[1]Università degli Studi di Milano, Milano, Italy

[2]Lausanne University Hospital, Lausanne, Switzerland

[3]Luigi Sacco University Hospital, Milan, Italy

[4]Fatebenefratelli Hospital, Milan, Italy

Biography

Professor Agostino Riva graduated in Medicine in 1990 and specialized in Infectious Diseases in 1994 at the University of Milan. He was a guest researcher and a visiting fellow in the Laboratory of Immune Regulation, NIAID, NIH from 1990 to 1997. Subsequently, he became attending physician at Luigi Sacco Hospital in Milan and Director of the laboratory of Molecular Immunology. In 2020 he became associate professor of Infectious Disease at University of Milan and in 2023 Director of research at the Department of Infectious Diseases at Luigi Sacco Hospital. He published over 200 papers on peer reviewed journals. H index 45. Citations: 10.244.

- The information from this work can address the question on the opportunity to vaccinate dialysis subjects and on the most recent XBB1.5 mRNA vaccine efficacy to protect against viral variants in these patients
- This research will give updates on SARS-COV-vaccine safety and efficacy to be employed in nephrology and vaccinology teachings

Immunosuppressive medications did not increase the risk of severe COVID-19 in solid organ transplant recipients diagnosed with SARS-CoV-2 infection

Due to conflicting data, it remains unclear whether immunosuppressive medications increase the risk of progression to severe COVID-19 disease in Solid Organ Transplant (SOT) recipients. Most of the available outcome data does not suggest a higher mortality rate in the SOT population. Even though immunosuppressive medications might be associated with worse outcome, its immunomodulatory effect might be beneficial.

Methods: We conducted a retrospective case-control study of SOT recipients diagnosed with COVID-19 at the University of Kansas Medical Center between January 1, 2020 and December 31, 2022. Severe COVID-19 was defined as development of hypoxia while the patient is on room air during a 21-day period after the COVID-19 diagnosis was established. We fit a logistic regression model with severe COVID-19 as the response variable and adjusted for prescription of mycophenolate, tacrolimus and prednisone and a set of covariates. To evaluate the effect of dose changes after the diagnosis of COVID-19 on the odds of developing severe COVID-19, we subset our data based on whether patients were taking mycophenolate (n=448), tacrolimus (n=536) or prednisone (n=386) at the time of diagnosis. Within each subgroup, we fit a logistic regression model with severe COVID-19 as the response variable and adjusted for the relevant immunosuppressant and a set of covariates.

Results: In our SOT population, 569 patients were diagnosed with COVID-19 (457 kidney, 73 liver, 54 heart, 43 pancreas, and 8 lung recipients). The median patient age was 53 years, 59% were male, and 70% were white. Severe COVID-19 disease developed in 127/569 (22.3%) patients. A total of 58/570 (10.2%) patients died. A multivariable analysis showed that age (OR=1.04; p<0.001), white race (OR=0.54; p=0.01), body-mass index (OR=1.04, p=0.04), heart disease (OR=1.84, p=0.01), chronic lung disease (OR=1.93; p=0.04), lack of prior COVID-19 vaccination (OR=2.05; p=0.01), and not receiving monoclonal antibodies (OR=3.79; p<0.001) were associated with severe disease. Being on treatment with mycophenolate, tacrolimus, or prednisone at the time of COVID-19 diagnosis was not associated with severe disease.

After adjusting for other covariates, a mycophenolate dose-reduction was not associated with progression to severe COVID-19. Similarly, tacrolimus dose reduction did not increase the risk of severe COVID-19. An increase or a decrease of prednisone dose was not associated with severe COVID-19.

Conclusion: Overall mortality in our SOT population was 10%. Patients receiving mycophenolate, tacrolimus, or prednisone at the time of COVID-19 diagnosis were not more likely to experience severe disease. Furthermore, the reduction of mycophenolate or tacrolimus dose when

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[5]Division of Cardiology

[6]Department of Biostatistics and Data Science, University of Kansas Medical Center, Kansas City, Kansas

Biography

Dr. Albert Eid received his medical degree from Saint Joseph University, Lebanon. He completed his Internal Medicine Residency at East Tennessee State University, Fellowship in Infectious Diseases at the Mayo Clinic. His focus has been infectious diseases in transplant recipients. He joined the Division of Infectious Diseases at the University of Kansas Medical Center (KUMC) in July 2007. He was promoted to Associate Professor in 2011. He has been involved in research projects addressing viral and fungal infections in transplant recipients. He has 36 peer-reviewed research articles. He is currently the Director of the Transplant ID at KUMC.

a SOT patient is diagnosed with COVID-19 was not associated with severe disease.

Audience Take Away Notes

- The presentation will be useful to clinicians managing solid organ transplant recipients diagnosed with COVID-19
- The presentation will provide guidance about management of immunosuppression in solid organ transplant recipients diagnosed with COVID-19
- Additional data in this area are needed to fully understand the impact of immunosuppression on COVID-19 outcome

The mechanisms of innate immune responses in Streptococcus pyogenes pathogenicity

A signature feature of Group-A Streptococcus pyogenes (GAS) infections in humans is dysregulated hemostasis. Hemostasis is a component of the innate immune system, which also includes inflammation and complement activation, all of which attempt to eliminate the invading bacteria. An initial response to GAS infection of the host is to activate the coagulation and inflammatory systems to entrap and eliminate the invading bacteria within a fibrin clot. The bacteria respond by conscription of the host protein, plasminogen, which is activated by the GAS-secreted plasminogen activator, streptokinase, to a potent protease, plasmin, which resides on the bacterial surface. Cell bound plasmin resolves the clot and liberates the bacteria to disseminate to deep tissue sites via its cell surface proteolytic activity. The clot is also an inflammatory mediator acting through attraction of leukocytes and induction of cytokines and chemokines. Additionally, during the process of clot formation, proteases are released that further stimulate the inflammatory system through cellular protease receptors. As a further component of the host defense system, the vasoactive and potent inflammatory peptide, bradykinin, is also formed, further stimulating inflammation and complement activation, again in an attempt to eliminate the microorganism. The inflammatory mediators then crosstalk with hemostasis system components to further upregulate thrombosis, thus continuing this vicious cycle of coagulation-inflammation. The complex interplay of these systems can lead to dire consequences for the host when hemostasis-inflammation is dysregulated bybacterial and host responses. In this discussion, we will assess the biological mechanisms that must be controlled in the tug of war for survival between GAS and the human host. A comprehensive understand ing of the mechanisms associated with GAS virulence and the host response to these infections could lead to novel approaches for altering the course of GAS infectivity.

Francis J. Castellino Ph. D

Kleiderer-Pezold Professor of BiochemistryDirector, W. M. Keck Center for Transgene Research University of Notre Dame, IN 46556

Biography

Francis J. Castellino, Ph. D. is the Kleiderer-Pezold Professor and Director of the W. M. Keck Center for Transgene Research at the University of Notre Dame. He received the B. S. in Chemistry from the University of Scranton, the M. S. and Ph. D. degrees from the University of Iowa and performed postdoctoral research Duke University. He joined the Notre Dame faculty as an Assistant Professor of Chemistry in 1970, was promoted to Associate Professor in 1974 and Full Professor in 1978. He became the Dean of the College of Science in 1979, a role in which he served for 23 years. In 1982, he was awarded the Kleiderer-Pezold Endowed Professorship in Chemistry and Biochemistry. In addition to serving on numerous internal committees for the University, he was a member and chair of severalNIH committees and review groups, is the editor-in-chief of Current Drug Targets and an associate editor in multiple journals. He has received many external awards, including an AAAS, AHA and NYAS Fellow, a MERIT Award from the NIH, the Wyeth-ISFP Research Prize in Fibrinolysis, the Distinguished Alumnus Award for Achievement from the Carver College of Medicine, University of Iowa and the Esteemed Career Award from theInternational Society for Thrombosis and Hemostasis. He also has honorary degrees from the University of Scranton and the University of Waterloo, where he was also a commencement speaker. Professor Castellino has published more than 500 peer reviewed manuscripts with >22, 000 citations. Interests of the laboratory are focused in the relationships between hemostasis and inflammation from the biochemical, biophysical and cell and molecular biological perspectives.

Are you doing enough to protect high risk patients from waterborne infections?

The incidence and range of infections associated with water and wastewater related to healthcare premises is increasing, with significant increased costs, length of patient stays and antibiotic use to healthcare organisations and the families affected. Whilst the development of water safety plans and multidisciplinary water safety groups has improved the management of water systems and associated equipment. Wastewater systems and their potential to cause cross contamination and infection has by in large been overlooked especially by those designing and engineering new build healthcare premises. This presentation will highlight the increasing range of range of infectious hazards associated with healthcare premises, the importance of multidisciplinary risk assessment and absolute necessity for a multidisciplinary approach to designing, constructing, fitting out, filling and commissioning new systems which should be considered from the concept stage of a new build to ensure the water and waste water systems are safe for the intended patient groups and factors to consider when designing for immunocompromised patients at high risk of infection.

Dr. Susanne Surman-Lee

Leegionella Ltd providing independent public health consultancy, legal and advisory services, UK

Biography

Dr. Surman-Lee is a Consultant Clinical Scientist Registered with the UK Health Professions Council. with >40y experience in clinical and public health microbiology and practical experience of auditing and investigating over 60 healthcare premises following colonization, cases and /or outbreaks of water systems and associated equipment including from Legionella, Pseudomonas aeruginosa, NTM) nationally and internationally. She has a strong scientific and research background with a PhD on Legionella growth within biofilms. Susanne. She has also worked as a temporary advisor to WHO and as a Member of the WHO working and editorial groups which published Legionella and the prevention of legionellosis (2007) and Water Safety in Buildings (2011).

Novel regulatory mechanisms of innate immunity and inflammation

Myeloid cells are the major players of innate immunity and inflammation. The functionality of myeloid cells is controlled by innate immune receptor signaling, which is critically regulated by a cytoplasmic adaptor protein termed TRAF3. Ablation of TRAF3 from myeloid cells does not affect the maturation or homeostasis of macrophages and neutrophils in young adult mice. However, aging myeloid cell-specific TRAF3-deficient (M-Traf3$^{-/-}$) mice spontaneously develop chronic inflammation, tumors and bacterial infection that affect multiple organs. Using a chronic inflammation model induced by repeated injections of heat-killed Bacillus Calmette-Guérin (BCG), we demonstrated that TRAF3 is an immune checkpoint that inhibits Myeloid-Derived Suppressor Cell (MDSC) expansion during chronic inflammation. Interestingly, our studies of mixed bone marrow chimeras revealed that TRAF3 restrains MDSC expansion via both cell-intrinsic and cell-extrinsic mechanisms. We next sought to identify the internal trigger of chronic inflammation and bacterial infection in these mice. We detected gut dysbiosis and transmigration of commensal bacteria to the liver in aging M-Traf3$^{-/-}$ mice using 16s rRNA gene sequencing of fecal bacterial DNA and bacterial culture of liver homogenates, respectively. To determine if gut dysbiosis and bacterial transmigration cause chronic inflammation and bacterial infection, we treated mice with broad-spectrum antibiotics. We found that depletion of commensal bacteria with antibiotics effectively prevented spontaneous chronic inflammation and bacterial infection in aging M-Traf3$^{-/-}$ mice. Taken together, our findings indicate that TRAF3 proteins expressed in myeloid cells critically regulate innate immunity and play indispensable roles in maintaining the symbiosis of gut microbiota and inhibiting chronic inflammation and commensal bacterial infection.

Audience Take Away Notes

- This study provides novel insights on how innate immunity and inflammation are regulated by innate immune receptor signaling
- Commensal bacteria could serve as key internal inducers of chronic inflammation and bacterial infection in genetically predisposed individuals
- For the design of new vaccines or vaccine adjuvants, genetic risk factors, commensal bacterial symbiosis and chronic inflammation need to be taken into consideration to improve their accuracy and efficacy

Ping Xie

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

Biography

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

Analysis of some societal factors constraining COVID-19, Dengue, Malaria and tick-borne Borreliosis control

The benefits conferred by recent scientific discoveries, e. g. new chemotherapeutics, monoclonal antibodies for diagnosis and treatment, recombinant protein antigens for diagnosis and vaccines for infectious diseases like COVID-19, dengue and malaria, are widely appreciated. However, some societal factors that limit the application of new scientific advances for improving the control of COVID-19, dengue, malaria and tick-borne borreliosis are less well understood. This article separately analyses specific societal constraints in each of these four diseases with the objective of broadening understand ing and promoting the development of appropriate measures to mitigate the constraints.

Audience Take Away Notes

- Better understand relevance of recent scientific advances for controlling important infectious diseases
- Participants will usefully consider the relevance to their own local context
- The knowledge will be valuable for teaching and research into infectious diseases, vaccines and vector control
- Knowledge gained can be applied directly to better control infectious diseases in a public health context
- Stimulate innovative thinking in infectious diseases control

Ranjan Ramasamy

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

Biography

Ranjan Ramasamy graduated in 1971 and then a PhD in 1974 from the University of Cambridge, UK. He was the Chairman of the National Science Foundation of Sri Lanka, Professor of Life Sciences at the Institute of Fundamental Studies in Kand y 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, Cambridge, UK and Scripps Clinic and Research Foundation, La Jolla, USA. He has more than 280 publications.

Why antimicrobial resistance is a global threat and its impact on everyone

Antimicrobial Resistance (AR) is an urgent and major global public health threat, killing at least 1. 27 million people worldwide and associated with nearly 5 million deaths in 2019, a report from The Lancet. In the U. S., more than 2. 8 million antimicrobial-resistant infections occur each year and more than 35, 000 people die each year from these infections, based on the CDC's 2019 AR Threats report. When a bacterium such as Clostridioides difficile, which normally is not resistant to antibiotics becomes resistant, it can cause deadly diarrhea. The U. S. toll of all the threats in the report exceeds 3 million infections and 48, 000 deaths.

The estimated national cost to treat infections caused by six multidrug-resistant germs frequently found in the health care settings amounts to more than $4. 6 billion annually, according to a CDC study.

The CDC is concerned about the emergence and spread of new forms of resistance and rising resistant infections in the community. Community infections puts more people at risk, makes identifying and containment more difficult and threatens the ability to protect patients in hospitals.

The AR Threats Report noted that when there is dedicated prevention and infection control efforts in the U. S., deaths from antimicrobial-resistant infections were reduced by 18% overall and by nearly 30% in hospitals. However due to pand emic, all progress was diminished and antimicrobial resistance is rapidly rising again. The pand emic pushed healthcare facilities, health departments and communities to nearbreaking points in 2020, making it very hard to maintain the progress made in combating antimicrobial resistance.

Combating this challenge requires a 5 prong approach. All five approaches need to be incorporated to ensure we preserve the effectiveness of existing treatments and our ability to fight infectious diseases in the future:

1) Appropriate and responsible antibiotic usage;

2) Better hygiene practices;

3) Development of new classes of antibiotics;

4) Global collaboration among healthcare sectors; and

5) Prepared readiness - responding and anticipating trends.

These five prong approach will be addressed in more detail. Slowing antimicrobial resistance is critical to preserving the effectiveness of existing treatments and ensuring our ability to fight infectious diseases in the future.

Regina Au

BioMarketing Insight, Boston, Massachusetts, USA

Biography

Regina Au, CEOat 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 scientificand 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.

Audience Take Away Notes

- Everyone, healthcare, non-healthcare professionals and industry will learn that Antibiotic resistance (AR) is a critical threat not only to patients but to the community as well
- They will also learn the enormous negative impact that it has on everyone
- Good hygiene is the easiest and most simplest approach to fighting AR. However, good hygiene needs to be instilled as a critical daily routine, most plans/protocols are observed when infections are up but then people get complacent about protocols and infections rises again
- In this 5 prong approach some can be implemented quickly and easily and some require more long term planning commitment
- It will make people more conscious about why these protocols need to be in place and the impact if it is not
- If they are doing research, more people need to focus on doing more research in this areas and developing newer classes of antibiotics
- Other faculty could use to expand their research or teaching because antibiotic resistance is a global problem not an isolated problem
- This provides a practical solution to a problem that could simplify or make a designer's job more efficient
- It will improve the accuracy of a design, or provide new information to assist in a design problem
- Stakeholders will realize that more collaboration is need between pharma/biotech companies, academics, government, private institutions and other countries to solve this global threat

Human challenge clinical trial of vaccines for infectious diseases–A necessary evil

Human Challenge Trials (HCT) or controlled human infection model (CHIM), which involve purposeful or intentional exposure of infectious microorganisms to healthy human volunteers, have a long history in medicine and have contributed significantly to our understand ing of the science behind vaccine development.

Human challenge studies are unique in their ability to investigate and understand the onset and progression of disease in a secure and carefully monitored environment, observe and analyse complex interactions between bacteria/ viruses and the human immune system and to identify strategies to disrupt and prevent infections.

Nevertheless, such research may seem to be in conflict with the guiding principle in medicine to 'do no harm'. But, it's important to realize that administering injections intravenously or using a biopsy needle might also be seen as "causing harm".

Although HCT are not a required element of every vaccine development program, there are reasons why a vaccine developer may want to conduct a "challenge-protection" study in humans, which might normally be conducted in animals. (164 words)

Audience Take Away Notes

- An understand ing of what is HCT, some examples, benefits and challenges

Sudhakar Bangera

Aileen Clinical Research Services, Hyderabad, Telangana State, 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".

Nanomedicine for the prevention, diagnosis and treatment of infectious diseases

Nanomedicine has already provided dozens of FDA approved products improving the lives of billions. Most notably, nanomaterials have been used to develop vaccines for COVID, improved spinal implants, developed anti-infection materials without using antibiotics and fabricated numerous drug delivery vehicles. This invited talk will provide a summary of in vitro, in vivo and human experiments in which nanomaterials have been used to improve the prevention, diagnosis and treatment of infectious diseases. This talk will also cover an over 25 year journey in which nanotextured orthopedic implants were developed, approved by the FDA and over 30, 000 implanted in humans with no cases of infections (the industry stand ard is 5 – 10% failure due to infections). Moreover, this presentation will provide how nanotechnology is driving the prevention of infectious diseases by encapsulating micro-organisms and killing them once in the body. Lastly, nanomedicine will be presented in which nanomaterials can bind to micro-organisms to aid in the detection and then activated for treatment, in the so-called field of theranostic nanomedicine. Throughout this talk, efforts will be emphasizedin which research is being commercialized into real products helping human health.

Audience Take Away Notes

- Definition of nanomedicine for infectious disease
- How nanomedicine is being used to prevent, diagnose and treat infectious disease
- The future of nanomedicine for treating infectious diseases

Thomas J. Webster

School of Health Sciences and Biomedical Engineering, Hebei University of Technology, Tianjin, China

Co-founder, Interstellar Therapeutics, Mansfield, MA, USA

Biography

Thomas J. Webster's (H index: 125; Google Scholar) degrees are in chemical engineering from the University of Pittsburgh (B. S., 1995; USA) and in biomedical engineering from RPI (Ph. D., 2000; USA). He has served as a professor at Purdue (2000-2005), Brown (2005-2012) and Northeastern (2012-2021; serving as Chemical Engineering Department Chair from 2012 - 2019) Universities and has formed over a dozen companies who have numerous FDA approved medical products currently improving human health in over 20, 000 patients. His technology is also being used in commercial products to improve sustainability and renewable energy. He is currently helping those companies and serves as a professor at Brown University, Saveetha University, Vellore Institute of Technology, UFPI and others. Dr. Webster has numerous awards including: 2020, World Top 2% Scientist by Citations (PLOS); 2020, SCOPUS Highly Cited Research (Top 1% Materials Science and Mixed Fields); 2021, Clarivate Top 0. 1% Most Influential Researchers (Pharmacology and Toxicology); 2022, Best Materials Science Scientist by Citations (Research. com); and is a fellow of over 8 societies. Prof. Webster is a former President of the U. S. Society for Biomaterials and has over 1, 350 publications to his credit with over 55, 000 citations. Prof. Webster also recently formed a fund to support Nigerian student research opportunities in the U. S. He was recently nominated for the Nobel Prize in Chemistry.

Studies on microbial infections associated with azoospermia in male mouse model and multifaceted insights into the potential mechanisms of spermatogenic failure

Male infertility, an intricate interplay of genetic, anatomical and environmental factors, underscores the notable influence of urogenital infections. Azoospermia, a multifactorial disorder characterized by absence of sperm in seminal plasma, silently challenges reproductive health, thwarting parenthood aspirations. It is categorized into Obstructive Azoospermia (OA) and Non-Obstructive Azoospermia (NOA) and recent evidences highlight the substantial role of microbial infections in both OA and NOA development, with more attention traditionally given to OA. Notably, the etiological understand ing of idiopathic NOA remains elusive despite extensive research. Focusing on this untapped scientific land scape, this study explores the relationship between uropathogens and NOA. The representative sperm impairing uropathogens viz., Sperm-Agglutinating (SA) Escherichia coli, Klebsiella pneumoniae and Serratia marcescens and Sperm-Immobilizing (SI) Staphylococcus aureus, already available in the laboratory were used for intratesticular administration into male mice exclusively in the right testis with an inoculum of 108 cfu in 20 µl PBS and for control groups, 20 µl of PBS alone, was administered. On the 7th day, the mice were euthanized and the bacterial load within the reproductive tissues, namely the testis, epididymis and vas deferens was quantified to discern the bacterial migration across these reproductive organs. Bacterial enumeration revealed a conspicuous pattern in the bacterial log cfu/g, displaying a descending sequence. This progression was observed from the right set of tissues-specifically, from the right testis to right epididymis followed by the right vas deferens and reverse pattern was observed on the left side, from the left vas deferens to the left testis via left epididymis. Moreover, as expected, right set of reproductive organs showed higher bacterial count as compared to the left set. However, mice subjected to PBS administration exhibited a complete absence of viable counts. To illustrate the impact of uropathogens colonization on the spermiogram of mice from right and left vas deferens, fundamental parameters including sperm count, motility and viability % were evaluated. As compared to the control groups, right vas deferens of test groups inoculated with SA microorganisms exhibited zero sperm count as evident by the absence of spermatozoa (azoospermia) and, therefore, none of the seminal parameters could be evaluated. However, for SI inoculated test group, significant reduction in the sperm count on the right side was observed exhibiting significantly reduced motility and viability percentages. Furthermore, only minimal presence of sperm count was observed on the left side for SA/SI inoculated test groups. The few sperms detected on the left side were predominantly immotile or nonviable. The histopathological examination of the testis of test groups showed

Garima Upadhyay, Renu Jaiswal, Ishwerpreet Kaur Jawanda, Thomson Soni, Vijay Prabha*

Departmentof Microbiology, Panjab University, Chandigarh, India

Biography

Vijay Prabha is a former Professor in the Department of Microbiology, Panjab University, Chandigarh, India. She has 32 years of teaching and 42 years of research experience. Her area of expertise is “Role of microorganisms in male and female infertility, exploitation of microbial factors as male and female contraceptive agents, molecular mimicry between bacteria and spermatozoa, understand ing bacteria sperm interaction at the receptor ligand level to develop immunocontraceptives, Probiotics and their role in amelioration of infertility, Cloning and characterization of sperm impairing factors isolated from microorganisms and their development as vaginal contraceptives, Protein profiling in unlocking the basis of microorganisms’ associated infertility”. She has guided number of M. Sc. and Ph. D students. She has 107 publications in national and international journals. She has also presented her work in various national and international conferences as an invited speaker and keynote speaker.

altered histology indicating severe hypospermatogenesis and serum testosterone levels exhibited a prominent reduction. To comprehend alternative mechanisms influenced by SA and SI on spermatogenesis, oxidative stress when evaluated through Malondialdehyde (MDA) levels, Catalase (CAT) activity, Peroxidase (POD) activity, showed significantly high levels and Glutathione (GSH) and Superoxide Dismutase (SOD) levels exhibited a decline. In conclusion, serum testosterone levels and ROS can act as important biomarkers in diagnosing azoospermia and may have promising implications for treatment strategies aimed at addressing male infertility caused by uropathogens.

Audience Take Away Notes

- The audience will learn that uropathogenic microorganisms can be one of the causative agents of azoospermia leading to male infertility
- This study also provides the probable mechanism of azoospermia caused by microorganisms
- Interventions that mitigate oxidative stress could offer new avenues for enhancing male fertility and improving the quality of life for affected individuals

She is life member of Association of Microbiologists of India and Panjab University Research Journal of Science. She is national advisory editorial board member, editor and editorial board member of various national and international journals. She has been also DBT nominee in various Biosafety committees.

Feuling drug research and development process with patient-centric and clinically relevant animal models

Despite promising advancements in drug Research and Development (R&D), the transition from preclinical studies to clinical success remains challenging, particularly in oncology where the success rate is only about 5%. This talk provides an insightful analysis of the challenges and opportunities in translational research within the pharmaceutical industry, advocating for a pivot towards approaches that prioritize patient needs and clinical relevance. It emphasizes the need for innovative preclinical models that reflect the complexity of human diseases, including cancer, auto-immune and cardiovascular diseases.

We call for increased collaboration among translational researchers from various fields and organizations to adopt and enhance these advanced methodologies. Highlighting the work at ClinBridge Biotech, we show our dedication to developing translational models that significantly advance drug development. This paper not only shares valuable insights and expert opinions but also reviews the capabilities and future strategies of ClinBridge Biotech in enhancing translational research.

We discuss important efforts in the industry, such as the creation of sophisticated orthotopic tumor models that mimic the TME and clinical conditions, the expansion of humanized cancer models for testing a broader spectrum of immuno-oncology therapies and the need for robust stand ard in vivo cancer pharmacology platforms for initial drug testing. The paper also explores the development of in vitro and in vivo pharmacology using Patient-Derived Xenograft (PDX) tumor organoids and resistant cancer cell lines, progress in autoimmune disease models and the creation of models for cardiovascular and cerebrovascular diseases in large animals.

In conclusion, this presentation aims to steer the pharmaceutical R&D sector towards more effective, patient-centered and clinically applicable translational research models, ultimately improving the translation of drug development from the laboratory to clinical application.

WenQing Yang

ClinBridge Biotech Inc Ltd, Nanjing, China

Biography

Dr. Yang finished his Ph. D. on Cell Biology and completed an extensive Post-Doctoral training at University of Calgary/Tom Baker Cancer Centre, Canada. He has ~30 years of translational and innovative drug development experience on cancer and inflammation from a range of leading pharmaceutical organizations, including Celgene, Amgen, Crown Biosciences, Kosan Biosciences and ImaginAb Inc. 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-III development. Dr. Yang's expertise focuses on translational medicine and translational research in cancer and inflammation and he has published ~100 research papers or reports. Dr. Yang currently serves as an Executive Director on translational sciences, State Key Laboratory of Translational Medicine and Innovative Drug Development, Simcere Pharma Group. He held several management positions in the biotech industry including Executive Director, Cancer Biology, Global Scientific Research Innovation Organization of Crown Biosciences, Senior Director of Cancer Pharmacology, Crown Biosciences and Head of Pharmacology at ImaginAb Inc.

BOOK OF ABSTRACTS

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SPEAKERS

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Epidemiological situation of 2023 dengue fever outbreaks in ecowas region: Implications for strengthening preparedness and response

Introduction: The Economic Community of West African States (ECOWAS) experienced a significant surge in Dengue Fever (DF) outbreaks in 2023, posing new important challenges to public health systems. This paper reviewed the epidemiological situation during the outbreaks and highlighted these challenges and key implications for strengthening preparedness and response strategies in the ECOWAS region.

Methods: We characterized DF outbreaks in ECOWAS from January to December 2023 using multiple methods comprising an extensive desk review of available literature on dengue in the region, the analysis of a self-administered questionnaire by key informants in the Member States to obtain the current epidemiologic situation, response, and control efforts), and the organizing a two-day regional stakeholder meeting.

Results: As of epidemiological week 52, ten (66%) of the 15 Member States reported a total of 164,406 suspected cases, including 72,799 confirmed and probable cases and 748 deaths (case fatality rate: 1.0 %) from Benin, Burkina Faso, Cabo Verde, Côte d'Ivoire, Ghana, Guinea, Mali, Senegal, Nigeria, and Togo. Burkina Faso accounted for 98% of the confirmed and probable cases (71,299) and 95% of fatalities. The highest case fatality rate of 33.3% was reported from Benin. Females (56.8%) and the age group 20-49 years (47.5%) constituted the highest number of cases, and the main circulating viral strains were DENV3 and 1.

Member States faced various health system, environmental, epidemiological, and political challenges with the response to the outbreaks such as limited access to diagnostics, limited public awareness, weak health system, sub-optimal vector and entomology control, and lack of cross-border collaboration.

Conclusion: Our findings call for improved surveillance, strengthened vector control measures, and fostering regional cooperation towards better data quality, updated risk maps, laboratory diagnosis, research, and cross-border collaboration.

Key Words: Dengue Fever, Outbreaks, Preparedness, Response, ECOWAS.

Audience Take Away Notes

- The extent and severity of the Dengue Fever (DF) outbreaks in the Economic Community of West African States (ECOWAS) in 2023
- The methodology used to characterize the outbreaks, including literature review, key informant questionnaires, and regional stakeholder meetings
- Epidemiological data from the outbreaks, including the number of suspected and confirmed cases, fatalities, and demographics of affected populations

- The distribution of cases across ECOWAS Member States and the disparities in cases and fatalities
- The challenges faced by Member States in responding to the outbreaks, including limitations in diagnostics, public awareness, health system capacity, vector control, and cross-border collaboration
- The identification of key priorities for strengthening preparedness and response strategies in the ECOWAS region, including improved surveillance, vector control measures, regional cooperation, data quality, risk mapping, laboratory diagnosis, and research

Biography

Dr. Aishat Bukola Usman is a Consultant Public Health Physician and Field Epidemiologist with over 15 years of experience in public health workforce development and health systems strengthening. She holds a PhD in Public Health from the University of Central Nicaragua, a Fellowship from the West African College of Physicians (Community Health), a master's in public health (Epidemiology and Medical Statistics) from the University of Ibadan Nigeria, and a Bachelor of Medicine and a Bachelor of Surgery from Ladoke Akintola University of Technology Nigeria. She received further training in Field Epidemiology Practice from the Nigeria Field Epidemiology and Laboratory Training Program (NFELTP). She is currently the Technical Advisor on Cross Border Surveillance at the ECOWAS Regional Center for Surveillance and Disease Control, West African Health Organization. She has published more than 40 articles in peer-reviewed scientific journals.

Ala O A[1*], Abdel Rahim M El Hussein[2], Isam M Elkhidir[3], Mohamed O Mustafa[2], Khalid A Enan[2]

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Prevalence and molecular detection of West Nile Virus (WNV) among renal transplant patients in Khartoum state, Sudan

Background: West Nile Virus (WNV) is an arbovirus from the Flaviviridae family. West Nile now represents one of the most common arboviral diseases worldwide that causes febrile illness. Also, significant number of patients develop severe neurological disease including meningitis, encephalitis and acute paralysis. This study was carried out to detect the frequency of West Nile virus IgM antibodies and virus nucleic acid among renal transplant patients in Khartoum state.

Methods: This was a descriptive study in which serum specimens were collected from 93 patient (68 male, 25 female) and investigated for WNV specific Immunoglobulin M (IgM) using Enzyme- Linked Immunosorbant Assay (ELISA) and for WNV RNA using Real Time PCR (RT-PCR). The study group age ranged from 20 to 80 years old.

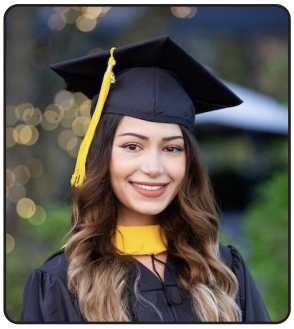
Result: Out of the 93 patients tested, 7(7. 5%) were positive for IgM and 86 (92. 4%) were negative and no positive RTPCR results were recorded.

Conclusion: The frequency of West Nile virus among renal transplant patients in Khartoum State, Sudan was documented through detection of specific IgM antibodies.

Keyword: West Nile Viruses (WNV), IgM. ELISA and Real-Time PCR.

Biography

Dr. Ala Omer Abdelaziz from Sudan have been working as a research assistant in the microbiology department at Al Neelain University in Khartoum, Sudan. His primary area of research revolves around flaviviruses such as West Nile virus and dengue virus ...etc.



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On a road to enhance VSV as an oncolytic agent: Deciphering the underlying mechanisms of resistance by some cancer cells

Vesicular Stomatitis Virus (VSV) has been suggested for use as an oncolytic agent, due to its wide host range and its ability to suppress host antiviral responses. Conceptually, a good oncolytic agent is able to selectively kill cancer cells while sparing normal healthy ones. It is believed that antiviral signaling pathways are perturbed in most cancer cells, rendering them susceptible to selective killing by VSV. However, some cancer cells still retain an intact antiviral response and are therefore “resistant” to oncolysis. Our previous work suggests NFkB-dependent antiviral signaling responsible for the inherent resistance to VSV in resistant human Prostate Cancer (PrCa) cells. Here, we follow-up our previous findings with a transcriptomic approach to identify targets underlying resistance vs sensitivity in two well-established human PrCa cell-lines (LNCaP and PC3 cells) infected with wild-type and mutant VSV strains. Our results show that the resistant cells (PC3) exhibit enrichment of several antiviral pathways and upregulation of multiple antiviral target genes. Validation of such targets through functional confirmation would provide another layer of confidence in the underlying cause of resistance to VSV in PrCa cells. The significance of this research lies in understand ing host responses to VSV in cancer and therefore paving the way to enhancing VSV’s use as an oncolytic agent, especially for better customization of individualized therapies.

Audience Take Away Notes

- Challenges facing the use of oncolytic viruses for cancer therapy
- Vesicular Stomatitis Virus is an excellent cand idate oncolytic agent
- Transcriptomics analysis is a powerful method for identifying genes that may contribute to resistance to VSV infection

Biography

Ms. Alaa studied Biotechnology and Molecular Biosciences at the Rochester Institute of Technology, NY, supervised by Dr. Maureen Ferran and graduated with her BS in 2020. She then joined the Biomedical Genetics PhD program at the University of Rochester (UR) School of Medicine and Dentistry and received her MS degree from the UR in 2022. Currently, she continues her graduate research as a fifth year PhD student supervised by Dr. Stephen Dewhurst. She has published one original research article in Current Protocols in Microbiologyand a few others are being finalized for submission for publication.

Dr. Amr Mousa
Internal Medicine Trainee, East Lancashire Teaching Hospitals, Blackburn, UK

A rare case of urogenital schistosomiasis in an African asylum seeker: Diagnostic and management challenges

Background: Schistosomiasis is a parasitic disease caused by trematode worms of the genus Schistosoma. Schistosomahaematobium is primarily responsible for urogenital schistosomiasis, commonly presenting with haematuria and bladder pathology. This case highlights the diagnostic and management challenges of a rare presentation of urogenital schistosomiasis in a non-endemic region.

Case Presentation: A 15-year-old male asylum seeker from Eritrea presented with intermittent haematuria for six months and intermittent Per Rectum (PR) bleeding for one year. His past medical history included pulmonary tuberculosis and chickenpox with scarring. Social history revealed he traveled through multiple endemic regions before arriving in the UK. Physical examination was generally unremarkable, with no visible haematuria on gross examination of the urine and no blood on digital rectal examination.

Investigations: Initial laboratory investigations, including FBC, CRP and urine culture, were unremarkable. Stool pathogen PCR and microscopy were negative. Ultrasound of the urinary tract revealed focal bladder wall thickening without vascularity. Diagnostic cystoscopy under general anaesthetic showed sand y patches in the bladder but no other abnormalities. Definitive diagnosis was confirmed by the presence of Schistosoma haematobium ova in urine microscopy.

Management: The patient was treated with Praziquantel 1. 2 g, the drug of choice for schistosomiasis, with an expectation of a curative outcome.

Discussion: Schistosomiasis is endemic in Eritrea and other parts of Africa. The patient's journey through multiple endemic regions increased his risk of infection. Haematuria and PR bleeding in this case indicated involvement of both the urinary and gastrointestinal tracts. The intermittent nature of symptoms and chronic timeline were consistent with a long-stand ing infection, rare in the UK but common in endemic areas.

Conclusion: This case underscores the importance of considering schistosomiasis in patients with compatible travel history and unexplained haematuria or PR bleeding. Prompt diagnosis and treatment are crucial to prevent long-term complications. This case also emphasizes the need for heightened clinical awareness and thorough history-taking for patients from endemic regions presenting with atypical symptoms in non-endemic areas.

Audience Take Away Notes

- **Recognize Clinical Presentations:** Understand key symptoms of urogenital schistosomiasis,

including haematuria and PR bleeding and their relevance to travel history

- **Diagnostic Process**: Learn the importance of comprehensive history-taking, laboratory tests, imaging and cystoscopy in diagnosing schistosomiasis
- **Treatment Protocols:** Gain knowledge about the use of Praziquantel for treating schistosomiasis and the importance of timely intervention to prevent complications
- **Clinical Awareness:** Appreciate the need for heightened awareness and consideration of tropical diseases in patients from endemic regions, even in non-endemic settings
- **Case Significance:** Recognize the complexities and challenges in managing rare tropical diseases in diverse healthcare environments, illustrated by this case

Biography

Amr Mousa has completed his medical degree from Charles University in Prague, Faculty of Medicine in Pilsen and graduated First in His Class. He has since moved to the UK where he has worked in a busy London Hospital and is starting in the UK National Internal Medicine Training Program in August 2024.

Anant Marathe
Parul Institute of medical sciences and Research, Parul University, India

Exploring association between host factors and different virulence \ factors of Enterococcus spp. With treatment outcome in Entrococcal BSI. (causing Blood stream infections)

Introduction: Enterococci are normal human of the oral cavity, gastrointestinal tract, and vaginal vault. Although they are relatively a virulent, they evolved as leading cause of nosocomial bacteremia with very high fatality rate of 68% (65) In one large study of nosocomial sepsis due to Gram positive pathogens, enterococci were independently associated with a high risk of death (227).

Enterococci can cause variety of human infections including blood stream Infection. Amongst many species isolated from clinical specimens Enterococcus faecium and E.faecalis are two major species frequently isolated from blood stream infection cases. Majority of infections are caused by E.fecalis. Evolution of Enterococci from commensal to most frequent pathogen of nosocomial blood stream infections required lot many changes in the Enterococci including adaptation to different environment, evading the host's immune attack and causing toxin mediated damage.

In the present study we have attempted to explore association between the host factors like co-morbidities and virulence factors of Enterococci causing nosocomial blood stream infections. Virulence genes of Enterococci

Adherence to Host Tissues (Adhesin): Adhesins play a significant role in adhesion to eukariotic cell surface or mucosal serface that makes them remained adhered strongly to remain and proliferate as commensals.

Invasion of Host Tissues: In some cases of nosocomial bacterimia the source of infection is identifiable but in large nuber of cases it is not possible to trace the source and in such case cases the source presumably is Intestinal tract. (1, 234). In some animal studies have hypothesized translocation of Intestinal Enterococci via Phagocytic leucocytes to regional lymphnodes to blood stream. The prior therapy with Cephalosporins kill the normal bacterial flora and allow the growth of Enterococci that are tolerent and evetually dominated the flora. (129, 161, 242) and are consistently associated with development of enterococcal bacteremia (6, 90, 93, 113, 175, 243, 244).

Modulation of Host Immunity: Lipoteichoic Acids od Enterococci are studied for their potency to induce Tumour necrosis factor and Interferons. (221) Enterococcal lipotechoic acid has been found to bring about immunemodulation.

Pheromones: E. faecalis strains are known to secrete Pheromones that are small peptides, comprising only 7 to 8 amino acids. Pheromones have potential to act as chemoatrractants for neutrophils (64).

Protease (Gelatinase): Protease produces by E.faecalis is capable of hydrolyzing gelatin. collagen, casein, haemoglobin and other small biologically active peptides (212) Coque et al. (47) analyzed 95 enterococcal isolates from patients with endocarditis and other nosocomial infections and found that 54% produced protease.

Hyaluronidase: It is suggested that enterococcal hyaluronidase could play a role in invasive disease. No studies, however, address this issue for enterococci.

AS-48: AS-48 is a 7.4-kDa peptide produced by E. faecalis inhibits and lyses a wide spectrum of gram-negative and gram-positive bacteria, including enterococci (80). The significance of this bacteriocin remains uncertain, however, since the prevalence of AS-48-producing strains among human commensal and infection isolates has yet to be defined. No activity of AS-48 against eukaryotic cell membranes has been reported.

Biography

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

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Genome-wide identification and functional analysis of dysregulated alternative splicing profiles in sepsis

Background: An increasing body of evidence now shows that the long-term mortality of patients with sepsis are associated with various sepsis-related immune cell defects. Alternative splicing (AS), as a sepsis-related immune cell defect, is considered as a potential immunomodulatory therapy target to improve patient outcomes. However, our understand ing of the role AS plays in sepsis is currently insufficient.

Aim: This study investigated possible associations between AS and the gene regulatory networks affecting immune cells. We also investigated apoptosis and AS functionality in sepsis pathophysiology.

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

Results: For the first time, we used systematic RNA-seq analysis of sepsis-related AS and identified 1505 variable AS events that differed significantly (p <= 0. 01) across the four groups. In the sepsis group, the genes related to significant AS events, such as, SHISA5 and IFI27, were mostly enriched in the cell apoptosis pathway. Furthermore, we identified differential splicing patterns within each of the four groups. Significant differences in the expression of RNA Binding Protein(RBP) genes were observed between the control group and the sepsis group. RBP gene expression was highly correlated with variant splicing events in sepsis, as determined by co-expression analysis; The expression of DDX24, CBFA2T2, NOP, ILF3, DNMT1, FTO, PPRC1, NOLC1 RBPs were significant reduced in sepsis compared to the healthy group. Finally, we constructed an RBP-AS functional network.

Conclusion: Analysis indicated that the RBP-AS functional network serves as a critical post-transcriptional mechanism that regulates the development of sepsis. AS dysregulation is associated with alterations in the regulatory gene expression network that is involved in sepsis. Therefore, the RBP-AS expression network could be useful in refining biomarker predictions in the development of new therapeutic targets for the pathogenesis of sepsis.

Biography

Baihetinisha Tuerdi is a Chief Physician of ICU. She is an Associate Professor, Master's Supervisor and also the Medical accident technical appraisal expert of Xinjiang Medical Association. She is a Famous Doctor of The First Affiliated Hospital of Xinjiang Medical University. Her representative publications are Genome-wide identification and functional analysis of dysregulated alternative splicing profiles in sepsis, Journal of Inflammation, 2023, 20(31). Downregulation of miR-155 attenuates sepsis-induced acute lung injury by targeting SIRT1, Int J Clin Exp Pathol, 2018, 11(9): 4483- 4492. Safety and efficacy of regional citrate anticoagulation in continuous blood purification treatment of patients with multiple organ dysfunction syndrome, Brazilian Journal of Medical and Biological Research, 2018, 51(1).

Carly Contri, Med
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Leveraging power BI to assess community immunization efforts

Vaccine hesitancy has increased as pediatric immunization rates have decreased, with lowest rates for children experiencing social determinants of health. To address these issues, 24 immunization partnership grants were awarded to practices and organizations across the United States to implement community-based vaccine initiatives. Funding prioritized rural, under-resourced, or historically hesitant communities and those immunizing children under 5.

Mixed method approaches were utilized to evaluate outcomes and impact and visualized within Power BI. To evaluate the effectiveness of the funded initiatives, data was collected from grantees through mid and final-project reports through SurveyMonkey (n=48) from February to July 2023. Grantees were asked to rate their level of agreement in which funding increased opportunities to 1) improve vaccine confidence, 2) improve vaccination uptake and 3) support pediatricians in delivering on-time vaccinations. Through grantee project activities, 88% reported they were better able to support pediatricians in delivering on-time vaccinations to children and 96% reported improved confidence in vaccines for rural and underserved communities. Overall, 92% of grantees felt there was an improvement in vaccination uptake within their communities and more than 1, 200 pediatric immunizations were administered.

The interactive Grantee Immunization Activities Power BI Dashboard, which centralized data sources and visualized programmatic outcomes, was shared with program stakeholders through a collaborate site. Data visualized community priorities, allowed users to filter outcomes by organization, geography, communities served and strategies implemented and demonstrated the collective impact across initiatives. Organizations evaluated grant deliverables and outcomes relative to others as they identified novel approaches that successfully impacted vaccination outcomes.

Centralizing cross-program data within Power BI increased data accessibility by sharing data with partners, increased knowledge of successful community initiatives and increased public health capacity. Data highlighted the positive impact of customizable strategies to reach individual communities. Lessons learned include database best practices and enhanced visualizations for future grants.

Audience Take Away Notes

- Summarizethe importance of customizable vaccination strategies on community-based pediatric immunization programs and vaccination uptake
- Describe how Power BI can be utilized as a tool to centralize data sources to reflect outcome achievement on immunization initiatives
- Apply database best practices and data visualizations to show how you can highlightimmunization impact and outcomes for stakeholders and funders

Biography

Carly Contri is a data scientist, evaluator and dashboard enthusiast. She currently works at the American Academy of Pediatrics managing evaluation initiatives across immunization and infection prevention and control programs. Carly graduated with an MEd in Measurement, Evaluation, Statistics and Assessment from the University of Illinois at Chicago. She is passionate about improving data centralization, increasing data accessibility and creating self-service dashboards and data visualizations to enhance storytelling with Power BI. She has recently worked on data disaggregation to understand community needs at the intersectionality of their identities and incorporating equitable evaluation into pediatric programs.

Chitra Upadhyay*, Priyanka Gadam Rao
Division of Infectious Disease, Department of Medicine, Icahn School of Medicine at Mount Sinai, 1 Gustave L. Levy Place, New York, NY 10029, USA

Distinct mechanisms regulate the exposure of broadly neutralizing antibody epitopes on HIV-1 particles

Background: Despite extensive research, an effective prophylactic vaccine against HIV-1 remains elusive. Currently, substantial focus is directed toward developing vaccines that can induce broadly Neutralizing Antibodies (bNAbs) capable of neutralizing multiple HIV-1 strains. However, HIV-1 employs various strategies to conceal the cross-reactive and conserved epitopes targeted by these bNAbs, resulting in an inadequate and non-protective immune response.

Goal: This study aimed to map the antigenic land scape of HIV-1 Envelope (Env) on virions and identify mechanisms to expose these epitopes.

Methods and Results: To achieve our goal, we designed a flow cytometry-based assay capable of detecting antibody binding on virus particles. Using three HIV-1 isolates and a panel of monoclonal Antibodies (mAbs), we demonstrated that specific epitopes—such as V2i, gp120-g41 interface and gp41-MPER—are accessible by mAbs, while others (V3, V2q and CD4bs) remain hidden. Prolonging virus-mAb interaction did not unmask these epitopes, but allosteric changes induced by pre-binding of specific mAbs rendered them accessible. This led us to explore whether similar changes are necessary for bNAbs to neutralize the virus. To test this, we assessed HIV-1 neutralization under two conditions: incubating the virus-mAb mix or not before adding target TZM. bl cells. Interestingly, both conditions yielded similar neutralization levels, suggesting that the interaction between virus and target cells sensitizes the virions for neutralization via bNAbs. Additionally, we found that lectin-glycan interactions can also expose these epitopes, with effectiveness depending on lectin specificity.

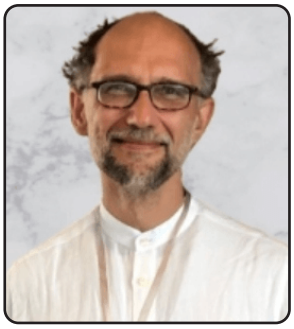
Conclusion: These findings deepen our understand ing of how HIV-1 strategically conceals critical epitopes from the host immune response. They also provide valuable insights for designing potent antibody combinations for therapeutic purposes. Furthermore, these findings pave the way for exploring innovative vaccine regimens involving Env-mAb or Env-lectin complexes. Such regimens have the potential to effectively present bNAb epitopes to the host immune system.

Audience Take Away Notes

- Improve our understand ing of how HIV-1 strategically conceals critical epitopes from the host immune response
- Use the information to enhance the exposure of the desired epitopes
- Improve the design of combination antibody therapy

Biography

Dr. Chitra Upadhyay received her PhD degree in 2003 from India. She then and moved to USA in 2005 for her postdoctoral training. She took a career break from 2009-2012 to raise her family and later she joined NYU Langone Medical Center for a second post-doc. In 2015 she joined Icahn School of Medicine at Mount Sinai as an Instructor after which in 2017 she obtained the position of Assistant Professor at the same institution. Her research primarily focusses on HIV-1 pathogenesis and vaccine development.



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Structural deformations in the superior tubular of the hypothalamus and their impact of autoimmune antibody production: A study of long COVID patients

Background: Post/Long COVID is a complex multisystemic post-viral syndrome characterized by heterogeneous symptoms, potentially associated with viral or immune-mediated disruption. The superior tubular of the Hypothalamus, responsible for the Immune response and control, plays a pivotal role in this interaction. Structural imaging, specifically Diffusion Tensor Imaging (DTI), revealed deformations and holes in cubic millimeters, suggesting degenerated cells leading to persistent firing and excessive toxic production of antibodies from the immune system.

Methods: This case study investigated the effects of testing different antibodies over six months in 10 LongCOVID patients, 10 Post-COVID patients and ten recovered patients (all female). The freesurfer and CONN toolbox, along with the 2D Elisa penel (antibodies), were utilized for displaying MRT DTI. Autoantibody profiles were determined and baseline and follow-up scans using Fractional Anisotropy were conducted. Diagnosis Long/Post COVID patients were established through clinical diagnosis, self-report measures, Canadian Consensus Criteria for CFS and ICD-10 coding.

Results: Structural deformation, particularly in the area of the hypothalamus responsible for the immune responce, were evident through holes in the structural imaging. The deformations are hypothesized to trigger chaotic cell behavior, leading to persistent firing and increased autoantibody production, predominantly observed in Long COVID patients and occasionally in post-COVID cases. Patients who had recovered still exhibited structural defects upon re-measurement with MRI.

Discussion: These findings suggest that altered structural integrity in the superior tubular may lead to the release of overdriven immun autoantibodies, potentially explaining the toxic autoimmune reactions due to long-term disturbance in brain function in patients with Long COVID. Clarifications is needed regarding whether the observed holes are causative or resultatant of volume changes in the superior tubular.

Biography

Christof Peter Ziaja is currently a guest scientist at the University Hospital Hamburg Eppendorf in neuroradiology, where he is researching the interaction of neuromuscular fatigue and processing using in Fractional Anisotropy (FA) imaging techniques. Additionally, he is also affiliated with the Prof. Stark's institute in Hamburg where he treats roughly 30 patients a week with differing clinical/somatic profiles. Examples are elderly who receive training to prevent falls, interventions to aid with neurodegenerative illnesses (such as Parkinson, MS) and athletes suffering from Overtraining Syndrome. His work consists of both diagnostics and treatments. Examples are the recording of measurement parameters (EEG measurements, gait analysis, EMG measurements, ECG and HRV measurements) as well as the therapeutic design and creation of an individual movement therapy. His Areas of expertise are individual trainability and regulation abilities (such as the cool down phase). He has an international publication record, teaching experience and experience with supervision. He has taught at the department of Health Sciences of the Fresenius University of Applied Sciences and the department of Movement Sciences of the University of Hamburg. Additionally, He has supervised students at the Fresenius University of Applied Sciences in Hamburg in the completion of their bachelor theses and accompanied their oral final exams.

Dalinda Eusébio[1, 2*], Milan Paul[3], Swati Biswas[3], Zhengrong Cui[2], Diana Costa[1], Ângela Sousa[1]

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[3]Nanomedicine Research Laboratory, Department of Pharmacy, Birla Institute of Technology & Science-Pilani, Hyderabad Campus, Jawahar Nagar, Medchal, Hyderabad, Telangana, India

Targeted delivery of a minicircle DNA vaccine against COVID-19 to antigen-presenting cells using mannosylatedpolyethylenimine-cholesterol-based nanoparticles

Coronavirus disease (COVID-19) is an infectious disease caused by the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), which has resulted in 775 million confirmed cases and approximately 7 million deaths reported by the World Health Organization (WHO) as of 31 March 2024. Nucleic acid vaccines have emerged as a novel approach to induce efficient and safe immune responses against COVID-19. DNA vaccines have advantages over mRNA vaccines, given their superior stability, simpler manufacturing process and cost-effective manufacturing and storage, qualifying them as desirable candidates for global vaccination efforts, particularly in low-income countries. Minicircle DNA (mcDNA) presents a safer alternative to conventional plasmid DNA, as it lacks bacterial-derived sequences that are often associated with safety concerns. In this work, different systems based on polyethylenimine (PEI) were investigated for delivering Parental Plasmid (PP) and mcDNA vectors encoding the Receptor-Binding Domain (RBD) of SARS-CoV-2 spike protein to antigen-presenting cells (APCs). Three polymeric systems were evaluated: PEI alone, PEI functionalized with cholesterol (PEI-CHOL) and PEI functionalized with both cholesterol and mannose ligand (PEI-CHOL-MAN). Different ratios of protonatable Nitrogen groups (N) in the polymer to anionic phosphate groups (P) in DNA were investigated and nanocomplexes were characterized in terms of DNA encapsulation efficiency, surface charge, size and Polydispersity Index (PDI). Fourier Transform Infrared Spectroscopy (FTIR) analysis revealed the successful formation of PEI complexes and confirmed DNA encapsulation. Scanning Electron Microscopy (SEM) verified that the formulated nanosystems exhibited a spherical shape and homogenous structure. Stability assays demonstrated that the formulated nanosystems were effective in protecting the DNA vector after incubation with cell culture media, trypsin and 10% FBS. Decomplexation assays confirmed that DNA was able to maintain its integrity and supercoiled conformation after being released from the nanocomplexes. In addition, in vitro transfection studies were conducted using immature dendritic cells (JAWS II) and human fibroblast cells (hFibro). Viability studies assured the safety of all nanocarriers, nevertheless, nanosystems functionalized with cholesterol seem to reduce the inherent cytotoxicity associated with PEI. Fluorescence confocal microscopy studies conducted in JAWS II cells confirmed the intracellular localization of nanosystems, demonstrating enhanced cellular uptake with PEI-CHOL and PEI-CHOL-MAN compared to PEI alone. Regarding RBD expression, cells transfected with the mcDNA vector exhibited higher levels of RBD transcripts compared to those transfected with the PP vector. Furthermore, the PEI-CHOL-MANsystem formulated with the mcDNA-RBD vector displayed higher levels of both transcripts and proteins in JAWS II cells. These findings suggest that mannose ligand s facilitated the specific recognition by mannose receptors, which are overexpressed on the surface of APCs, in contrast to cells lacking this receptor (hFibro). Additionally, dendritic cell maturation was successfully induced by the nanosystems, resulting in a significant increase in pro-inflammatory cytokine production. This study highlights the potential for improving DNA vaccine efficacy by combining the mcDNA vector with mannosylated polymeric delivery systems. This innovative approach shows promise for enhancing immune

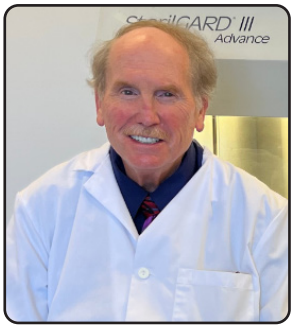
responses against SARS-CoV-2, contributing to the fight against COVID-19, while also holding promise for addressing other infectious diseases.

Audience Take Away Notes

- The importance of DNA vaccines in mitigating the impact of emerging infectious diseases
- The unique features and benefits of the cutting-edge minicircle DNA vector
- The potential of using polymeric nanosystems to deliver mcDNA vaccines to antigen-presenting cells

Biography

Dalinda Eusébio completed her BSc in Biotechnology in 2016 and her MSc in Biomedical Sciences in 2018 at the University of Beira Interior, Portugal. Currently, she is pursuing her Ph. D. Degree in Biomedicine at the Health Sciences Research Centre of the University of Beira Interior (CICS-UBI) in collaboration with The University of Texas at Austin, supported by a Ph. D. fellowship from the Portuguese Foundation for Science and Technology (FCT). Her research focuses on pharmaceutical nanobiotechnology, specifically on the production, purification and targeted delivery of the innovative minicircle DNA vector for gene therapy and DNA vaccine applications.



Jacob Hoadley[1], Emily Wright[1], Michael Bowe[1], Peter Pushko[2], Brian Backstedt[3], Casey Gardner[3], Micah Short-Freeman[3], Swagata Kar[3], David Craig Wright M. D[1*]

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Immunogenicity and efficacy of a subcutaneously administered, adjuvanted vaccine containing modified s1 spike protein of SARS-CoV-2 variant C. 1. 2

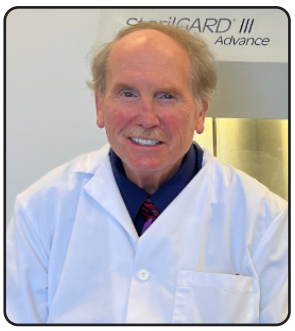
During the COVID-19 pand emic, vaccines have produced protective immunity sufficient enough to cause a decrease in hospitalizations and deaths; however, the pand emic continues due to mutational events, predominantly occurring in the S1 sequence of the spike protein of SARS-CoV-2. We have developed a baculovirus-expressed, modified S1 SARS-CoV-2 protein based on the C. 1. 2 variant, which was first identified in South Africa. This was encapsulated in a vitamin E containing, nonphospholipid liposome (SubATVax™), which was then used to subcutaneously immunize Syrian hamsters with 25 gauge needles. This vaccine, when administered at day 1 generates IgG responses that react to the modified C. 1. 2 S1 protein; full-length spike proteins from Wuhan-Hu-1, Delta, Omicron BA. 1; and the Omicron recombinant variant XBB. 1. 5 in 100% of the animals. The second dose administered subcutaneously on day 28 demonstrated anamnestic response in the quantitative IgG assay to the Wuhan-Hu-1 spike Receptor Binding Domain (RBD). In addition, antibody IgA and IgM responses in sera were demonstrated. Serum IgG antibody responses to the spike proteins of the modified C. 1. 2 S1 and full-length spike proteins Wuhan-Hu-1, Delta, Omicron BA. 1 and Omicron recombinant XBB. 1. 5 variants are elevated for over 120 days. Challenge of vaccinated and unvaccinated hamsters at day 126 of the study with an Omicron BA. 1 resulted in a difference in weight change and viral load based on the qRT-PCR assay seven days after challenge. We have completed a two-year stability study on the vaccine and it is stable when stored at 4 degrees C. Photomicrographs and real-time videos of the structures will be presented. In summary, we have developed a new adjuvant system for protein-based vaccines which allows for subcutaneous immunization in a one- or two-dose format.

Audience Take Away Notes

- We have designed proprietary, patented delivery vehicles for vaccines, called SubATVax™, which can be administered either subcutaneously or intramuscularly
- Our adjuvanted vaccine containing the C. 1. 2 SARS-CoV-2 modified S1 sequence of the Spike protein is immunogenic and generates IgG, IgM and IgA antibody responses in a one- or two-dose format
- Our adjuvanted vaccine cross-protects in an Omicron BA. 1 challenge study in hamsters
- Our adjuvanted vaccine is administered through a 25-gauge needle subcutaneously. Structures can be loaded into and administered in needle-free injector systems
- We have completed immunogenicity studies with two different proteins and a polypeptide using our SubATVax™ technology

Biography

Dr. Wright studied Biology at the University of Virginia (1968-1972) and attended the University of Virginia Medical School (1972-1976). He completed his internship at Harlem Hospital in New York City (1976-1977), his residency in Internal Medicine at Walter Reed Army Medical Center (WRAMC) (1980-1982) and his three-year infectious disease fellowship at WRAMC (1983-1985), working in the laboratory of Dr. Gerald Sadoff at Walter Reed Army Institute of Research. He has been an Infectious Disease practitioner since 1985 and has co-founded three companies: Univax Biologics, Novavax and D4 Labs, LLC. Dr. Wright holds 20 U. S. patents and has numerous publications.



David Craig Wright* M. D, Jacob Hoadley, Emily Wright
D4 Labs, LLC, Pacific Grove, California, USA

Preparation of subatvax™ adjuvanted vaccines against inactivated poliovirus, diphtheria toxoid, tetanus toxoid, acellular pertussis, neisseria meningitidis, streptococcus pneumoniae and haemophilus influenzae polysaccharide conjugates for subcutaneous administration

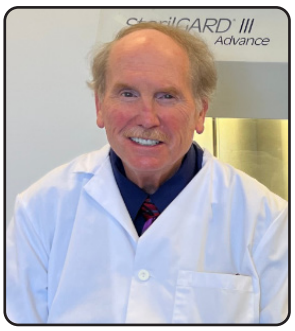
In developing nations the cost of commercial vaccines to immunize children against Polio virus, Diphtheria, Tetanus, Pertussis, Neisseria meningitidis, Streptococcus pneumoniae and Haemophilus influenzae can be prohibitive. If one could develop inexpensive adjuvants for these approved vaccines, put multiple vaccine antigens in said adjuvant, decrease the volume and number of immunizations and administer these vaccines subcutaneously, then more children could be immunized at a fraction of the current cost. During the COVID-19 pand emic, we developed just such an adjuvant system, SubATVax™, for baculovirus expressed proteins which generated systemic levels of IgM, IgG and IgA with a subcutaneous immunization schedule. With our adjuvant system, we have now successfully formulated a Diphtheria toxoid, Tetanus toxoid and acellular Pertussis vaccine, along with an inactivated Poliovirus vaccine, as well as a multiantigen polysaccharide conjugate vaccine directed against 20 serotypes of Streptococcus pneumoniae, four serotypes of Neisseria meningitidis and Haemophilus influenzae capsular type b. These were encapsulated in a vitamin E containing, nonphospholipid liposome (SubATVax™). Both adjuvanted vaccines were packaged into 1 mL syringes and a needleless injector technology. Both packaged vaccines were placed on two-year stability studies in 2024. Data on stability testing, to include sizing data, photomicrographs and real-time videos of the structures, will be presented. In summary, we have developed a new adjuvant system for protein-based vaccines, polysaccharide conjugate vaccines and inactivated whole virus vaccines for potential testing and use in resource-constrained countries.

Audience Take Away Notes

- We have designed proprietary, patented delivery vehicles for vaccines, called SubATVax™, which can be administered either subcutaneously or intramuscularly
- The audience will learn how to easily produce our adjuvant system for local use with approved vaccines
- Our adjuvanted vaccines can be administered subcutaneously through a 25-gauge needle. Adjuvanted vaccines can also be loaded into and administered in needle-free injector systems

Biography

Dr. Wright studied Biology at the University of Virginia (1968-1972) and attended the University of Virginia Medical School (1972-1976). He completed his internship at Harlem Hospital in New York City (1976-1977), his residency in Internal Medicine at Walter Reed Army Medical Center (WRAMC) (1980-1982) and his three-year infectious disease fellowship at WRAMC (1983-1985), working in the laboratory of Dr. Gerald Sadoff at Walter Reed Army Institute of Research. He has been an Infectious Disease practitioner since 1985 and has co-founded three companies: Univax Biologics, Novavax and D4 Labs, LLC. Dr. Wright holds 20 U. S. patents and has numerous publications.



David Craig Wright[1*] M. D, Jacob Hoadley[1], Emily Wright[1], Daniel Sweet DVM[2]

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

[2]Sweet River Equine Clinic, Inc., Modesto, California, USA

Preparation, characterization and stability of subatvax™ adjuvanted commercial veterinary vaccines using six commercial vaccines, including rabies, leptospirosis and an encephalomyelitis combination vaccine for subcutaneous administration

In resource-constrained nations, the cost of commercial vaccines to immunize animals can be prohibitive. For example in the USA the cost of a single dose of rabies vaccine for horses is US $7. The encephalomyelitis combination vaccine for horses is US $28. Various combination vaccines for dairy cows and cattle range from US $5. 30-$9. 60 per dose. We have recently used our SubATVax™ adjuvant technology, which was originally designed to prepare adjuvants for SARS-CoV-2 spike proteins, to prepare adjuvanted vaccines using commercially available vaccines for horses, dairy cows and cattle, sheep, swine, dogs and cats. Specifically, we have prepared adjuvanted vaccines directed against rabies, leptospirosis, combination products like the Zoetis encephalomyelitis combination vaccine and three other combination vaccines. We will present three-month stability data on the first six commercial animal vaccines encapsulated with our patented SubATVax™ adjuvant, including lazer sizing data, photomicrographs and video of said adjuvanted vaccines. A demonstration of how veterinarians can encapsulate a vaccine will be performed on a commercial vaccine against rabies. In summary, we have developed a simple method to locally prepare adjuvanted commercial vaccines for subcutaneous administration in mammals. Developing inexpensive adjuvants for approved vaccines, putting multiple vaccine antigens in said adjuvant, decreasing the volume and number of immunizations and administering these vaccines subcutaneously should allow more animals to be immunized at a fraction of the current cost.

Audience Take Away Notes

- We have designed proprietary, patented delivery vehicles for veterinary vaccines which can be administered either subcutaneously or intramuscularly
- The audience will learn how to easily produce our adjuvant system for local use with approved veterinary vaccines
- Our adjuvanted veterinary vaccines can be administered subcutaneously through a 25-gauge needle. Adjuvanted veterinary vaccines can also be loaded into and administered in needle-free injector systems

Biography

Dr. Wright studied Biology at the University of Virginia (1968-1972) and attended the University of Virginia Medical School (1972-1976). He completed his internship at Harlem Hospital in New York City (1976-1977), his residency in Internal Medicine at Walter Reed Army Medical Center (WRAMC) (1980-1982) and his three-year infectious disease fellowship at WRAMC (1983-1985), working in the laboratory of Dr. Gerald Sadoff at Walter Reed Army Institute of Research. He has been an Infectious Disease practitioner since 1985 and has co-founded three companies: Univax Biologics, Novavax and D4 Labs, LLC. Dr. Wright holds 20 U. S. patents and has numerous publications.

Erez Shmueli*, Dan Yamin
Department of Industrial Engineering, Tel-Aviv University, Tel-Aviv, Israel

Higher sensitivity monitoring of reactions to vaccination using smartwatches

The absence of sufficient vaccine safety information is one of the key contributors to vaccine hesitancy. In this presentation, I will discuss the methodology and findings of four of our recent studies that evaluated the safety profile of the second and third BNT162b2 mRNA COVID-19 booster vaccines using data from a retrospective cohort (based on EMR data) and a prospective cohort, in which all participants wore a Garmin Vivosmart 4 smartwatch and completed a daily questionnaire via smartphone. Both our retrospective and prospective analyses supported the safety of the second and third boosters, with our findings reflecting physicians' diagnoses, patients' subjective reactions and importantly - patients' objective physiological measures. Interestingly, we found that that the smartwatches were able to detect physiological responses following vaccination that were not captured by patient self-reporting.

Audience Take Away Notes

- Safety profiles of vaccines should consider both physicians' diagnoses, patients' subjective reactions and objective physiological measures
- The ubiquity of smartwatches provides an opportunity to gather improved data on patient health, including active surveillance of vaccine safety

Biography
Erez Shmueli is an Associate Professor, Head of the Big Data Lab and Co-Head of the Data Science undergraduate program at Tel-Aviv University. Holding a BA degree (with honors) in Computer Science from the Open University of Israel, he earned his MSc and PhD degrees in Information Systems Engineering from Ben-Gurion University of the Negev. His postdoctoral fellowship at the MIT Media Lab further enriched his academic journey. Erez's research is dedicated to developing Artificial Intelligence (AI) models for understand ing, predicting and influencing human behavior using real-world data from sources like smartphones and wearable devices. Over the past years, his focus has particularly shifted towards the intersection of AI and healthcare.

Fisseha Shiferie[1,2*], Samson Gebremedhin[3], Gashaw And argie[1], Dawit A. Tsegaye[1], Wondwossen A. Alemayehu[4]

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[4]Project HOPE Headquarter, Washington D. C., United States

Decomposition analysis of socioeconomic inequalities in vaccination dropout in remote and underserved settings of Ethiopia

Background: Despite increments in immunization coverage over the past decades, substantial inequality due to wealth status has persisted in Ethiopia. This study aimed to decompose the concentration index into the individual factors contributing to socioeconomic-related inequalities leading to vaccination dropout among children aged 12–35 months in remote and underserved settings in Ethiopia using a decomposition approach.

Methods: A wealth index was developed by reducing 41 variables related to the women's household living stand ards into nine factors using Principal Component Analysis. The components were further totaled into a composite score and ultimately divided into five quintiles (poorest, poorer, middle, richer and richest). Vaccination dropout was calculated as the proportion of children who did not get Pentavalent-3 among those who received the Pentavalent-1 vaccine. The concentration curve and concentration index were used to estimate socioeconomic-related inequalities in childhood vaccination dropout. The concentration index was also decomposed to examine the contributing factors to socioeconomic inequalities in childhood vaccination dropout.

Results: The overall concentration index was -0. 179 and statistically significant (p<0. 01), which confirmed the concentration of vaccination dropout among the lowest wealth strata. The decomposition analyses showed that wealth index was a significant contributor to inequalities in vaccination dropout (49. 73%). Place of residence also explained -16. 15% of the inequality in vaccination dropout. Skilled birth attendance and availability of health facility in the kebele were also significant positive contributors to inequality, contributing 33. 64% and 12. 55% to inequalities in vaccination dropout, respectively.

Conclusions: Vaccination dropout was concentrated among the lowest wealth strata. Wealth index, place of residence, skilled birth attendance and availability of a health facility in the kebele largely contributed to this inequality. Policymakers need to address the pro-rich inequality in childhood vaccination by strengthening women's utilization of healthcare services and accessibility of health facilities in rural kebeles.

Audience Take Away Notes

- Main predictor variables that contribute to childhood vaccination dropout in Ethiopia
- How concentration curve and index can be used to estimate inequalities in childhood vaccination dropout
- How decomposition analysis approach is used to examinecontributing factors to socioeconomic inequalities in childhood vaccination dropout

Biography

Fisseha Shiferie completed his master's in international public healthfrom the French School of International Public Health in Paris, France and his Master of Pharmacology from Addis Ababa University, Ethiopia. Currently, he is a 3rd year PhD student at Addis Ababa University. He has been working for over 15 years in managerial, researcher and academician positions in research organizations, international NGOs and GOs including higher academic institutions. He has also worked as an expatriate in France, South Sudan, Ethiopia and Ugand a. He is currently leading the Research, Learning and Publication unit at Project HOPE.

Fisseha Shiferie[1,2]*, Samson Gebremedhin[3], Gashaw Andargie[1], Frank DelPizzo[4], Kidist Belete[5]

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Spatial distribution of zero-dose children in Ethiopia: Evidence for a targeted intervention from a large-scale evaluation survey

Background: Ethiopia is the fourth leading contributor to the global total of zero-dose children (those who lack the first dose of the pentavalent vaccine) and has substantial regional variations in zero-dose children. This study explored the spatial pattern of zero-dose children aged 12-35 months in Ethiopia.

Methods: A survey was conducted in pastoralist regions, developing regions, newly-established regions, conflict-affected areas, underserved urban populations, hard-to-reach areas, internally displaced populations, and refugees and included a total of 3,646 children aged 12-35 months. Spatial autocorrelation was measured using the Global Moran's I statistic. Getis-Ord Gi* statistics was applied to calculate the spatial variability of the high and low prevalence rates of zero-dose children. The spatial interpolation technique was also applied to estimate unknown values that fall between known values. Inverse distance weighting interpolation method was used to predict the risk of zero-dose children. ArcGIS version 10.8 was used for the spatial analysis.

Results: The spatial distribution of zero-dose children aged 12–35 months in Ethiopia was non-random (Global Moran's I=0.178971, $p<0.001$). According to the hotspot analysis, Somali and Afar regions had the highest load of zero-dose children (hotspot areas) followed by the Northeastern part of Amhara and peripheral areas of Oromia region. On the other hand, SNNP, Sidama, and the Eastern part of the Southwest Ethiopia region were identified as cold spot areas. The spatial interpolation analysis corresponded with the hotspot analysis results where Afar and Somali regions were identified as high-risk areas for zero-dose children followed by the Northeastern part of Amhara and peripheral areas of Oromia region. However, Addis Ababa, Dire Dawa, Harari, Southern Nations, Nationalities, and Peoples, Sidama, Southwest Ethiopia, and parts of Oromia were found to be low-risk areas for zero-dose children.

Conclusion: The spatial analysis identified that zero-dose children had a significant spatial variation across the study areas where high clusters of zero-dose children were detected in Afar and Somali regions, followed by the Northeastern part of Amhara and peripheral areas of the Oromia region. Implementing routine and mop-up vaccination campaigns in the identified hotspot areas will help Ethiopia to improve coverage and reduce immunization inequalities.

Audience Take Away Notes

- Spatial distribution of zero-dose children aged 12-35 months in Ethiopia
- Areas with the highest load of zero-dose children (hot spot areas)
- Evidence to design interventions in the identified areas
- The different techniques to map zero-dose children which can also be applied to other public health problems

Biography

Fisseha Shiferie completed his master's in international public health from the French School of International Public Health in Paris, France and his Master of Pharmacology from Addis Ababa University, Ethiopia. Currently, he is a 3rd year PhD student at Addis Ababa University. He has been working for over 15 years in managerial, researcher and academician positions in research organizations, international NGOs and GOs including higher academic institutions. He has also worked as an expatriate in France, South Sudan, Ethiopia and Uganda. He is currently leading the Research, Learning and Publication unit at Project HOPE.

Gashaw Andargie Biks (PhD, Professor of child health and Public Health)[1*], Fisseha Shiferie[1], Dawit Abraham Tsegaye[1], Wondwossen Asefa[2], Legese Alemayehua, Tamiru Wondie[1], Gobena Seboka[1], Adrienne Hayes[2], Uche Ralph Opara[2], Meseret Zelalem[3], Kidist Belete[4], Jen Donofrio[5], Samson Gebremedhin[6]

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In-depth reasons for the high proportion of zero-dose children in underserved populations of Ethiopia: Results from a qualitative study

Background: Increasing attention is being given to reach children who fail to receive routine vaccinations, commonly designated as zero-dose children. A comprehensive understanding of the supply and demand -side barriers is essential to inform zero-dose strategies in high-burden countries and achieve global immunization goals.

Objectives: This qualitative study aimed to identify the barriers for reaching zero-dose and under-immunized children and what and explore gender affects access to vaccination services for children in Ethiopia. Data was collected between March-June 2022 using key informant interviews and focus group discussions with participants in underserved settings.

Results: The high proportion of zero-dose children was correlated with inadequate information being provided by health workers, irregularities in service provision, suboptimal staff motivation, high staff turnover, closure and inaccessibility of health facilities, lack of functional health posts, service provision limited to selected days or hours and gender norms viewing females as responsible for childcare. Demand -side barriers included religious beliefs, cultural norms, fear of vaccine side effects and lack of awareness and sustained interventions.

Conclusion: Recommendations to increase vaccination coverage include strengthening health systems such as services integration, human resources capacity building, increasing incentives for health staff, integrating vaccination services, bolstering the EPI budget especially from the government side and supporting reliable outreach and static immunization services. Additionally, immunization policy should be revised to include gender considerations including male engagement strategies to improve uptake of immunization services.

Key words: Supply And Demand Barrier, Gender Norms, Key Informant Interview, Focus Group Discussion.

Audience Take Away Notes

- By understand ing the various factors health policymakers and practitioners can use this knowledge to develop comprehensive information campaigns that tackle the misconceptions and fears surrounding vaccines while providing accurate, accessible and culturally sensitive information to caregivers

- Understand ing the diverse range of barriers contributing to the high proportion of zero-dose children is crucial for professionals in their job. By addressing these barriers comprehensively, professionals can ultimately contribute to reducing vaccine-preventable diseases and safeguarding the health and well-being of children
- The findings highlight the importance of addressing issues such as inadequate information provision, irregularities in service provision, staff motivation, accessibility challenges, gender norms and demand -side barriers. By incorporating these key findings into their own research or teaching, faculty members can contribute to the collective efforts aimed at improving vaccination coverage and reducing the prevalence of zero-dose children
- the high proportion of zero-dose children is influenced by both the supply and demand sides of immunization. Addressing this complex issue requires a comprehensive and integrated approach that strengthens the health system, promotes gender equality and fosters community engagement. By adopting these multifaceted strategies, we can work towards ensuring every child receives the life-saving benefits of vaccination, simplifying the task of designers and making the process more efficient
- By recognizing and understand ing these barriers, interventions can be designed to improve the accuracy of design, providing new information to assist in designing effective interventions. A multidimensional approach that targets health worker training, service provision, staff motivation, gender norms and demand-side barriers is crucial for achieving comprehensive immunization coverage and ensuring that every child has access to life-saving vaccines

Biography

Professor Gashaw Andargie Biks studied Public Health at the University of Gondar, Ethiopia and graduated with a diploma in 1992. He then joined the University of Gondar as a Graduate Assistant. He received his BSc degree at Jimma University 2001 and later obtained his master's degree in public health from Addis Ababa University. Furthermore, in 2013, he was awarded his PhD degree from the University of Gondar. Prof. Gashaw has worked at the University of Gondar in various capacities, including as vice president, lecturer and researcher. Currently, he has been working as a Senior Implementation Sciences Advisor at Project HOPE for the last two years. He has published over 120 research articles in SCI(E) journals.

Ghazala Rubi
Lahore General Hospital/Post Graduate Medical Institute Lahore, Pakistan

Covid-19 waves with associated variants & scenario in Pakistan

Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) is an enveloped RNA beta-coronavirus virus that is corona viridae-related. It originated in Wuhan, China in December 2019 and is known to cause COVID-19 illness. SARS-CoV-2posed a major threat to the world in concern of health along with trade and medical facilities. COVID-19 patients experience comorbid conditions like severe fever, typhoid, myocarditis, and a fatal black fungus attack. World Health Organization declared COVID-19 as an emergency on 30th January 2020 and a pandemic on 11th March. As of right now, COVID-19 has been verified to have infected over 100 million people across 210 nations, and 2 million of those infections have resulted in death. RT-qPCR (Reverse transcriptase qualitative PCR) test is performed if any symptoms exist, and isolation is necessary for three to five days after the confirmation. In Pakistan, it was reported firstly on 26th February 2020 by the Pakistan government when two persons were found infected with the disease. SARS-CoV-2 changes its genome constantly and results in the emergence of different variants in different waves. Pakistan has faced 6 sequential waves since 2020 to date, each associated with different variants and overlapping variants. The first wave was associated with B.1, B.1.471, B.1.36, second with B.1.36.31, B.1.247, B.1.1.1, B.1.160, B.1.471, B.1.562, B.1.1.7, B.1.1.250, B.1.261, B.1.351, P.1, third with B.1.1.7, B.1.351,P.1, B.1.617.2, B.1.36, B.1.468, B.1.1.413, A.27, fourth with P.1, B.1.617.2, fifth with Omicron (B.1.1.529) and sixth with new sub variants of Omicron (BA.4 & BA.5). In terms of severity and infectivity, Omicron and its sub variants differ from Delta and other SARS-CoV-2 variants. In this review, we have discussed SARS-CoV-2 spike mutations, its variants along with their origin& association to wave(s), and its scenario in Pakistan. Keywords: COVID-19; Coronavirus Variants; Waves in Pakistan; Mutations in SARS-CoV-2; Covid Prevalence.

Biography

Ghazala Rubi completed her Post graduation from Surrey University UK, trained at Royal Free London Hospital. She went back Pakistan & established Molecular Pathology services for Hospitals. She got another post-graduation from Bradford University. She got PhD in Human Genetics & Molecular Pathology. Vast experience of Molecular Genetics Pathology. She is Director of Research & Molecular Genetics Pathology, completed 26 Research Projects. National & International speaker at Conferences. She worked as frontline worrier for COVID-19 & did RT-PCR of 355000 tests of Patients. She got multiple awards for her tremendous work as WHO awarded her worth PCR Multiplex Machine.

Kaningini Furaha Gisèle
National Institute of Biomedical Research (INRB), Kinshasa, Democratic Republic of Congo

Enhancing vaccine supply chains

The Democratic Republic of Congo (DRC) faces multifaceted challenges in vaccine supply and logistics, hindering the efficient delivery and distribution of life-saving vaccines. This presentation delves into the complexities surrounding vaccine supply chains within the context of the DRC, exploring the intricate interplay of infrastructural limitations, geographical barriers, political instability, and socio-economic factors. For example, in July 2016, the Ministry of Health decided to delegate vaccine supply chain management functions from the Medical Stores Department (MSD) to the Expanded Program on Immunization (EPI) to reduce storage and distribution costs. A retrospective cost-minimization study was carried out to estimate the costs associated with storing and distributing vaccines to the EPI and MSD in 2018. In addition to delineating these barriers, the presentation will offer innovative strategies and best practices for optimizing vaccine supply chains in the DRC, such as:

1. **Predictive Analytics:** Using data analytics to forecast vaccine demand accurately for better planning and allocation.
2. **Cold Chain Optimization:** Implementing solar-powered refrigeration and temperature-monitoring devices to maintain vaccine integrity during storage and transportation, particularly in remote areas.
3. **Just-in-Time Manufacturing:** Adopting agile manufacturing processes to produce vaccines in response to real-time demand fluctuations, preventing overproduction or shortages.

Efforts are also underway in the DRC to strengthen governance frameworks, ensuring transparency, accountability, and equitable distribution of vaccines. These efforts include establishing guidelines for distribution, monitoring systems for tracking vaccine allocation, and addressing disparities in access to vaccines.

Audience Take Away Notes

- Insights into the logistical and infrastructural challenges of vaccine supply in the DRC
- Strategies for optimizing vaccine distribution using data analytics and cold chain innovations
- Governance mechanisms to ensure equitable access to vaccines across the country
- As for job, this information will equip the audience with practical solutions for improving vaccine logistics, which can be applied to enhance vaccine delivery systems in low-resource settings

Biography

Gisèle Kaningini is a senior logistician at the National Institute of Biomedical Research (INRB), with extensive experience in healthcare supply chain management. Passionate about healthcare logistics, she is dedicated to addressing the challenges of vaccine distribution in the DRC. Gisèle has led various initiatives aimed at optimizing supply chain processes, with a focus on ensuring equitable access to life-saving vaccines.

Harald Eugen Helling[1]*, Iewa Martinaityte[1], Rex Segadimo[2]
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A comprehensive intervention for TB-HIV co-infected patients in francistown, botswana: Integrating geriatric principles into infectious disease care

Background: Tuberculosis (TB) and HIV co-infection remains a significant public health challenge in Botswana, with a high mortality rate among affected individuals. While standard pharmacological treatments are effective, they often fail to address the broader health and wellness needs of these patients.

Objective: This study aims to evaluate the effectiveness of a comprehensive, non-pharmacological intervention program for TB-HIV patients in Francistown, Botswana. The complex intervention combines elements of traditional sanatoria treatment with a rational, pragmatic geriatric approach, focusing on enhancing physical health, nutritional status, treatment adherence, and geriatric medical follow-up.

Methods: A pilot study will be conducted with 60 TB-HIV co-infected patients, randomly assigned to either an intervention group or a control group. The intervention group will receive tailored physical training, nutritional support, and continuous geriatric monitoring. The control group will continue with standard care. The primary outcome measures will be mortality rate reduction, reduction in hospital admissions, and frequency of recurrent infections. Secondary outcomes include improved health-related quality of life and treatment adherence.

Results: While the study is ongoing, we anticipate that the integrated intervention will significantly reduce mortality and improve the overall health and quality of life of TB-HIV patients in the intervention group compared to the control group.

Conclusion: This study proposes a novel approach to managing TB-HIV co-infection by drawing on geriatric principles. If successful, this approach could be adapted and transferred for broader use in high-burden settings, particularly in areas requiring integrated care for chronic infectious diseases. We warmly welcome collaboration with other researchers, healthcare organizations, and funding bodies interested in joining us to further develop this project.

Audience Take Away Notes

- TB-HIV co-infected patients share similarities with geriatric patients, such as vulnerability and reduced health reserves.
- Geriatric medicine's holistic approach, which addresses the full spectrum of a patient's needs, could reasonably be applied to TB-HIV patients to improve outcomes
- Through this presentation, we aim to demonstrate the potential of integrating geriatric principles into the management of high-burden infectious diseases.

- We would welcome collaboration with other researchers, healthcare organizations, and funding bodies interested in joining this innovative project in Botswana.

Biography

Harald Eugen Helling is a senior consultant in geriatric medicine at the university hospital of Nothern Norway with additional specialty in both family medicine and internal medicine. He received a master degree in Business Administration with interest in international public health issues. He conducts a study where he compares Nursing Homes in Netherlands, Germany and Norway. He has research experience in coagulation disorders in critical care patients.

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

Experience and advice from single medical center: What we have learned from COVID-19 to unexplained serious Pneumonia?

During the past four years, the people all over the world have been struggling with COVID-19 and other terrible infectious disease. Fortunately, we have accumulated amounts of clinical experience in the diagnosis and treatment of unexplained pneumonia from COVID-19 that wasnot be listed in the literature.

The first serious COVID-19 patient with intubation in the Guangdong province, a case of severe ARDS with oxygenation index in 50, was successfully rescued in our ICU during the early outbreak stage in mid-January, 2020. Although we did not fully understand the terrible disease at that time, we had taken benefit treatment measures for unexplained pneumonia. And they have been consistently applied in clinical practice to this day.

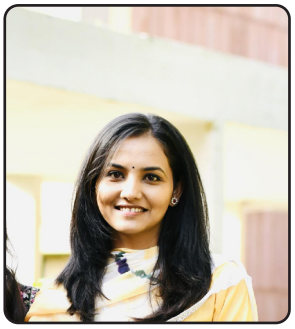
Performing intubation and sending mNGS for inspection in severe hypoxemia associated with infection as soon as possible, can greatly shorten our diagnosis time in around 24 hours. Large dose of vitamin C (4–10 g/day) for the fulminant myocarditis and sepsis is required to alleviate oxidative stress. Acute exudative lesions or alveolar consolidation follows the subpleural pathway may be related to immune reaction which make methylprednisolone therapy in need. It also means the possible lesions of distal branches of pulmonary blood vessels. Hemoptysis, thrombosis in situ, acute pulmonary fibrosis like changes and pulmonary hypertension indicate that the pathogen has affected the pulmonary vascular endothelium. Refractory hypoxemia is often a thorny problem that needs to be solved for unexplained pneumonia. Its treatment strategy not only includes prone ventilation and early CRRTbut also includes continuous anticoagulation, reducing pulmonary hypertension and protection of alveolar epithelium and vascular endothelium. Nafamostat, as a new anticoagulant targeting immune thromboembolism has shown promising potential in alleviatingacute fibrosis in some patients.

Audience Take Away Notes

- mNGS can quickly provide important clues for unknown infectious diseases
- Corticosteroids, vitamins and low molecular weight heparin have unique effects in unexplained pneumonia. They directly or indirectly protect the alveoli, myocardium and pulmonary vascular endothelium, respectively
- The lesions distribution of immune related unexplained pneumonia havetheir own characteristics. They may be distributed in the outer periphery of the lung field more than in the center
- Stubborn hypoxemia caused by unexplained infections may imply simultaneous involvement ofalveoli and pulmonary vessels

Biography

Dr. Hua Luo, MD, Chief Physician, Director of Medical Intensive Care Unit, Peking University Shenzhen Hospital, SCIE Journal reviewer, had published more than 10 papers. Dr. Hua Luo graduated from Peking University (PKU) and works in the affiliating hospital of Peking University. He specializes in Critical Care Medicine (CCM) as well as Pulmonary Vascular Diseases (PVD). He isproficient in treatment for complicated hypoxemia, thrombosis, sepsis, MODS, etc. He was absorbed as the collaboration member of famous international trials SAFE TRIP and FLUID TRIP. In 2020, hefirst reported the phenomenon of acute pulmonary hypertension induced by COVID-19 in the world.



Ishwerpreet Kaur Jawanda*, Thomson Soni, Seema Kumari, Vijay Prabha

Department of Microbiology, Panjab University, Chandigarh, India

Identifying key proteins associated with infertility induced by sperm immobilizing staphylococcus aureus in murine vaginal lavage fluid

In the context of a rapidly growing global population, the struggles and suffering of infertile couples deserve attention, underscoring the paradox of waning concerns about fertility. This research is based on the overlooked role of bacterial infections in female infertility. The study explores the proteomic analysis of pooled vaginal lavage fluid obtained from female BALB/c mice administered with 108 cfu of sperm immobilizing S. aureus in 20 µl PBS (test group, n=10) or 20 µl PBS alone (control group, n=10) via the intravaginal route for ten consecutive days; with a particular focus to detect the anti-fertility signature protein(s) associated with S. aureus induced infertility. Nano-LC-MS/MS analysis yielded five distinct bacterial proteins in the test group and no bacterial proteins in the control group, indicative of a vigorous proteomic response to bacterial exposure. Using gel filtration chromatography, the elution profile of test Vaginal Lavage Fluid (VLf) revealed a single prominent peak in the test group sample, that was further assessed for purity with SDS-PAGE indicating one unique protein band (~36 kDa). This protein aligned with GMP reductase, identified through protein profiling. Further, when the purified protein was tested for its impact on sperm parameters, the results showed that it impaired the sperm motility and viability in a concentration-dependent manner and disrupted sperm structural integrity when studied by using FE-SEM. Moreover, when the binding studies using FITC-labelled purified protein were conducted, it depicted presence of green fluorescence over entire surface of mouse spermatozoa. These results were akin to Sperm Immobilization Factor (SIF), already isolated and characterized in our laboratory, from culture supernatant of S. aureus, causing sperm impairment. Hence, taking into account all these factors, this protein (VLf) was designated as Vaginal Lavage fluid-derived Sperm Immobilization Factor (VLf-SIF). Through in-silico analysis, superimposition of VLf-SIF and SIF, already known to show sequence homology to cysteine-tRNA ligase, revealed close structural alignment, suggesting functional equivalence in sperm immobilization. Henceforth, this investigation provides compelling evidence for VLf-SIF, identified as GMP reductase, as a pivotal anti-fertility factor behind this bacterial-induced infertility.

Audience Take Away Notes

- This research highlights the significant influence of bacterial infections on female infertility, providing crucial insights into the antifertility factors involved.
- Attendees will learn about the significant impact of Staphylococcus aureus-derived proteins on female infertility, specifically focusing on the identification of VLf-SIF as an anti-fertility factor.
- By identifying key proteins associated with bacterial-induced infertility, this research aims to establish a basis for developing reliable diagnostic biomarkers, paving the way for innovative approaches to address this pressing global health issue.

Biography

She is currently pursuing a Ph.D. in the Department of Microbiology at Panjab University, Chandigarh, India under the supervision of Dr. Vijay Prabha and Dr. Seema Kumari. She completed her integrated undergraduate and postgraduate program as a gold medalist at the Department of Microbiology, Punjab Agricultural University, Ludhiana, India. She has 14 publications in both national and international journals.

Jamie Platt[1]* PhD, Yoichi Furuya[2] PhD, Andrea Kinga[3] PhD
[1]Pictor Inc., San Diego, California, USA
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[3]Pictor Ltd., Auckland, New Zealand

Next-generation proteomics for increased access to infectious disease testing for both human and animal health

Global access to accurate diagnostics for infectious diseases remains a critical challenge, particularly in low-resource settings. Access to accurate, sensitive infectious disease testing, is especially important in managing population health, epidemics and pandemics that have major health economic impacts. Affordable and accurate testing is crucial for improving healthcare access and reducing the global burden of infectious diseases. Traditionally, the most affordable testing is based on a single analyte, often requiring follow-up or reflex testing to rule out causative agents. However, multiplexing enables testing for multiple diseases (diagnostic breadth) or detecting disease at various stages (diagnostic depth) in a single test with a streamlined workflow, thereby increasing diagnostic yield.

Pictor has developed an advanced ELISA-based proteomics platform aimed at delivering precise and efficient diagnostic solutions for complex and infectious diseases in both animal and human health. This platform significantly boosts productivity by incorporating multiple antigens or antibodies into each well of a 96-well plate, delivering comprehensive diagnostic information in less than 2.5 hours from multiple specimen types, including saliva. Analytical performance data from several human infectious disease panels, including HIV/Hepatitis panel, Dengue/Zika panel, and SARS-CoV2 will be discussed. In addition, data from extensive validations of Mycoplasma bovis for animal health will also be presented. The presentation will highlight the flexibility of the platform for applications spanning research, clinical diagnostics, to epidemiological surveillance, and as a robust tool for improving health economic outcomes and the global burden of infectious diseases.

Audience Take Away Notes

- They will learn about a new technology to assist with their research or other applications for infectious diseases in humans and animals
- It will provide them with information about a more productive tool and ideas for how they may be able to multiplex their biomarker testing
- Other faculty could use this research to expand their research or teaching, as it also highlights information about non-traditional specimen types
- It provides a practical solution
- It will provide new information with the potential to better address a problem

- Opportunities to accelerate research through an affordable proteomics solution

Biography

Jamie brings 20 years of progressive leadership in genomics and molecular diagnostics, guiding teams in developing, validating, and commercializing more than 40 innovative, high-complexity molecular tests for US and global firms (both LDTs and IVDs). Dr. Platt earned her Ph.D. in Molecular & Cellular Biology from Oregon State University and completed Post-Doctoral studies at University of California at Berkeley. She is founder and CEO of BRIDGenomics, a molecular diagnostic laboratory consulting firm and serves on the boards of Pictor, Ltd., DxTerity Diagnostics and bioAffinity [BIAF]. Jamie is passionate about leveraging her expertise in product development and clinical laboratory operations using Six Sigma methodologies to create innovative products impacting clinical markets. She is an industry-recognized peer educator and speaker, holds multiple US and international patents and has authored numerous peer-reviewed publications.

Kadesh Daniels[1*], Chistopher L. Kiker[2]

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[2]Family Medicine, Northeast Georgia Physicians Group, Toccoa, GA, USA

Blind spot: A case of ocular syphilis in a patient with HIV

Ocular syphilis is a rare and potentially blinding complication of localized Treponema pallidum infection. Unlike the typical progression of syphilis through the primary, secondary, latent and tertiary stages with distinct, accompanying symptoms, ocular syphilis can occur at unpredictable intervals during the course of T. pallidum infection with vague symptoms that often mimic other diseases. Therefore, high clinical suspicion is necessary for accurate diagnosis— especially in the absence of common manifestations such as palmar rash, genital lesions and vision changes.

Furthermore, the synergistic interaction of HIV and Syphilis not only increases the likelihood of coinfection but also increase the risk of neurosyphilis in HIV patients. The case aims to highlight the clinical manifestations of ocular syphilis in an HIV patient and underscore the importance of considering this diagnosis in high-risk populations with unexplained ocular symptoms.

This is a case of a 37 YO male, with a history of HIV and suppressed viral load, who presented with a one-week duration of pressure-like pain, swelling, conjunctivitis and purulent discharge of the right eye with accompanying right-sided pressure-like headache. Patient stated that one month prior, eye examination revealed increased pressure of the right eye without vision changes or additional symptoms. Patient reported HIV medication compliance and review of medical records confirmed suppressed viral load but, with an increased viral load and decreased CD4 count compared to 3 months prior. Patient denied sexual activity during the past year. HEENT and Neurologic examinations were positive for bilateral conjunctivitis with crusted discharge but otherwise unremarkable. Lab results were significant for inflammatory markers (elevated platelets, C reactive protein and erythrocyte sedimentation rate). Head CT was negative for abnormalities. Initial trial of Valacyclovir and Polymyxin B sulf-trimethoprim failed to resolve symptoms. Patient then presented with worsening of initial symptoms in addition to bilateral otalgia, tinnitus and facial maculopapular rash. Further testing demonstrated a positive RPR and patient was referred to the hospital where additional testing demonstrated positive treponemal Ab with titer of 1: 128. CSF analysis showed elevated protein and white blood cell count– lymphocyte predominant–but negative CSF VDRL. Based on these findings, treatment with penicillin G was commenced with resolution of symptoms following treatment.

Due to the rise in syphilis cases globally and potential complications of undiagnosed disease, healthcare providers must maintain a high index of suspicion for ocular syphilis, particularly in patients with risk factors such as HIV infection or multiple sexual partners. Early detection and intervention is necessary to prevent severe complications and improve patient outcomes.

Audience Take Away Notes

- Demonstrate the vague presentation of ocular syphilis in order to emphasize the importance of heightened clinical suspicion for the diagnosis
- Highlight the association between syphilis and HIV whereas neurosyphilis may be more likely to occur in HIV positive patients
- Emphasize the importance of early intervention to provide resolution of symptoms and betterment of patient outcomes
- Serve to underscore public health awareness of the increasing incidence of syphilis cases and emphasizes the need for physician-patient discussion of safe sex practices and STD testing

Biography

Kadesh Daniels is a passionate fourth year medical student at the Medical College of Georgia. Her intellectual curiosity and commitment to lifelong learning has fueled her involvement in research since her freshman year of college and throughout medical school. As such, she has had the privilege of achieving multiple publications and presentations at national conferences. As an aspiring Anatomic and Clinical Pathologist, she hopes to forage a career as a physician scientist to aid in the collect effort of medical advancement.

Lindsay Parish* PhD, Daniel Wolfe PhD
Division of Chemical, Biological, Radiological and Nuclear (CBRN) Countermeasures, Biomedical Advanced Research and Development Authority (BARDA), Administration for Strategic Preparedness and Response (ASPR), U. S. Department of Health and Human Services (HHS), Washington, DC, USA

Current investments and future directions of biomedical advanced research and development authority's CBRN vaccines portfolio

The mission of the Biomedical Advanced Research and Development Authority (BARDA) as part of the Administration for Strategic Preparedness and Response within the U. S. Department of Health and Human Services, is to enhance the U. S. government's capability to respond to Chemical, Biological, Radiological and Nuclear (CBRN) threats, pand emic influenza and emerging infectious diseases by investing in the advanced development and procurement of an array of medical countermeasures. Anthrax, smallpox and multiple different filovirus species are priority biological threats addressed within BARDA's current portfolio of CBRN vaccine advanced development and procurement programs. Over the past ten years, some of these CBRN vaccine investments have helped contain outbreaks and prevent further spread of diseases, such as Ebola and Mpox, that pose public health concerns. To enhance preparedness for priority CBRN threats as well as other emerging threats, BARDA is focusing on three Areas of Interest in the BARDA Broad Agency Announcement (BAA-23-100-SOL-00004). First, BARDA seeks proposals for development of flexible vaccine manufacturing technologies that can be applied to rapidly develop and manufacture a range of different vaccines against a range of threat agents. Second, BARDA is interested in the proof-of-concept application of needle-free delivery technologies for a licensed vaccine for a CBRN threat to improve the operational logistics of vaccine administration in a response scenario. Finally, since there are currently no licensed vaccines for Orthomarburgvirus and Orthoebolavirus sudanense, BARDA seeks to advance the development of vaccines for these filoviruses. BARDA looks to engage vaccine developers through the BAA and other funding opportunities. Any vaccine or vaccine-related technology developer interested in working with BARDA is encouraged to apply to the TechWatch program to receive feedback before submission of an application to the BAA.

Audience Take Away Notes

- The audience will gain insight into BARDA's current CBRN vaccine portfolio, BARDA's funding opportunities for vaccine development against CBRN threats and the plans to improve preparedness for biological threats using vaccine and manufacturing technologies
- This presentation provides an overview of funding opportunities available at BARDA to support vaccine development, including flexible manufacturing technologies and platforms, improvement of operational logistics of mass vaccine administration and advanced development for vaccines against priority threat pathogens
- The presentation will highlight opportunities and ways to connect with BARDA for funding and vaccine development support
- By understand ing BARDA's priorities for vaccine development, a researcher/designer could incorporate these requirements early in the development process to enhance the chances of success for obtaining future funding from BARDA

- This presentation will provide information on criteria to consider in vaccine cand idate design for threats such as anthrax, filoviruses, smallpox and other emerging infectious diseases
- Participants will have a better understand ing of federal resources available at BARDA to support vaccine development as well as funding opportunities

Biography

Dr. Lindsay Parish joined the CBRN Vaccines team at BARDA in 2020 and is supporting vaccine development programs for Marburg virus, Sudan ebolavirus and anthrax. Prior to joining BARDA, Lindsay was a Program Manager and Senior Infectious Disease Advisor with the US Agency for International Development (USAID). At USAID, Dr. Parish led partnerships between US and international universities and research centers, utilizing her expertise in infectious diseases to help improve global health security. Lindsay did postdoctoral training at the Johns Hopkins Malaria Research Institute, earned her Ph. D. in Microbiology from the University of Alabama at Birmingham and her B. S. in Microbiology from the University of Texas at Austin.

Madhu Khanna[1]*, Nilanshu Manocha[2], Daphne Laubreton[3], Jacqeline Marvel[3], Prashant Kumar[2]

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Development of a polyepitope-based immunogen for inducing cellular immunity against all dengue virus serotypes

Dengue, a significant global health challenge, is caused by four co-circulating serotypes (DENV 1-4) of the virus. Viral infections not only result in health complications and fatalities among infected individuals, but it also depletes limited resources intended for preventing infections. The only licensed vaccine against dengue exhibit variable efficacy based on host factors and primary stimulate humoral response. It also has low efficacy in children and dengue-naive individuals. The development of an effective vaccine is critical to minimize the spread and impact of this infection. In our study, we address this challenge by developing a polyepitope-based immunogen that induces active cellular immunity against DENV all serotypes. Our preclinical investigation explored the potential of priming CB6F1 mice with CD8+ T cell epitopes from all four DENV serotypes simultaneously to induce protective cellular immunity against all serotypes. A chimeric peptide, comprised of T-cell epitopes from conserved domains of the DENV envelope protein, was designed and validated using advanced immunoinformatics tools. Subsequently, the cellular immune response was demonstrated by the development of IFNγ and TNFα producing CD8+ T cells in immunized mice. These specific CD8+ T cell responses were elicited against a pool of DENV peptide epitopes from all serotypes, evident in both ex-vivo and in-vitro experiments.These results provides a robust basis for conducting in-vivo evaluations, representing a substantial advancement towards comprehensive and effective dengue vaccine.

Biography

Professor Madhu Khanna heads the Virology Unit at the Department of Microbiology, Vallabhbhai Patel Chest Institute, University of Delhi, India. Professor Khanna has dedicated over 30 years in research and diagnosis of viral diseases. Her work involves developing innovative antiviral and vaccine delivery strategies to mitigate outbreak risks from emerging and re-emerging viruses, like, influenza, dengue, chikungunya, SARS-CoV-2. Professor Khanna is honored with numerous international and national awards. She has several publications in journals of national and international repute. Her laboratory is designated ICMR-'Virus Research & Diagnostic Laboratory' and was instrumental in providing diagnostic services during influenza and COVID-19 pandemics.

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Parvovirus B19 infection and auto-immunity diseases

Human Parvovirus B19 infection is responsible for a wide range of human diseases ranging from mild erythema infectiosum in immunocompetent person to fetal loss in primary infected pregnant women and aplastic anemia or lethal cytopenias in adult immunocompromised patients. A variety of further manifestations are associated with the infection such as arthralgias, arthritis, leukopenia and thrombocytopenia, anemia and vasculitis, spontaneous abortion and hydrops fetalis in pregnant women. Both in children and adults Parvovirus B19 infections have been frequently implicated as a cause or trigger of various forms of autoimmune diseases affecting joints, connective tissue and vessels. In addition, autoimmune neutropenia, thrombocytopenia and hemolytic anemia are known as sequelae of B19 infection.

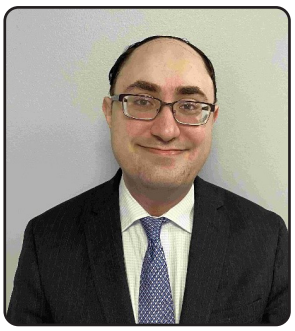
Since persistent viral infection is responsible for an autoimmune response and clinical symptoms can mimic autoimmune inflammatory disorders, parvovirus B19 is the object of intense efforts to clarify whether it is also able to trigger autoimmune diseases. Indeed, the virus has been implicated as the causative or the precipitating agent of several autoimmune disorders including rheumatoid arthritis, systemic lupus, antiphospholipid syndrome, systemic sclerosis and vasculitides.

Production of a variety of autoantibodies has been demonstrated to occur during B19 infection and these have been shown to be key to the pathogenesis of the particular disease process in a significant number of cases, for example, production of rheumatoid factor in cases of B19-associated rheumatoid arthritis and production of anti-glutamic acid decarboxylase (GAD) in patients with B19-associated type 1 diabetes mellitus.

Molecular mimicry between host and viral proteins seems to be the main mechanism involved in the induction of autoimmunity. By means of a rand om peptide library approach, we have identified a peptide that shares homology with parvovirus VP1 protein and with human cytokeratin. Moreover, the VP peptide shares similarity with the transcription factor GATA1 that plays an essential role in megakaryopoiesis and in erythropoiesis. These new data sustain the role played by molecular mimicry in the induction of cross-reactive (auto)antibodies by parvovirus B19 infection.

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 of Mohammedia in Morocco and also with a university degree in Advanced Immunology. Majda BOURADDANE is a PhD student researcher from the CLAUDE BERNARD University of Lyon-2012-2016 in allergology immunology. Majda BOURADDANE research 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 in Marrakech, Morocco 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.



Mazen A. Hasan
Department or Internal Medicine, Garden City Hospital, Garden City, MI

Hyperlactatemia in septic shock, unmasking the false notion; An intriguing case report

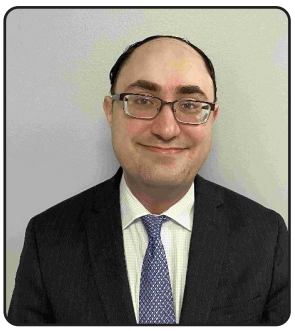
Sepsis is defined as a life-threatening dysregulated body response and systemic inflammation to an infection. Septic shock is a subset of sepsis which has cellular, metabolic and circulatory abnormalities leading to the shift of aerobic respiration to an anaerobic pathway with resultant lactic acidosis. It is a vasodilatory shock and a continuum of severity extending from infection and bacteremia to septic shock. A patient with septic shock progresses from a compensated state (flash capillary refill less than 2 seconds, warm extremities) to a decompensated state (cold, clammy skin, delayed capillary refill and thready pulses). The burden of sepsis and septic shock has consistently increased over the years, affecting millions of people around the globe every year.

This study illustrates a case of 49 years old female, who presented to the emergency department with intractable back pain, attributed to her caregiver services for her disabled sister. On examination, she was febrile, hypotensive with MAP less than 65 mm Hg, cool, mottled skin and capillary refill was greater than 5 seconds. Based on surviving sepsis campaign guidelines, balanced crystalloid and empiric antibiotics were initiated immediately. The patient was started on vasopressors because she did not respond to fluid resuscitation and was ultimately transferred to the intensive care unit. Diagnostic studies were carried out which revealed MRSA bacteremia on blood culture, elevated C reactive protein and pulmonic valve vegetation on transesophageal echocardiogram. Interestingly, white cell counts and lactate levels were normal throughout the hospital stay. The patient had a contributing risk factor of a recent glucocorticoid injection leading to sepsis and septic shock. The diagnosis was particularly made based on the clinical features of fluid refractory hypotension, fever and signs of end-organ hypoperfusion such as delayed capillary refill.

Conclusion: Clinical examination is becoming obsolete with time and clinicians are relying more on laboratory findings. This study emphasizes that a thorough bedside physical examination should always remain the cornerstone of clinical practice in managing the patient during the initial hours of critical illness and laboratory values supplement the diagnosis of sepsis and septic shock. Furthermore, early identification of septic shock and appropriate treatment within the first three hours have a positive impact on quality of life as well as morbidity and mortality.

Biography

Mazen Hasan was born and raised in the Detroit metropolitan area. He earned his undergraduate degree in Biomedical Sciences from Oakland University, and his Masters in Physiology at the University of Michigan before earning his Doctor of Osteopathic Medicine degree at the Chicago College of Osteopathic Medicine. He is currently completing his internal medicine residency at Garden City Hospital in Michigan, and he has a strong passion for infectious disease, and he particularly interested in how infectious diseases have shaped human history. He hopes to one day work as an infectious disease physician.



Mazen A. Hasan[1]* DO, Leonard B. Johnson[2] MD, FACP

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Psoas abscess due to group B streptococcus presenting as diabetic ketoacidosis

Introduction: Psoas abscess is an uncommon infection that typically presents with fever and back pain. The most frequently identified pathogen is Staphylococcus aureus. We present a diabetic patient presenting with Diabetic Ketoacidosis (DKA) due to a Streptococcus agalactiae psoas abscess.

Case: A 60-year-old male with a past medical history of type 2 diabetes mellitus presented to the hospital with a chief complaint of right-sided back and leg pain. He also reported polyuria and polydipsia but denied any fevers or chills. He also reported abdominal pain and a 30-pound weight loss over the last month. On presentation, his physical exam revealed no abdominal tenderness but some weakness in the right leg. He was found to be in DKA and started on insulin and IV fluid infusion but his DKA failed to resolve despite appropriate treatment. A CT of the abdomen and pelvis was performed and revealed a 4.5 x 4.7 cm right psoas muscle abscess and an adjacent 5.2 x 2.5 cm right inferior posterior pararenal abscess with concurrent right hydronephrosis. A urine culture revealed mixed urogenital flora with 5,000-10,000 CFU of S. agalactiae and he was started on ceftriaxone and metronidazole. Percutaneous drainage of the abscess also grew S. agalactiae. His symptoms and DKA resolved following these interventions and he was later discharged on oral cephalexin for 8 weeks with plans to have repeat imaging as an outpatient.

Discussion: Psoas abscesses typically occur either through hematogenous spread from another infection site or direct spread from another closely located structure such as in vertebral osteomyelitis, diverticulitis, appendicitis, and pyelonephritis. Signs and symptoms can often be nonspecific and include fevers as well as abdominal, back, and leg pain. As with our patient, the lack of specific symptoms may delay the diagnosis. As always in patients presenting with DKA, underlying infection should be ruled out. Streptococcus agalactiae is an uncommon pathogen, causing 1% of psoas abscesses but invasive group B streptococcus infections are increased among diabetics. Clinicians should consider appropriate imaging in patients with back pain and an increased suspicion of underlying infection such as in patients presenting with DKA.

Audience Take Away Notes

- Provide an example of an atypical presentation of infection which was not diagnosed initially at presentation and how to recognize similar cases
- Explore the common pathogens, presentations, and sequelae of psoas abscesses including potential spread to nearby structures and the importance of timely diagnose due to morbidity and mortality
- Discuss how a symptoms of leg pain can be a sign of numerous intra-abdominal pathologies and infections
- Discuss the value and significance of the Psoas Sign on a physical examination, and how it can be used as a sign of not just appendicitis

Biography

Mazen Hasan was born and raised in the Detroit metropolitan area. He earned his undergraduate degree in Biomedical Sciences from Oakland University, and his Masters in Physiology at the University of Michigan before earning his Doctor of Osteopathic Medicine degree at the Chicago College of Osteopathic Medicine. He is currently completing his internal medicine residency at Garden City Hospital in Michigan, and he has a strong passion for infectious disease, and he particularly interested in how infectious diseases have shaped human history. He hopes to one day work as an infectious disease physician.

Surya Suvvari, Megha Mummalaneni*, Gary Nguyen
University of Nevada, Reno, School of Medicine, Reno, Nevada, United States

Using google trends to gain insight into COVID-19 hesitancy distribution in the United States

Google Trends, launched on May 11, 2006, serves as a valuable research tool across various healthcare topics. It analyzes daily Google Searches in the United States, offering geographic and temporal pattern data for searched terms. Instead of surveying user-stated preferences, it provides insight into actual user behaviors. Widely regarded as a reliable, fast and cost-effective data collection method, Google Trends is utilized in social sciences research. However, concerns about data reproducibility and inconsistencies have been raised over time. In the context of the ongoing debate on vaccines in the United States, vaccine hesitancy, ranging from acceptance to refusal, has gained prominence. Research indicates a significant rise in vaccine hesitancy, particularly in the Americas compared to Europe and the Western Pacific Region. This study aimed to determine whether Google Trends data can predict vaccine hesitancy in the United States by comparing it with CDC reports. It was hypothesized that specific Google Trends search terms would accurately reflect the COVID-19 vaccine hesitancy distribution reported by the CDC.

CDC county vaccination hesitancy rates were averaged for each state as a control. After comparing multiple search terms, the two with the highest search rates during the same period as the CDC study were “COVID vaccine near me” and “COVID vaccine side effects”. For each search term, the relative search rate on a scale from 1 to 100 was obtained from Google Trends. A linear regression was calculated between the values for each state for the search term “COVID vaccine side effects” and the average vaccination hesitancy from CDC. The search term “COVID vaccine near me” represented the inverse of vaccination hesitancy, so the values were subtracted from 100 to represent vaccination hesitancy. Following that subtraction, a linear regression was calculated between the values and the CDC vaccination hesitancy values.

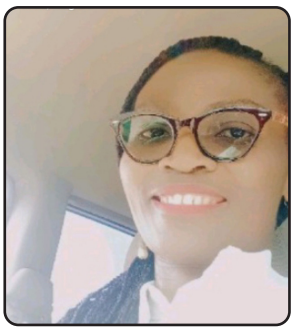
There was no significant correlation between CDC vaccination hesitancy and the Google Trends search term "COVID vaccine near me" ($F1, 48=2.19$, $p>.05$). However, a significant correlation existed between CDC vaccination hesitancy and the search term "COVID vaccine side effects" ($F1, 47=17.9$, $p<.05$), emphasizing the need for refining search terms in Google Trends. Limitations of Google Trends include assumed correlations between chosen search terms and negative connotations of vaccine hesitancy. For instance, searches for "COVID vaccine side effects" could indicate preparation for vaccination or hesitancy. Despite these limitations, Google Trends offers nuanced insights into public sentiment on topics likeCOVID-19 vaccine hesitancy, avoiding the Hawthorne Effect present in traditional surveys. Utilizing anonymized Google Search Histories, it captures unfiltered public sentiments on debated topics. Future studies could compare Google Trends data with research on political affiliations regarding attitudes toward COVID-19 vaccination, distinguishing between pro and anti-vaccine sentiments.

Audience Take Away Notes

- This presentation demonstrates how Google Trends can present data similarly to those provided by organizations such as the CDC
- This experiment emphasizes the importance of using refined search terms in Google Trends when attempting to formulate a research hypothesis
- The advantages and disadvantages of using a set of information from a nuanced database such as Google Trends

Biography

Megha graduated from the University of Nevada, Reno with a BS in Neuroscience in May of 2023. She is currently a first-year medical student at the University of Nevada, Reno, School of Medicine with an interest in the specialty of Psychiatry. She is working in a research group under Dr. John Westhoff, MPH, MD–Assistant Dean of Student Research and board-certified Emergency Medicine Physician.



Mmuoegbulam Augusta Oluchi
Department of Microbiology, Faculty of Biological Sciences, University of Calabar, Calabar, Cross River State, Nigeria

Microbiological and phytochemical analysis of Curcuma longa and evaluation of the antibacterial activity of the phytochemical components

The inefficiency of current drugs in the treatment of diseases orchestrated by bacterial resistance has been a global public health challenge. This work was therefore conducted to evaluate the microbiological quality, phytochemical and antibacterial potentials of three different *Curcuma longa* samples-fresh (rhizoid) and powdered (refined and locally processed) *C. longa*. The mean bacterial count in the samples ranged from 3. $4x10^6$ CFU/g for refined *C. longa*, 5. $1x10^6$ CFU/g for locally processed *C. longa* to 9. $6x10^6$ CFU/g for fresh *C. longa*, while the result of the mean fungal count was $5.3x10^s$ CFU/g for fresh *C. longa*, 1. $4x10^s$ CFU/g and 1. $2x10^6$ CFU/g for locally processed and refined *C. longa* samples respectively. The bacterial isolates from the three samples were of the genera *Staphylococcus*, *Bacillus*, *Listeria*, *Pseudomonas*, *Escherichia* and *Salmonella*, while the fungal isolates enumerated were of the genera *Cand ida*, *Fusarium*, *Aspergillus* and *Rhizopus*. Out of the four phytochemical constituents (steroids, alkaloids, phenols and flavonoids) qualitatively analyzed for in the fresh and the two powdered *C. longa* samples, three (steroids, flavonoids and alkaloids) were present while phenol was absent in all the samples. Only the alkaloid constituent from all samples exhibited antibacterial activity against clinical *Pseudomonas aeruginosa*, *Klebsiella Pneumoniae* and *Escherichia coli* isolates at 100% concentration, whereas *Staphylococcus aureus* was resistant to the same alkaloid isolated from all samples at 100% concentration. However, the antibacterial activity of the alkaloid from fresh *C. longa* was slightly increased based on its higher zones of inhibition compared to the results from the powdered samples.

Audience Take Away Notes

- The presentation highlights the major phytochemical constituents of *Curcuma longa* and their antibacterial potential against important disease pathogens
- The antibacterial activity property of the evaluated component emphasizes the importance of alkaloids in the treatment of disease and its incorporation during drug discovery especially in synergism with available antibiotics
- Researchers can leverage from this presentation and explore other pathogens that would be susceptible to the other phytochemical components of *C. longa* to which the clinical isolates in this study were resistant to
- This study proffers solution to antibiotic resistance as patients can easily incorporate powdered *C. longa* that are of microbiological stand ard into their diets for a quick relief through the synergistic effect of all the phytochemical constituents of *C. longa*

Biography

Mmuoegbulam Augusta Oluchi is a researcher and lecturer in the Department of Microbiology with specialization in Pathogenic Microbiology and Public Health. Mmuoegbulam Augusta Oluchi did Ph. D research internship in CPQBA, University of Campinas, Brazil. Mmuoegbulam Augusta Oluchi is an adjunct Faculty in Texila American University and currently a Research Scholar in Griffith Institute for Drug Discovery, Griffith University, Nathan Campus, Queensland - Australia.

Patrycja Dolibog[2*] PhD, Paweł Dolibog[1] PhD,, Klaudia Kierszniok[2] M. A

[1]Department of Biophysics, Faculty of Medical Sciences in Zabrze, Medical University of Silesia

[2]Department of Medical Biophysics, Faculty of Medical Sciences in Katowice, Medical University of Silesia

The influence of physical factors on recombinant human serum Albumin

Human serum albumin, a key blood plasma protein, plays an important role in vaccine production. It is not only a stabilizer, but also a basic ingredient of some preparations, which emphasizes its fundamental importance in medical biotechnology. Studying the effects of physical factors on recombinant human serum albumin is crucial for improving vaccine stabilization and production. During the presentation, I will discuss the fluorescence spectroscopy method as an effective tool for understand ing the structure and behaviourof albumin. Additionally, I will emphasize the importance of measuring viscosity and electrical parameters to fully understand its physical properties. This research has the potential to improve production processes and stabilize vaccines, which is an important step in the development of new protein-based therapies.

Biography

Patrycja Dolibog is a biophysicist whose research focuses on the use of modern physiotherapeutic methods and supporting the healing of soft tissues. Currently, Patrycja Dolibog serves as a research and teaching assistant professor and head of the Department and Department of Medical Biophysics at the Faculty of Medical Sciences in Katowice of the Medical University of Silesia. Patrycja Dolibog is the author and co-author of many scientific publications, including articles in renowned medical journals, which contributed to expanding knowledge about the impact of physical factors on the humanbody. Patrycja Dolibog research mainly focuses on examining the possibilities of therapeutic use of physical therapies in the wound healing process. Additionally, Patrycja Dolibog is a member of the Polish Society for Wound Treatmentand the Polish Society of Medical Physics. She completed a training internship at IDT Biologika Corporation (Rockville, USA).

Prachi Bhanvadia* MD, Roshniben Patel MD, Ravindra Karmarkar MD

Department of Internal Medicine, Ascension St Agnes, Baltimore, Maryland, USA

Rare case of clostridium cadaveris in an immunocompromised patient with metastatic rectal adenocarcinoma

Case of a 50 y/o patient with metastatic rectal adenocarcinoma on 5th line chemotherapy who presented with fever and anemia. Was found to have blood cultures positive for Clostridium cadaveris that remained positive for 10 days despite broad spectrum antibiotics. The case discusses the incidence, rarity and varied etiology and management of the infection. Clostridium cadaveris is rarely responsible for causing clinical pathology. Only 8 cases have been documented till date causing bacteremia from GI source, osteomyelitis or bacterial peritonitis. Usual underlying risk factors include immunosuppression, decubitus ulcer, cardiovascular disorders, diabetes mellitus, bowel necrosis etc. Significant mortality is associated with the infection. It is not clear if the infection itself is robust enough to cause the mortality or is it the underlying limited and poor prognosis due to immunosuppression that is responsible for causing the detrimental outcome.

In terms of management, no proposed regimen is available.

The case is unique in terms of its rare incidence. This presentation will be an opportunity to bring to light the details of such a case and reflect in brief regarding the finesse of management of such an infection in an already immunocompromised patient and the need to have a broad differential.

Audience Take Away Notes

- Understand the clinical presentation and epidemiology of the disease
- A preliminary diagnostic bundle for the infection, other contributing risk factors
- The importance of anaerobic blood cultures in susceptible cases and importance of close monitoring in an immunocompromised patient that can help other physicians in a similar situation
- Lastly, getting into the depth of possible first line management of the infection and choices of antibiotics given there is no regimen available till date

Biography

Dr. Prachi Bhanvadia, a second year resident physician in Internal Medicine from Ascension Saint Agnes Hospital. Joined residency in 2023 after graduating MBBS from Government Medical College Surat, India in 2022.

Priscilla
Atlanticare Regional Medical Centre, United States

Unilateral endophthalmitis caused by streptococcus pneuemonia

Introduction: Endophthalmitis is a rare infection of the interior eye by bacteria or fungi. These infections are usually exogenous and are caused as a complication of ophthalmic procedures or penetrating ocular traumaEndogenous endophthalmitis is a rare condition that carries a high risk of vision loss. Risk factors for developing endogenous endophthalmitis include having a systemic source of infection and one or more risk factors for immunosuppression. We present a case of a 62 year old female with recent cardiac surgery who presented with altered mental status and fevers, patient grew blood cultures positive for streptococcus pneumonia and subsequently developed right endogenous endophalthimitis.

Case report: A 62 year old female with a past medical history of hepatitis c (treated), severe aortic stenosis s/p bio prosthetic valve replacement 8 weeks prior to admission with altered mental status, fever and back pain.
Vitals revealed temperature 99. 4, heart rate 88bpm, blood pressure 128/71, respiratory rate 20 breaths per minute, oxygen saturation is 98%. labs revealed lactate 2. 79 and blood culture reveals gram positive bacteremia which turn out to be streptococcus pneumonia. She was started on ceftriaxone 2gram bid.

Patient started to complain of headaches with floaters in right eye, tte and tee was done which was negative for vegetation. Mri of the brain also revealed t_2 hyperintensity and diffusion restriction associated with the bilateral occipital horns without associated susceptibility artifact or ependymal enhancement. Findings were concerning for ventriculitis.

Patient had worsening symptom of pain and loss of vision in od>>>os, floaters. Ophthalmology was consulted and their examination revealed photosensitive eomi, marked edema od>>os, injected conjunctiva with copious drainage bilaterally with poor view of the fundus od>>os due to vitritis.

The next day, patient began to see black spheres with poor visual acuity on the right and left. His final visual acuity was no light perception in the right eye and 20/50 in the left eye. Patient was transferred to special eye center for further evaluation and intravitreal antibiotics.

Discussion: Our patient's medical sequelae demonstrate the importance of early detection of ee as an indicator of severe, potentially devastating systemic disease.

Despite the increasing volume of research, challenges remain in the diagnosis and treatment of bacterial ee. Previous retrospective studies show that incorrect diagnosis of ee occurs in up to 50% of casesEndogenous endophthalmitis comprises approximately 2 to 8% of endophthalmitis cases streptococcus pneumoniae is only found in 0% to 5% of all ee cases, bacterial ee is usually unilateral with bilateral disease occurring in just 12 to 14% of patients. ee is associated with systemic risk factors, such as recent surgery, urinary tract

infections, endocarditis, gastrointestinal tract infections, immunosuppressive diseases and therapies and chronic immune-compromising illnesses endogenous endopthalmitis is an ophthalmologic emergency with high morbidity and poor visual outcomes. Endogenous endophthalmitis occurs by hematogenous spread of a microorganism from one site in the body to another. Microorganisms more commonly affect the right eye because of the more direct hematogenous spread through the right carotid artery. Within bacterial ee, staphylococcus aureus is the most common organism in the developing world. Gram-negative species are known to be more common in the asian population. Streptococcus pneumoniae is only found in 0% to 5% of all ee cases. bacterial ee is usually unilateral, with bilateral disease occurring in just 12% to 14% of patients. endogenous endophthalmitis is associated with systemic risk factors, such as recent surgery, urinary tract infections, endocarditis, gastrointestinal tract infections, immunosuppressive diseases and therapies and chronic immune-compromising illnesses. 5the prognosis of ee is poor, frequently resulting in complete vision loss. Streptococcal endophthalmitis carries a particularly poor prognosis, as approximately 40% of patients have no remaining vision and 25% of patients require enucleation or evisceration. 4 currently, there are no established guidelines regarding management of ee. As first-line treatment, most experts recommend performing a vitreous tap followed by injection of intravitreous antibiotics ("tap and inject").

The prognosis of ee is worse than in other types of endophthalmitis. In a retrospective study on all-cause endophthalmitis, ee was an independent risk factor for evisceration or enucleation.

The predisposing factors are diabetes mellitus, use of intravenous drugs, recent surgery, valvular cardiac diseases, renal insufficiency, neoplasias, corticosteroid therapy and immunosuppressive therapy. The right eye is generally more affected than the left eye, which is probably due to direct blood flow from the heart.

The most common causes of endogenous endophthalmitis are meningitis, endocarditis, urinary tract infection and wound infection. Other sources of infection have included pharyngitis, pneumonia, septic arthritis, pyelonephritis, intra-abdominal abscess and gastrointestinal malignancy. About 25% of the cases are bilateral and usually caused by meningococcus, escherichia coli and klebsiella sp.

Conclusion: Diagnosing endogenous endophthalmitis early is essential to initiating a systemic evaluation for potentially life-threatening medical conditions, including sepsis, endocarditis and osteomyelitis. A high degree of suspicion, expeditious treatment and interdisciplinary collaboration are essential to maximizing patient outcomes.
We believe our emergent, collaborative efforts led to saving patient's left and right eye and ultimately his life. Continued efforts to quickly diagnose and treat patients with ee are essential to maximizing both ophthalmologic and systemic outcomes.

Hemanta Maity, Rajib Deb*, Gyanendra Singh Sengar, Seema Rani Pegu, Swaraj Rajkhowa, Vivek Kumar Gupta
ICAR-National Research Centre on Pig, Guwahati, Assam, India

Development and characterization of a virus-like particle-based subunit vaccine cand idate against Indian isolate of Porcine Circovirus 2d

Porcine Circovirus Type 2 (PCV2) is a major threat to pig farming in India, with emerging PCV2d strains causing vaccine failures. This study aimed to develop a recombinant Virus-Like Particle (VLP) vaccine targeting the Indian isolate of PCV2d capsid protein and evaluate its efficacy in a porcine model. The PCV2d capsid gene (ORF2) was cloned into a baculovirus expression system using Ascalapha odorata (Ao38) insect cells. Recombinant VLPs were produced, purified and characterized by western blotting and Transmission Electron Microscopy (TEM). The vaccine's immunogenicity was tested in pigs by measuring antibody titers and cytokine expression. The recombinant PCV2d capsid protein was successfully expressed in Ao38 cells, assembling into VLPs of 17-20 nm size. Stability analysis demonstrated that the VLPs remained structurally intact and functional at temperatures up to 45°C for six hours and were stable at acidic pH levels down to 5. In the porcine model, the adjuvanted VLP vaccine (PCV2dVLPadj) induced significantly higher antibody titers and cytokine responses (IL-12, IL-2, IL-4, IL-6, IFN-γ) compared to the non-adjuvanted group. The vaccine also showed potential as a diagnostic tool with 93. 75% relative accuracy. The developed VLP vaccine not only demonstrated strong immunogenicity but also exhibited significant thermal and acid stability, making it a robust and economical solution for preventing PCV2d infections in pigs.

Audience Take Away Notes

- Understand ing the development and characterization process for a VLP-based vaccine targeting PCV2d
- Insights into the challenges of current PCV2 vaccination strategies and the need for strain-specific vaccines
- Practical application of VLP technology for both vaccination and diagnostic purposes in porcine models
- The VLP vaccine offers a potentially cost-effective and strain-specific solution to control PCV2d outbreaks
- The approach can be adapted for other emerging strains, ensuring better protection and lower economic losses

Biography

Dr. Rajib Deb is a Senior Scientist at the ICAR-National Research Center on Pig, Guwahati, India. He holds a Ph. D. in Animal Biotechnology from the Indian Veterinary Research Institute and has completed post-doctoral fellowships in Brazil and the UK. Dr. Deb's work focuses on developing innovative diagnostic tools, vaccines and genetic solutions to improve livestock health. His research significantly advances veterinary biotechnology, contributing to livestock disease management and food safety in India and globally.

Hamza Saber[1], Riti Sanghvi[2]*, Ahmed Algohiny[1], Nivesh Yadav[1], Kirelos Younan[1], Tejas Nikumbh[1]

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[2]Department of Internal Medicine, Grant Government Medical College, Maharashtra, Mumbai, India

Gram-negative sepsis by multidrug-resistant hafnia alvei in a 76-year-old man with multiple sclerosis and neurogenic bladder

This case report describes a 76-year-old male with multiple sclerosis and neurogenic bladder who presented with altered mental status and a recent history of diarrhea. Despite empiric antibiotics, fluids, and vasopressors, the patient deteriorated. Subsequently, positive Polymerase Chain Reaction (PCR) results for Clostridium difficile (C. difficle) prompted adjusting antibiotics. However, the patient's clinical status exhibited no improvement, and blood cultures remained unyielding. This case ultimately unveiled a diagnosis of gram-negative sepsis originating from a Urinary Tract Infection (UTI) caused by multidrug resistant Hafnia alvei. This report emphasizes the significance of considering unusual pathogens, particularly in patients with neurogenic bladder and immunocompromised conditions, remaining vigilant for multidrug resistance patterns, and the limitations of using PCR as the sole diagnostic test for C. diff, potentially leading to incorrect diagnoses. Tailoring antibiotic therapy based on culture and sensitivity results is essential in achieving favorable patient outcomes.

Audience Take Away Notes

- This case demonstrates the imperative requirement for conducting a comprehensive septic workup in patients displaying altered mental status and indications of systemic inflammation, even in the absence of an immediately identifiable source of infection.
- In the case of urinary tract infections, it focuses on the critical importance of contemplating atypical pathogens and being vigilant for multidrug resistance patterns to ensure appropriate management and favorable patient outcomes.
- Additionally, it serves as a reminder of the necessity for antibiotic stewardship, advocating for the judicious use of antibiotics to combat the growing threat of antibiotic resistance.
- Furthermore, it highlights the limitations of relying solely on PCR for detection of Clostridium difficle, which lacks specificity in distinguishing between colonization and active infection, underscoring the importance of combining it with other diagnostic tools for more precise clinical decisions.

Biography

Dr. Riti Sanghvi graduated in 2022 with an MBBS degree from Grant Government Medical College, Mumbai, India. Driven by a passion for Internal Medicine and Preventive Medicine, Dr. Riti Sanghvi is preparing to apply for an Internal Medicine residency, with a commitment to advancing patient care and community health.

João Vitor Carvalho Constantini, Camila Cristina Baccetti Medeiros, Rodrigo Sorrechia, Rosemeire Cristina Linhari Rodrigues Pietro*
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Coffee industry by-products extracts: Evaluation of the repellent effect against the R (B.) microplus tick

Livestock plays a crucial role in the Brazilian economy, however, the ubiquitous presence of the Rhipicephalus (Boophilus) microplus tick represents a significant challenge, resulting in considerable economic losses. Additionally, ticks stand out as vectors of different microorganisms for humans and animals, such as Lyme disease, Babesiosis, Anaplasmosis, Tularemia and Rocky Mountain spotted fever. This parasite not only impacts animal production, but also increases veterinary care costs and excessive use of commercial acaricides leads to the development of resistance. The coffee industry generates by-products that offer an opportunity to explore new repellents. These by-products offer a unique opportunity to explore new tick repellents. In the phytotherapeutic scenario, herbal medicine emerges as a promising alternative for tick repellence. The objective of this study was to evaluate hydroethanolic extracts from by-products of the coffee industry, such as defective roasted beans, defective green beans and leaves, for their repellent effects against R. (B.) microplus. To obtain the extracts, the sonication process was carried out with EtOH-H_2O 7: 3 (v/v), using 500mg of sample for 5mL (plant material/solvent). The repellent activity was evaluated according to the methodology described in the literature. The extracts were solubilized in Milli-Q water and Tween 2%, at a concentration of 25 mg/mL and were tested at three-time intervals: 4, 12 and 24 hours of the extracts against ticks. The green grain and leaf extract only showed effects within 4 hours, with 0. 6% and 0. 7% repellence, respectively. The green grain extract demonstrated effects at intervals of 4 and 12 hours, with 7. 8% and 0. 6% repellence, respectively. The repellent effects of coffee by-product extracts provide insights for future research at different concentrations, methods of obtaining plant extracts and tested time intervals, as well as potential associations with biotechnological products. This approach aims to enhance the repellent percentage, enabling its use in tick control in cattle farming.

Audience Take Away Notes

- The audience will learn about the potential repellent effects of hydroethanolic extracts from coffee industry by-products against the Rhipicephalus (Boophilus) microplus tick
- They will understand the methodology used in the study, including the extraction process and the testing procedure for repellency
- The presentation will highlight the specific results obtained from testing different extracts at various time intervals, providing information on the efficacy of these extracts as tick repellents
- Attendees will gain knowledge about the potential applications of coffee by-product extracts in tick control and the need for further research to optimize their effectiveness
- Veterinarians and livestock farmers can explore alternative methods for tick control, potentially reducing reliance on conventional acaricides and mitigating resistance development
- Researchers in the field of veterinary medicine and agriculture can use this research as a basis for further studies on natural repellents and their application in pest management

- The findings may inspire collaboration between the coffee industry and livestock sectors to develop eco- friendly solutions for tick control, benefiting both industries and the environment
- This research contributes to the development of sustainable and cost-effective strategies for tick management, ultimately improving animal health and reducing economic losses in the livestock industry
- This research provides a potential practical solution to the challenge of tick infestation in livestock, offering a natural alternative to conventional acaricides
- This research providesopportunities for interdisciplinary collaboration between the agriculture and food industries, fostering innovation and sustainability
- Insights into the utilization of agricultural by-products for pest management, promoting waste reduction and circular economy principles
- New information on the repellent properties of coffee industry by-products, expand ing the repertoire of natural pest control options for farmers and veterinarians
- A foundation for future research endeavors aimed at optimizing the efficacy and applicability of coffee by-product extracts in tick control strategies

Biography

Rosemeire Cristina Linhari Rodrigues Pietro holds a degree in Biochemical Pharmacy from São Paulo State University Júlio de Mesquita Filho- UNESP (1978), a master's degree in Biochemistry from the University of São Paulo-USP (1985), a Ph. D. in Biochemistry from the University of São Paulo-USP (1991) and a post-doctorate from the University of São Paulo-USP (1995). She is currently an associate professor at São Paulo State University Júlio de Mesquita Filho-UNESP, at the Faculty of Pharmaceutical Sciences (FCFAR), in the Department of Drugs and Medicines, at the Pharmaceutical Biotechnology Laboratory. She was the coordinator of the Graduate Program in Pharmaceutical Sciences at FCFAR from 2013 to 2021. She is a Full Member of the Central Postgraduate Chamber-CCPG (2017-2019), UNESP. She was President of the Permanent Teaching Commission of FCFAR-UNESP. Full Member of the Congregation (2009-2024). She is the leader of the CNPq research group: Biotechnological Aspects of Studies of Enzymatic, Antimicrobial and Biological Activities. Full Member of the Departmental Council of the Department of Drugs and Medicines FCFAR (2008 - 2016; 2018-currently), being a substitute member from 2016 to 2018. Full Member of the Council of the Graduate Program in Pharmaceutical Sciences, FCFAR (2013-currently). She has experience in the area of Biochemistry, with emphasis on Microorganism Biochemistry and Biotechnology, mainly working on the following themes: enzymes, antimicrobial activity, acaricidal activity, plant extracts, natural products and microbiological analyses of biotechnological products.

Dr. Sabiha Imran
Professor, Department of Biotechnology, School of Engineering & Technology, Faridabad, Haryana, India

BacLI: A potential antibacterial agent against hospital-acquired lung infection

Hospital-acquired infections are infections that are not present at the time of admission to a hospital and thus include ventilator-associated pneumonia, hospital-acquired pneumonia, etc. Hospital-Acquired Pneumonia (HAP), also known as nosocomial pneumonia, is a lower respiratory bacterial infection that occurs 48 hours or more after hospital admission and does not appear due to intubation at the time of admission. Lung infection is a situation where a disease-causing microorganism causes damage and inflammation in the Lung airways or tissues caused by the accumulation of immune cells. There are a number of symptoms that are common with lung infections and they can occur regardless of the type of infection. Breathing difficulties, chest congestion and back pain are all common symptoms. Hospital-Acquired Pneumonia (HAP) is typically caused by bacteria, especially aerobic gram-negative bacilli, such as Pseudomonas aeruginosa, Escherichia coli, Klebsiella pneumonia and Acinetobacter species. Lung Infection is a very common sort of infection that will affect many generations irrespective of age, gender and the treatment which are available have very toxic side effects antibiotic resistance is also very common and to control lung infection strong antibiotics have to be given and these antibiotics have very severe toxic effects on several parts of the body. We are providing a solution for hospital-acquired lung infections. By using a potential antimicrobial agent i. e. Bacteriocin, Bacteriocins offer great potential in a wide range of fields around the world and both the medical and agricultural industries are conducting research on the use of bacteriocins as therapeutic agents. Bacteriocins have become an alluring tool for human health because they are ribosomal–synthesized antibacterial molecules of a protein family that inhibit growth and have the ability to eliminate certain microorganisms and are highly potent, exhibit antimicrobial activity at nanomolar concentrations and are harnessed for designing safer and better therapies for mankind. In addition to the discovery of bacteriophages and the development of antibiotics, bacteriocins did not receive the same level of attention as antibiotics due to a lack of understand ing of their biology, which resulted in difficulties in production and inconsistent control of microbial growth. Bacteriocins are a very potent and effective alternative to strong antibiotics for the treatment of Hospital Acquired Lung infections as the antibiotics cause many undesirable side effects. Bacteriocins are protein in their nature and when taken orally will be cleaved by stomach proteases. So, drug resistance problems could not be an issue with bacteriocin.

Audience Take Away Notes

- This presentation will open a window of thought for the treatment of hospital acquired infections particularly lung infections because the bacteria have developed resistance against the available antibiotics that makes this difficult to treat
- After discussing the unique properties and approach in presentation the audience will be benefited by acquiring new approach to save the life of patient

Biography

Dr. Sabiha Imran is a Professor in the Department of Biotechnology, School of Engineering & Technology. She did MSc M. Phil in Biotechnology and PhD is in Microbiology in 1995. Her area of specialization is medical biotechnology and Immunology. She has more than twenty two years of research and teaching experience. She has presented Research Papers in many International and National Conferences as key note and invited speaker. She has more than thirty publications in reputed Scopus and web of science indexed national and international journals. She has been awarded as Start Faculty and Manav Rachna KarmsetuKaushlam Puruskar (award) in September 2022. Many UG and PG students worked under her supervision for Dissertation and Research Project and startups.

Samson Gebremedhin[1*], Fisseha Shiferie[2], Dawit A. Tsegaye[2], Wondwossen A. Alemayehu[3], Tamiru Wondie[2], Solomon Zeleke[2], Belete Alebachew[4], Kidist Belete[5], Gashaw And arge Biks[2]

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The Ethiopian vaccine supply chain and logistics system's performance after the last mile delivery initiative: Phenomenological study

Background: Uninterrupted availability of potent vaccines requires robust Vaccine Supply Chain and Logistics System (VSCLS). With special focus on remote and underserved settings, we assessed the reach and bottlenecks to end-to-end delivery of the Ethiopian VSCLS after the initiation of the last mile transition.

Methods: We explored the perspectives of key stakeholders of the VSCLS using a qualitative phenomenological study. give spaces in the middle. We captured the viewpoints of the Ethiopian Pharmaceutical Supply Service (EPSS), the health system, partner organizations, health workers and community members through 327 in-depth interviews and 22 focus group discussions. The study was sequentially implemented over two phases to understand the bottlenecks at national and regional (Phase-I) and lower levels (Phase-II). Data were analyzed thematically using data-driven coding.

Results: After the transition, EPSS started supplying vaccines directly to health facilities bypassing intermediaries. The transition reduced supply hiccups and enabled the health sector to focus on its core activities. However, in remote areas achievements are modest and health facilities are receiving supplies indirectly through district health offices. By design, health posts collect vaccines from health centers, causing demotivation of health extension workers and frequent closure of health posts. Challenges of the VSCLS include artificial shortage due to ill-forecasting and failure to request needs on time, lack of functional refrigerators secondary to scarcity of skilled technicians and spare parts and absence of dependable back-up power at health centers. From EPSS's perspective, shortage of refrigerated tracks and unmanageably large catchment areas are major blockades. Vaccine wastages owing to poor forecasts, negligence and cold chain problems are common. The VSCLS has not sustainably embraced digital logistics solutions so far. The system is overstrained by frequent outbreak-responses and introduction of new vaccines.

Conclusion: The last mile delivery has improved the VSCLS. However, the reach remains suboptimal in remote areas, threatening national coverage and equity goals.

Keywords: Vaccine Supply Chain, Cold Chain Management, Vaccine Wastage, Last Mile Delivery.

Audience Take Away Notes

- Systematic redesigning of the vaccine logistic system, especially bypassing intermediaries, improves the availability of routine vaccines in LMICs like Ethiopia
- However, additional strategies need to be considered to reach to remote and underserved settings

Biography

Dr. Samson Gebremedhin is an Associate Professor of Public Health, at Addis Ababa University, Ethiopia. Recently he has served as the Principal Investigator for Bill and Melinda Gates Foundation funded research project “Reaching zero-dose and under-immunized children in Ethiopia” implemented by the Project HOPE. Dr. Samson has served in the academia for more than two decades.

Shikha
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To study the bacteriological episodes of urinary tract infection in different age group with relation to gender

A urinary tract infection is a condition in which one or more parts of the urinary system (kidneys, ureters, bladder and urethra) become infected. Urinary tract infection may be defined as the presence of bacteria undergoing multiplication in urine within the urinary drainage system. A count 105 organism/ml of urine denotes significant bacteriuria and indicate active urinary tract infection. Moreover, urinary tract infection is generally caused by one species, while contaminants are generally of mixed species. Urinary tract infection is one of the commonest bacterial infections. The *Enterobacteriaceae* are the most frequent pathogen detected causing 80% of urinary tract infection. Present study was conduct to achieve resistance summary of clinical isolates against commonly prescribed antibiotic. A total of 100 urine specimens were received and these were processed in the laboratory. Significant bacteria: (cultures with > 10^5 colony forming units (CFU) of bacteria/ml of urine). Gram-negative bacteria were more prevalent than Gram-positive bacteria. Identification was done on the basis of morphological, biochemical and phenotypic characteristics of the 100 isolates, the most commonly isolated bacteria were *Escherichia coli* 45, *Klebsiella pneumoniae* 22, *Pseudomonas aeruginosa* 19. The study shows the distribution of microbial species isolated from patients with urinary tract infection and their susceptibility pattern to antimicrobial agents. Microbial infection of the urinary tract infection is one of the most common infectious diseases worldwide. The present study was to describe the isolation and identification of *Pseudomonas sp.*, *Klebsiella sp.* and *E. coli* in urinary tract infection patients and to study antibiotic susceptibility patterning of these as well. As *E. coli* is first major pathogen that may lead to UTI after its *Klebsiella* and *Pseudomonas* play role. Out of 100 samples, 19 samples were isolated as *Pseudomonas sp.* and 22 *Klebsiella* and *E. coli* 47. The percentage of resistance by antibiotics were Amikacin (21. 05%), Ciprofloxacin (21. 05%), Gentamicin (10. 52%), Cefotaxime (84. 21%), Imipenem (5. 2%), Meropenem (10. 52%), Cefoperazone (0%), Tobramycin (5. 26%), Piperacillin-tazobactam (5. 26%), Cefepime (10. 52%), Ceftazidime (31. 57%), Norfloxacin (63. 15%).

Audience Take Away Notes

- To isolate and identify the pathogenic bacteria in urine sample
- To perform antibiotic susceptibility test of bacterial isolates
- To estimate the prevalence of Multi Drug Resistant microorganism from the isolates

Biography

Ms. Shikha studied M. Sc. in Clinical Microbiology at the Lovely Professional University, Phagwara, Punjab, India. Shikha received Post Graduated degree in 2018 at the same University. After that Shikha obtained the position of an Assistant Professor. From last 5. 5 years, Shikha is working as an Assistant Professor and presently Shikha is working at GNA University. Shikha is Board of Studies (BOS) member, Event coordinator and clinical laboratory in-charge. Shikha has published 4 research papers in various reputed journals. Shikha has attended prestigious conferences, faculty development programs, expert talks and seminars. Other than this, she attended and organized medical camps and workshops. Moreover, she participated in oral paper presentation at international conferences and bestowed with awards.

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Wohlfahrtiimonas chitiniclastica bacteremia: A rare case of a male with maggot-infested lower extremity wounds

Wohlfahrtiimonas chitiniclastica (W. chitiniclastica) is an emerging gram-negative bacillus rarely found in patients presenting with fly myiasis or parasitic larvae infection. Here, we present the case of a 58-year-old male who presented with W. chitiniclastica bacteremia from lower extremity wounds complicated by fly larvae infestation. Blood cultures were analyzed with matrix-assisted laser desorption ionization-time of flight mass spectrometry, which identified W. chitiniclastica. The patient was treated with empiric antibiotic therapy with piperacillin-tazobactam and de-escalated to ceftriaxone. We discuss the potential impact of environmental interactions with zoonotic vectors and the concern for the increasing incidence of this new emerging zoonotic infection. This appears to be the first reported case of W. chitiniclastica bacteremia in the southern United States and demonstrates a growing list of climates and locations in which this organism can be present. Further evaluation of potential vectors for W. chitiniclastica continues to be a priority for how cases are distributed and can present in patients.

Audience Take Away Notes

- It is important for providers to recognize Wohlfahrtiimonas chitiniclastica as a rare pathogen directly linked to myiasis
- Providers will need to be aware of the risk factors associated with this disease
- More research will need to be done with regards to alternative routes of transmission of this pathogen
- This is an emerging zoonotic infection which may be influenced by human interaction with flies and variations in climate

Biography

Dr. Sina Hedayatpour, DO graduated from the University of Houston with a B. S in Health in 2016. He then went on to graduate from medical school at Philadelphia College of Osteopathic Medicine- Georgia Campus in 2021. He is currently a resident of the Internal Medicine Program at Methodist Health System in Dallas, Texas.

Dr. Sunita Girish*[1] PhD, Preeti Sonje[2], Abhay Jagtap[3], Pradeep Borle[4]
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Comorbidities in COVID-19 patients: Are these associated with vitamin D deficiency and SARS-CoV- 2 infection grade?

Background: Vitamin D, recognized for its immunomodulatory effects, plays a crucial role in strengthening the body's defense mechanisms. Emerging evidence suggests that comorbidities associated with COVID-19 often exhibit lower levels of Vitamin D, predisposing them to heightened susceptibility to severe COVID-19 manifestations.

Objective: We aim to assets the COVID-19 positive individuals with demographic and laboratory parameters, comorbidities identified post COVID-19 infection acquired with vitamin D deficiency.

Materials and Method: This was a cross-sectional study. Estimation of serum 25(OH)D was done in conjunction with other blood tests including D dimer and complete blood count. All COVID-19 positive patients were check for the other health issues and medical emergencies. Data analysis was done using the SPSS (Statistical Package for the Social Science) Version 23 for Windows. The demographic variables, COVID-19 severity, Vitamin D level and comorbidity were calculated in number and percentage. The ANOVA test was used to find significant differences in Vitamin D, D Dimer, to COVID severity.

Results: Fifty patients who clinically diagnosed with positive COVID-19 by RT-PCR were included in this study. 74% (n=37) patients were vitamin D deficient. Eight percent patients were (n=4) were diagnose with insufficient vitamin D levels and 18% patients had adequate vitamin D levels. It was noted that after acquiring SARS-CoV-2 infection 62% (n=31) were diabetic, 36% (n=18) were obese and 42% (n=24) patients were suffering from hypertension. Other medical conditions such as NS (20%), TH (6%), TB (4%), CKD (2%) and COPD (2%) was observed. Correlation was observed in the severity grade of COVID-19 infection and comorbidities. Moreover, the positive correlation between the laboratory and demographic markers was also observed.

Conclusion: SARS-CoV-2 infection had an impact on individuals' medical health. Health comorbidities were associated to the COVID-19 severity. Plus, our study demonstrated that lower vitamin D levels also had a significant impact on demographic markers indicative of low and deficient vitamin D levels may be associated and responsible for infection severity and comorbidities.

Key words: COVID-19, Comorbidities, Vitamin D, Correlation of Infection Severity.

Biography

Dr. Sunita Girish has completed Ph. D in 2004 in leprosy at Pune University, Pune, India and completed Fogarty fellowship under John-Hopkins, USA, 2020Currently she is persuing her Ph. D degree in Covid-19. She obtained the position of an Associate Professor since 1999 at BJGMC, Pune India teaching Biochemistry. She has published more than 20 research articles in national and international journals.

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Pathoblockers: A novel anti-virulence approach to combat bacterial infections by targeting cholesterol-dependent cytolysins

Cholesterol-Dependent Cytolysins (CDC), a protein family of analogous pore-forming toxins that bind to cholesterol-rich membranes and exacerbate infections through diverse mechanisms, including direct toxicity and immune evasion. CDC are major source of virulence in various gram- positive bacteria (Streptococcus, Clostridium, Listeria, etc.) and independently cause the deleterious responses when released by bacteria during an infection. Thus, CDC are a legitimate health threat during invasive bacterial infection, responsible for nearly 2. 5 million deaths globally. Conventional antibiotics cannot curtail CDC, therefore, new therapeutic strategies are required. Our objective is to develop targeted small molecule inhibitors of homologous CDC that could be used as an anti-virulence therapy, alone or adjunct to antibiotics against various CDC-containing bacterial infections.

For the development of inhibitors, we utilized the archetypical CDC toxin Pneumolysin (PLY) from S. pneumoniae, which is an acknowledged drug target and a key contributor in the pathogenesis of bacterial pneumonia. S. pneumoniae is responsible for nearly 1 million fatalities among children under 5 years old worldwide. We employed a combination of virtual screening and in-vitro testing to obtain our first inhibitor named, Pathoblocker-1 (PB-1). Through structural optimization, PB-2 emerged, exhibiting a tenfold increase in potency. Subsequent optimization rounds culminated in the synthesis of PB-3, a more potent molecule exhibiting substantial efficacy in blocking CDC-mediated cytotoxicity during bacterial infection. Moreover, we identified the mechanism of PB molecules that enabled the application of PB compounds toward homologous CDC. Consequently, we validated the efficacy of PB inhibitors against perfringolysin, a CDC, homologous to PLY and belonging to C. perfringens. Our proof of concept has been recently published (U. B. A. Aziz et al. Nat. Commun. 15 (1), 3537 (2024).

We are continuing to enhance the potency and drug-like attributes of our lead and consequently, we synthesized a chemically distinct and more drug-like PB inhibitor than PB-3, which is under investigation in bacterial infection assays and subsequent animal studies. Our project has significantly advanced from the early preclinical studies to verge of animal studies and the promising developments indicate a trajectory towards future applicability of PB molecules.

Audience Take Away Notes

The presentation will provide the audience with a comprehensive overview of the challenges posed by virulence factors during bacterial infection, the imminent need of innovative therapeutic strategies against infectious diseases and a pragmatic workflow of pre-clinical studies in drug development. The major points are as follows:

- **Education and Research Expansion:** The audience will learn about the impact of virulence factors that have been underestimated for a long time. Virulence agents like CDC in aggressive bacterial

infections are the major source of morbidity and mortality. Furthermore, audience will understand the limitation of traditional antibiotics and why these are ineffective against CDC

- **Novel Therapeutic Strategies**: The presentation will emphasize on the immediate need of innovative anti-infective therapeutics in the context of virulence factors, as well as antimicrobial resistance. In addition, the work will introduce the audience to the concept of a novel anti- virulence therapy that specifically target CDC. The impact of an innovative approach like Pathoblockers will be communicated to the listeners that could work alone or as an adjunct to antibiotics for the treatment of multiple bacterial infections
- **Practical Application of Drug Development:** The research techniques and methods enabling the development of Pathoblockers will be shared with the attendees and this presentation provides a practical example of how modern techniques can be used to solve complex problems of new drug development, making it an excellent teaching resource for courses in drug target validation, drug design and pre-clinical study

Biography

Dr. Umer Bin Abdul Aziz earned his PharmD from GCUF, Pakistan in 2010 and gained substantial experience in clinical and hospital pharmacy in Pakistan and the UAE. Moving to Berlin in 2016, he completed MSc in Pharmaceutical Research in 2018, followed by a PhD in Medicinal Chemistry at Freie Universität Berlin, focusing on anti-infective drug development. Since 2023, he is leading a translational research project on anti-virulence therapies as a Project Leader in the lab of Prof. JörgRademann at Freie Universität Berlin. Dr. Aziz has published multiple research articles and specializes in pre-clinical studies.

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Metagenomic next-generation sequencing for diagnosing severe leptospirosis in a patient suspected COVID-19: A case report

Leptospirosis is a zoonotic and neglected waterborne disease caused by the pathogenic helical spirochetes. Several significant risk factors, such as climate, occupation, urbanization and poverty, can contribute to leptospirosis in humans. Symptoms of acute-phase leptospirosis include fever, severe headache, muscle aches, nausea, diarrhea, vomiting and chills, which significantly complicate diagnosis. Early diagnosis of leptospirosis remains challenging due to non-specific symptoms and the limited availability of rapid point-of-care diagnostic tests. Herein, we present a case where a patient suspected of having COVID-19, in 2021, was diagnosed with leptospirosis combined with pulmonary hemorrhage and multiple organ failure using metagenomic Next-Generation Sequencing (mNGS). The patient complained of persistent pain in both lower limbs for 5 days, fever with dyspnea and hemoptysis for 1 day. Timely antibiotic therapy and systemic multiorgan function support were immediately administered and the patient was cured following treatment. This case highlights the potential of mNGS to diagnose leptospirosis in the context of the COVID-19 pand emic.

Audience Take Away Notes

- mNGS is beneficial for rapid diagnosis of unknown pathogens. We used it to accurately diagnose leptospirosis at an early stage
- During the epidemic period of infectious diseases, it can play a role in rapid identification and diagnosis, thereby saving isolation resources
- PCR followed by Sanger sequencing also support the diagnosis

Biography

Wei-Jia Li MD, Vice Chief Physician, Intensive Care Unit, Peking University Shenzhen Hospital, had published more than 3 papers.

Xue Bai
Key Laboratory of Special Animal Epidemic Disease of Ministry of Agriculture and Rural Affairs, Institute of Special Animals and Plants, Chinese Academy of Agricultural Sciences, Changchun, China

Two residues in VP2 contribute to the enhanced replication and pathogenicity of raccoon dog parvovirus

Raccoon dog parvovirus (RDPV) is a highly contagious viral pathogen that causes acute and often fatal hemorrhagic enteritis, particularly in young raccoon dogs. Since 2016, epidemiological studies have reported frequent outbreaks of RDPV with increased virulence, yet the molecular mechanisms behind this heightened pathogenicity remain elusive. In our study, an alignment of all available full-length sequences of RDPV (n=38) revealed two consistent amino acid mutations that differed between RDPV before and after the 2016 outbreak were located at positions 27 and 297 in capsid protein VP2. Next, a series of mutant viruses witheither single or double amino acid replacements were generated from RDPV 2016 strains and RDPV 2010 strains infectious cDNA clones. Deletion of either of the amino acids led to a great impact of virus viability. In F81 cells, we observed that mutant viruses derived from RDPV 2016 showed reduced replication efficiency and attachment compared to the parental strain. Conversely, mutant viruses derived from RDPV-10 exhibited enhanced replication and attachment. Plaque growth assays showed clear differences between mutant and parental viruses. ELISA and BLI (Biofilm interferometry) assays demonstrated a significant reduction in transferrin receptor (TfR) binding by RDPV 2016 derived mutants. In infected racoon dogs, the pathogenicity of RDPV 2016 derived mutant viruses, assessed through clinical symptoms, viral load in sera and anal swabs, histopathology examination was reduced. Our results indicate that the amino acids at positions 27 and 297 in VP2 are involved in the replication efficiency of RDPV 2016 and contribute to enhanced pathogenicity. This study is the first to identify specific amino acids involved in RDPV replication or pathogenicity. These findings will contribute to understand ing the molecular mechanisms of RDPV replication and pathogenicity, leading to better therapeutic and prognostic options to combat the virus.

Audience take Away Notes

- This study providing insights into the molecular mechanisms underlying RDPV infection, which could inform the development of more effective therapeutic and prognostic strategies against the virus

Biography
Dr. Xue bai studied Veterinary Medicine at the Henan Agricultural University from 2001-2005 and graduated as MS at the Nanjing Agricultural University in 2008. Xue bai then joined the research group of Prof. Xijun Yan at the Institute of Special Animals and Plants, Chinese Academy of Agricultural Sciences (CAAS). Xue bai received PhD degree in 2019 at the same institution. She has published 13 research articles in SCI(E) journals.

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Development of nanobody-armored DC vaccine (BaizeDC) and its preliminary exploration in preventing solid tumor recurrence

Background: Dendritic cells (DCs) are pivotal in developing therapeutic cancer vaccine based on its function of crossing antigen presenting and induction of anti-tumor cytotoxic T lymphocyte response. To increase the efficacy of current anti-tumor DC vaccine, we developed a bi-specific anti-PD-1/CTLA-4 nanobody-armored DCs (BaizeDC) expressing tumor associated antigens (TAAs) p53 and Survivin. PD-1 and CTLA-4 are established immune checkpoints, p53 and Survivin are TAAs widely expressed in various solid tumors. The combination of immune checkpoint inhibition and TAA-specific T cell stimulation is expected to improve clinical response. A first-in-human study was initiated to explore the pharmacokinetics (PK), safety and preliminary efficacy of this novel DC vaccine.

Methods: *In vitro* synthesized mRNA encoding TAAs and anti-PD-1/CTLA-4 Tiniplasmid were electroporated into mature DCs induced from monocytes. DC viability and recovery, phenotype and migration efficacy were measured once thawed after 10-day cryopreserve. 24 hours post recovery, antigen expression, nanobody level and pro-inflammatory cytokines of DCs were analyzed. IFN-γ and activated T cell surface markers were tested after co-culturing DCs and autologous T cells for 3 days. A single-arm, open-label, early phaseI study approved by the Institutional Review Board was conducted in Shanghai Mengchao Cancer Hospital (NCT06015269). Subjects meeting the inclusion and exclusion criteria and signing the informed consent were enrolled in the study. Total 8 doses were intradermally injected to patients with 1E7 DCs each dose on Day0, 7, 14, 21 and Month2, 3, 4 and 5. Adverse events (AEs) were monitored throughout study. PK of anti-PD-1/CTLA-4 nanobody were tested on Day0, 1, 3, 5, 7, 28 and immune response was examined on Day0, Month2 and 3 by TAA-specific T cell response. Preliminary efficacy was assessed by disease free survival.

Results: The thawed DCs exhibited a purity of >90% and viability of >80%. More than 90% BaizeDC expressed co-stimulation molecules CD80, CD86, maturation marker CD40, HLA-ABC and chemokine receptor CCR7. The expression of Survivin, p53 and antiPD-1/CTLA-4 nanobody was 1. 65ng/mL, 15. 8 ng/mL 138. 6 ng/mL respectively. TNF-α and IL-12 secretion by DCs exceeded 200 pg/mL. T cells activation by BaizeDC was evidenced by an IFN-γ level of 1563. 45 pg/mL, surface marker analysis revealed CD69 positivity in 40% CD4+ and 20% CD8+ T cells, CD25 positivity in 40% and 60% of CD4+ and CD8+T cells. Four patients with a median age of 44 years post-solid tumor resection were enrolled in the clinical study. Anti-PD-1/CTLA-4 nanobody increased rapidly on Day1 with Cmax 6pg/mL and remained detectable until Day28. The most common AEs were injection site induration, no grade II or higher treatment-emergent adverse events happened. TAA-specific T cell response was detected in 3/4 patients with strongest immune reaction at Month2 or 3. There was no tumor recurrence identified with a median 8. 6 months follow-up.

Conclusion: Autologous BaizeDC expressing p53 and Survivin armed with bispecific anti-PD-1/CTLA-4 nanobody enables to activate T cells *in vitro*. It is safe in multiple injections and provokes T cell specific

responses in human. The effectiveness of BaizeDC in preventing cancer recurrence or metastasis requires continuing follow-up and involving more subjects.

Audience Take Away Notes

- The audience will gain insights into the innovative approach of integrating immune checkpoints inhibition with anti-tumor T cell activation stimulation in the design and development of therapeutic cancer vaccine
- Meeting participants will be informed about the pioneering observations of anti-PD-1/CTLA-4 nanobody in humans, persisting for an average duration of 7 days, with the longest recorded presence lasting up to 28 days post-administration of therapeutic dendritic cell (DC) vaccines
- The audience will be presented with findings from a first-in-human clinical trial that evaluated the safety and effectiveness of the novel vaccine in preventing the recurrence of tumors

Biography

Dr. Liu earned her MD from Shanghai Jiao Tong University School of Medicine in China and her PhD from the University of Amsterdam in the Netherlands. She subsequently completed a postdoctoral fellowship at the Royal Netherlands Academy of Arts and Sciences (KNAW). Dr. Liu has extensive experience in innovative drug development, having held various leadership roles at several global pharmaceutical companies. These include Chairman and CEO at Dendreon (China), General Manager of Medical and Drug Development at Daiichi Sankyo (China), Head of Medical and Regulatory Affairs at Genzyme (China), Medical Head at Novartis Vaccines (China), and Clinical Research Physician at AstraZeneca (China). She currently serves as the CEO of Shanghai Cell Therapy Group Pharmaceutical Technology Inc.

M. Madiba[2], Dr. Z Gulube[1*], M Patel[2]

[1]Department of Oral Biological Sciences, School of Oral Health Sciences, Faculty of Health Sciences, University of the Witwatersrand, Johannesburg, South Africa

[2]Clinical Microbiology and Infectious Diseases, School of Pathology, Faculty of Health Sciences, University of the Witwatersrand and National Health Laboratory Services, Johannesburg, South Africa

Anti-streptococcus mutans, anti-adherence and anti-acidogenic activity of Uvaria chamae P beauv

Dental caries is the most prevalent oral infection resulting from accumulation and multiplication of bacteria in the oral cavity. It is caused by demineralisation of the tooth due to the acids produced by Streptococcus mutans from fermentable carbohydrates. Pathogenic characteristics of S. mutans include biofilm formation, production of extracellular polysaccharides, acidogenicity and aciduricity. Dental caries can be prevented by controlling bacterial biofilm also called plaque with antimicrobial oral hygiene products. Medicinal plants have shown antimicrobial activity against these oral bacteria. Uvaria chamae have been used to treat various infections. It has proven antiparasitic, antiplasmodial, antidiabetic, antimicrobial and antioxidant properties. Although the anti-S. mutans activity of this plant has been reported, its effect on the virulence properties has not been studied. Therefore, this study aimed to investigate the antimicrobial activity of U. chamae roots extracts on S. mutans virulence factors.

Methods: The plant extracts were prepared using methanol, dichloromethane, hexane, ethanol and methanol: water. Minimum Bactericidal/MIC Concentrations (MBC) were obtained against S. mutans using double dilution technique. Subsequently, best effective solvent was selected for antivirulence study. The MIC, ½ and ¼ MIC concentrations of the dichloromethane extract were evaluated for their effect on biofilm formation, acid and extracellular polysaccharides production by S. mutans. The effect of the plant extract on the expression of virulence genes (gtfB, gtfC, spaP, IDH, atpD, vicR, brpA and gbpB) was also investigated using RT-qPCR. The results were analysed using the one-way ANOVA and Wilcoxon Rank Sum Test.

Results: The mean MIC of U. chamae roots extracts against S. mutans ranged between 0. 02 and 1. 25 mg/ml and the MBC ranged between 0. 04 and 1. 25 mg/ml. The dichloromethane plant extract showed the best antibacterial activity against all the five cariogenic S. mutans strains with an average MIC and MBC of 0. 02 and 0. 04 mg/ml respectively and was used in the subsequent experiments such as the biofilm, acid, EPS and RT-qPCR assay. At 6 hours, exposure to 0. 005, 0. 01 and 0. 02 mg/ml of the plant extract reduced biofilm formation by 39. 70, 59. 17 and 76. 82 %. At 24 hours, the percentage reduction of the biofilm counts significantly improved up to 91 %. Not much difference in the test results was observed between 24 and 30 hours. The plant extract also significantly inhibited acid production ($p < 0. 01$). The roots extract did not inhibit the production of soluble and insoluble extracellular polysaccharides. Furthermore, a significant decline in the transcription of virulence genes (gbpB, vicR, brpA, spaP, gtfB, gtfC, atpD and IDH) was observed in the presence of the plant extract.

Conclusion: The Uvaria chamaeextracts showed the best antibacterial activity. At subinhibitory concentrations, this plant extract significantly inhibited biofilm formation, acid production and virulent gene expression by S. mutans. Therefore, this suggests that U. chamae has the potential to control and prevent dental caries.

Audience Take Away Notes

- They should target virulence rather killing microbes
- She enjoys the application of logical thinking as a tool for exploring and satisfying curiosity about microbes and the world
- Research is set to explore and make mysterious discoveries to improve the quality of life
- It provides a practical solution to the world of microbes
- Render pathogens avirulent and less infectious

Biography

Dr. Zandiswa Gulube graduated BSc Honors in Biochemistry from the University of the Western Cape South Africa. In 1999, she joined Wits University South Africa to pursue her Masters in Biotechnology and was later worked with Prof. M Kew in Molecular Hepatology Research Unit from 2003. She moved to Gauteng Department of Health/Wits University on a joint appointment in 2007 where she completed PhD in Clinical Microbiology and Infectious Diseases in 2019. Dr Gulube has persuaded research in medicinal plants in search of therapeutic agents. She is a recipient of SA-NRF/Nagoya Japan, NRF Thuthuka, SEED FRC, Female Academy Leaders Fellowship (FALF). Currently collaborating with Federal, Bells University in Nigeria and Mintek South Africa. Her research portfolio has produced internationally recognized scientific outputs, postgraduate graduates and reviewed journal manuscript.

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Vaccines Congress

POSTERS

Anant Marathe
Parul Institute of medical sciences and Research, Parul University, India

Phenotypic changes in salmonella typhi

Salmonella enterica serotype Typhi (Hereafter referred to as S.Typhi) is the causative agent of Typhoid. Evolution of drug resistance in S.Typhi, initially as MDR strains (Strains resistant to Chloramphenicol, Ampicillin, and co-cotrimoxazole) to resistance to Fluoroquinolones after a decade. Currently, ceftriaxone (3rd cephalosporin) has been the drug of choice for treatment. Recently there have been reports from different parts of the world and from Gujarat of Ceftriaxone resistant S.Typhi because of the acquisition of blaCTX-M 15.1 The bacilli exhibited Bipolar staining (Safety-pin appearance). With this phenotypic change, we hypothesize its possible association with the resistance pattern.

Introduction: Salmonella is a genus of Gram-negative bacilli of the family Enterobacteriaceae. It has two species Salmonella enterica and Salmonella bongarii. S.enterica is further divided into six subspecies2 that contain over 2600 serotypes3. Salmonella species are non-spore-forming, mostly motile with peritrichous flagella, measuring 0.7-1.5 μm in diameter and 2 - 5 μm in length.4 The Centers for Disease Control and Prevention (CDC) is currently using the Salmonella nomenclature system suggested by the World Health Organization (WHO) Collaborating Centre as a nomenclature system.: Species: Salmonella enterica serotype Typhi.5

The evolution of drug resistance in Salmonella Typhi is a great public health concern. Multi-Drug Resistance (MDR) that emerged in 1990 is defined, in the case of S.Typhi, as resistance to Chloramphenicol, Amoxicillin, and Co-cotrimoxazole. This was followed by a decreased susceptibility to Fluoroquinolones and high-level fluoroquinolone resistance emerged and spread throughout the world.6 Clinicians relied, then, more on third-generation cephalosporins and Azithromycin. Recently there have been reports from different parts of the world and from Gujarat of Ceftriaxone resistant S.Typhi because of the acquisition of blaCTX-M 15.1

Clinicians in Vadodara, during recent upsurge of S.Typhi cases, experienced that even in cases of Ceftriaxone susceptible Salmonella Typhi infections the patients required prolonged treatment (up to two weeks) to render the patient afebrile.

We observed a conspicuous phenotypic change in S. Typhi bacilli in the gram-stained smear made directly from positive blood cultures.

Material and methods: The study was carried out at the Central Laboratory of Parul Sevashram Hospital of Parul Institute of Medical Sciences and Research. Our Central Laboratory is NABL accredited and the blood cultures are performed on an automated system. Identification and Drug Susceptibility of the bacterial Isolates is done on VITEK 2.

Result: The study comprised of 25 Blood culture positive typhoid cases in last three months. Recently our city (Vadodara) experienced a sudden upsurge in the cases of Typhoid and the cases were more severe requiring prolonged antibiotic treatment.

We observed that Gram's stained smears made from positive blood culture bottles, revealed conspicuous changes in the bacilli. The bacilli showed Bipolar staining (Safety pin appearance) under the Oil immersion Objective.

Discussion: We hypothesize an association between emerging phenotypic change in the bacilli and the changes in their tolerance to antibiotics and requiring prolonged antibiotic therapy. Since the 1990s, it has been well-accepted that a key component of the pathogenesis of B. pseudomallei is its ability to survive intracellularly in both phagocytic and non-phagocytic cells.7 Our findings open a new window for further genotypic studies to explore the association between phenotypic change and acquisition of virulence factors.

Recent trends in S typhi bacteremia: The temporal change in trends of antimicrobial resistance in Salmonella typhi bacteremia has been observed in the state of Gujarat in the last few months. Cephalosporins have been the mainstay of management of MDR S Typhi infections for the past several years. Perhaps cephalosporins failed as empirical therapy in a substantial number of cases as we observed a rise in ESBL XDR S.Typhi infections in recent outbreaks. Also, the children especially required longer hospital stays due to delayed fever defervescence. Average days for fever defervescence were observed to be 6-8 days of Intravenous therapy. Prolonged fever in most children was observed to be due to immune dysregulation or exaggerated immune response as we ruled out other causes, such as persistent bacteremia, deep-seated abscesses, or secondary HLH. Culture-proven S typhi bacteremia was also observed in children who were vaccinated with 2 doses of Typhoid conjugate vaccine. Relapse and complications were observed in those who were treated with inappropriate antibiotics and for inadequate duration. Distant complications such as osteomyelitis and spondylodiscitis were also observed in children treated for enteric fever.

Traditionally, a Bipolar staining pattern was used for probable identification of Burkholderia species especially pseudomallei in blood culture in patients with community-acquired pneumonia or B.cepacia in case of VAP. The other bacilli having similar staining patterns include Yersinia pestis and Fransisella tolerances.

Since the 1990s, it has been well-accepted that a key component of the pathogenesis of B. pseudomallei is its ability to survive intracellularly in both phagocytic and non-phagocytic cells7Our findings foster a probable association of the phenotypic characteristic with the acquisition of some virulence factors by S.Typhi and open a new window for further genotypic studies to find factors responsible for the intracellular survival of these strains.

Conclusion: This is the first observation study regarding the phenotypic change in the staining property of Salmonella Typhi. We hypothesize an association between the phenotypic change and change in the behavior of typhoid infections. We suggest further studies in S.Typhi virulence mechanisms and to develop new guidelines for the treatment of typhoid to tackle the menace.

Ethical statement: The study was approved by the institutional ethics committee, with reference no. IEC-INT/2022/Study-134, dated April 12, 2022. The patient gave informed consent for the publication.

Biography

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

Asmamaw Moges Bihonegn
Department of Public Health, Bahir Dar City Administrative Health Department, Bahir Dar, Amhara, Ethiopia

Comprehensive analysis of immunization program efficacy in Bahir Dar city: A six-month retrospective study

This presentation elucidates the findings of a rigorous six-month evaluation of the Expand ed Program on Immunization (EPI) conducted by the Health Department of Bahir Dar City. Utilizing a robust dataset extracted from the District Health Information System 2 (DHIS2), this analysis provides a granular look at immunization coverage trends, encompassing critical vaccines such as Penta1, Penta3, MCV1 and MCV2. The report meticulously assesses vaccine coverage rates, the productivity of Health Facilities (HFs) and delineates the immunization coverage disparities across various facility levels.

Key performance indicators reveal significant challenges including the rotation of trained staff, recurrent vaccine stock shortages, notably of Rota and OPV antigens and high dropout rates that collectively impede the efficacy of the immunization programs. Moreover, persistent issues in data quality and the operational hurdles posed by infrastructural limitations are highlighted. The presentation will propose a series of methodologically sound recommendations aimed at enhancing the integrity of immunization data and optimizing the distribution and utilization of vaccine resources.

Audience Take Away Notes

- **Attendees will gain:** A deep understand ing of the dynamics and operational challenges of running immunization programs in an urban Ethiopian context
- Insight into methodological approaches for analyzing health data to assess program performance comprehensively
- Strategies to mitigate common logistical and administrative challenges in vaccine program implementation
- **Professional Relevance:** The findings furnish pivotal insights that can aid public health professionals in enhancing vaccine distribution strategies and immunization program efficiency
- The detailed analysis serves as a blueprint for similar urban settings grappling with public health management challenges, particularly in low-resource environments
- **Academic Contributions:** The study offers a rich dataset for academic exploration, suitable for incorporation into public health curriculum and further scholarly research
- It provides a critical examination of field-specific challenges that could inform future research directions and policy formulations
- **Design and Innovation:** By addressing data integrity and staff training issues, the presentation introduces innovative solutions for improving the design and administration of immunization programs
- It outlines data-driven strategies that can be employed to refine program monitoring and evaluation frameworks, thereby enhancing overall program efficacy

Biography

Asmamaw Moges Bihonegn was born and raised in Northern Ethiopia. He graduated from Bahir Dar University of Ethiopia in Bachelor of Nursing in 2008 with honors. Since then he has been working as a leader in deferent public health and health administration positions in Amhara region until he left to attend his Master's Degree in advanced nursing practice and medical technology in 2023. As such, He has developed high level nursing skills and health sector leadership skills as part of my past achievements. The following is his work experiences: Master's degree student in Advanced Nursing Practice and Medical technology at Central South University of China in Changsha City, Hunan Province since Sept, 2023. Worked as Head of Bahir Dar City Zonal Health Department, Amhara Region, Ethiopia from Jan 2019 until Sept, 2023. Head of District health office, Amhara Region, Ethiopia from Jan 2011–Dec, 2018. Head of Health Center in Amhara Region Ethiopia from 2008–2010.

Hemant Garg*, Raphael Tze-Chuen Lee
Bioinformatics Institute, Agency for Science Technology and Research (A*Star), Bioinformatics Institute (BII), United States

Evolutionary trends and positive selection sites in major SARS-CoV-2 variants

The SARS-CoV-2 virus was first detected in Wuhan China in 2019. The virus rapidly dissipated to various continents leading to a global pand emic by acquiring rapid mutations in different regions of the viral genome including the highly studied spike protein. The mutation rate of the SARS-CoV-2 genome has thus been estimated at 1×10^{-3} substitutions per base (30 nucleotides/genome) per year under neutral genetic drift conditions or 1×10^{-5} to 1×10^{-4} substitutions per base in each transmission event. The rapid mutation/ evolution of the virus has resulted in the emergence of Variants of Interest (VOIs), Variants Under Monitoring (VUMs) and Variants of Concern (VOCs).

This study was undertaken to determine whether positive selection sites and mutation rate changes across SARS-CoV-2 variants. Furthermore, we also wanted to determine whether positive selection sites and mutation rate are the same throughout different Spike protein domains which is a major determinant of virus transmission and pathogenesis as well as immune response.

Fourteen different SARS CoV-2 variants were identified for further analysis. A sampling strategy was developed to limit the number of sequences to be analyzed. We selected 2 sequences from each variant per week per state from the more than 16 million full length genomes in the GISAID EpiCoV database. Each variant was aligned using the MAFFT multiple alignment software. Mutation rates for different regions were calculated using Mega7 software.

This study will help gain a better understand ing of the frequency, distribution and nature of mutations in SARS-CoV2. Our findings could provide important insights into vaccine design and drug discovery along with predictions into future evolution of novel variants. A detailed analysis of our findings will be presented.

Biography
Hemant Garg is a rising senior at North Penn High School, USA. He is a student intern at the Bioinformatics Institute, Agency for Science Technology and Research (A*Star) researching the evolution of the SARS-CoV-2 genome under the leadership of Dr. Lee. He is interested in pursuing a degree in Data Science or Statistics in college.

Srishty Agarwal, Vaishnavi Rathod, Muhammad Hussain*, Justin Oring
Department of Infectious Diseases, Mayo Clinic, FL, USA

Disseminated histoplasmosis in post-transplant patient: A bone marrow biopsy diagnosis

Background: Histoplasmosis is considered a rare disease following immunosuppression in an allogeneic bone marrow transplant patient or a solid organ transplant patient, even in hyper-endemic areas, with an incidence of ≤ 1%. The majority of cases occur within the first two years of transplantation. This is a case of a post-transplant patient from North Carolina with disseminated Histoplasmosis diagnosed on bone marrow biopsy, with no symptoms to suggest a histoplasmosis infection.

Case: A 51-year-old female presented with fever and pancytopenia on day 46 post-liver transplant. An extensive infectious disease workup that followed showed streptococcus pneumoniae antigen, she began receiving adequate antibiotics for Community-acquired pneumonia. Her CT chest revealed bilateral ground glass opacities with an admixed picture of pulmonary edema, dependent atelectasis and superimposed aspiration. Nodular consolidations were seen in the lateral basal lobe. A multi-disciplinary approach that followed resulted in bone marrow aspiration, which grew fungal yeasts and later revealed PCR-positive Histoplasmosis. This finding was backed up by the growth of histoplasma in broncho-alveolar lavage as well. Therefore, the treatment for disseminated Histoplasmosis was initiated with Amphotericin B, after which the patient's condition improved. She was discharged on Itraconazole, which was later switched to Posaconazole due to possible tinnitus. She feels better seven months post-treatment and is on continued treatment to complete a 12-month course.

Discussion: Histoplasmosis is an opportunistic infection with documented cases in immunocompromised patients, most commonly in patients who have HIV. Limited cases of disseminated Histoplasmosis have been seen with solid organ transplants. Fungal spores are present in the soil or bird and bat droppings, which, when aerosolized, can be inhaled by the host, leading to an infection. It is particularly common in chicken coops, old barns, caves and parks. Recent surveillance from 2018-2019 revealed that simple activities like gardening, hand ling plants or trees, land scaping and digging soil were also associated with an increased risk. 28% of individuals were reported to be participating or were near construction, demolition, or renovation. About 25% of patients could not recall any of these exposures. While an immunocompetent individual may develop self-limiting respiratory conditions, an individual with suppressed immunity might have disseminated or a life-threatening condition. Our patient lived in a rural setting in North Carolina with a very low incidence rate and no endemicity for Histoplasmosis. Apart from immunosuppression and DM-type 2, the patient did not account for an increased risk for the infection. To the best of our knowledge, the patient could not recall exposure to bird or bat droppings or being around a construction site recently, or traveling to an area of high endemicity. She did not have exposure to caves, barns or chicken coops. It was thus difficult to pinpoint the cause of infection in our patient.

Conclusion: The lack of specific symptoms, delay in histoplasma isolation in fungal culture and false negative

antibody titres complicates the diagnosis of histoplasmosis. In a recent survey, nearly 12% histoplasmosis patients with Medicare beneficiaries and 20% patients among private care belonged to a region which was considered as non-endemic for Histoplasmosis. Additional cases of histoplasmosis have been addressed from non endemic regions like Michigan, Mexico and New York city, among others. Specific exposures in sporadic casesappear to be less obvious and could be further complicated to pin-point particularly if the person participates in leisure activity like gardening which may increase the exposure chances. Disseminated histoplasmosis should thus be considered as a potential differential in the setting of immunocompromised hosts, especially in newly transplanted recipients, along with other common opportunistic infections, irrespective of geography and a defined risk factor.

Keywords: Disseminated Histoplasmosis, Post-Transplant, Liver Transplant, Bone Marrow Biopsy.

Images:

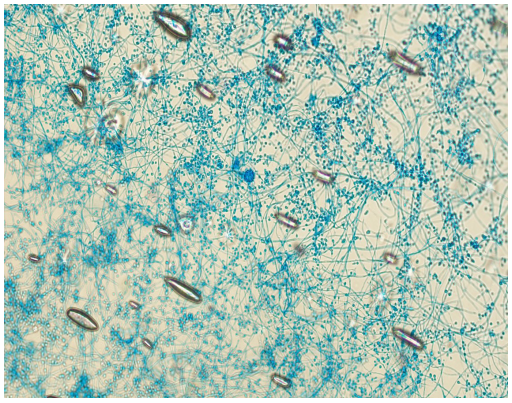


Figure 1: Microscopy consistent with Histoplasmosis due to the presence of hyphae and macroconidia.

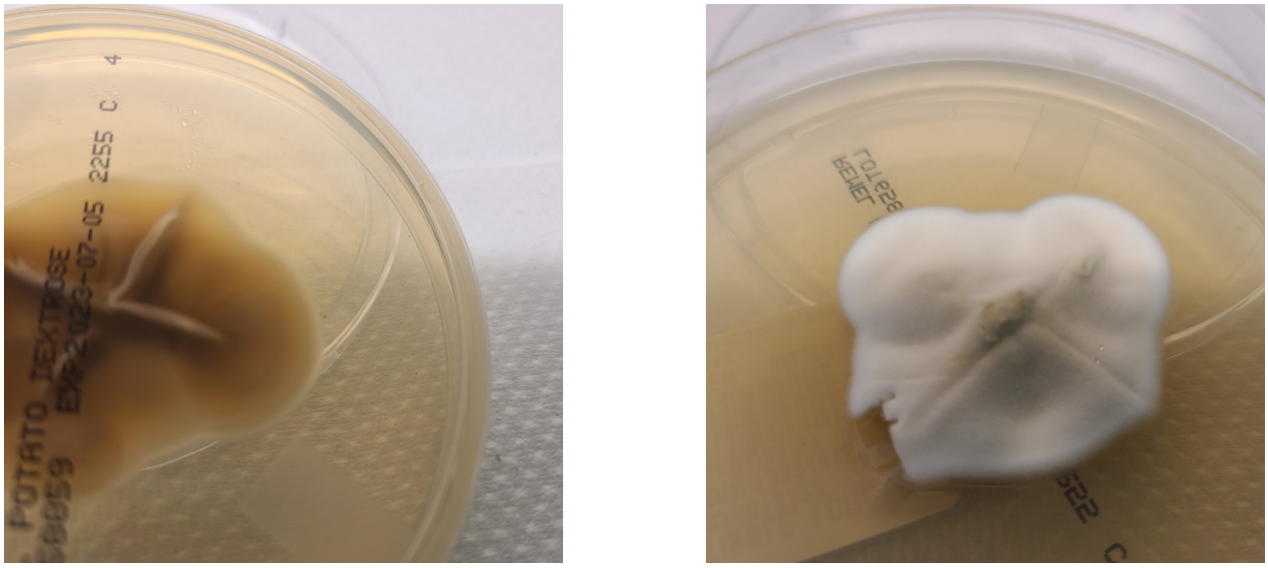


Figure 2: Growth of Cottony White Mold Colony of Histoplasmosis Capsulatum on Potato Dextrose Agar.

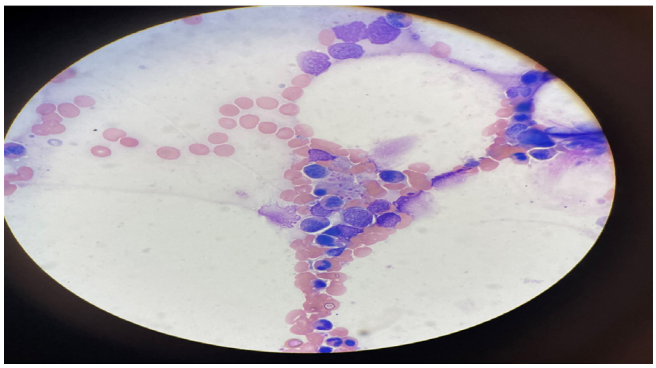


Figure 3: Bone Marrow Biopsy, not the presence of Histiocytes with fungal components, concerning for disseminated histoplasmosis.

Audience Take Away Notes

- This is an atypical presentation of Histoplasmosis infection in a transplant patient with no identified exposure factor. This qualifies as a great teaching case for healthcare providers to consider the possibility of infection even in absence of typical symptoms
- Even in regions with no reported endemicity for the infection, the risk for developing this infection must not be ruled out without a proper work up. Timely intervention can lead to favorable outcomes, if the differential is kept in mind
- A high degree of clinical suspicion is required to make the diagnosis of rare infection in a transplant patient especially when the diagnosis is complicated by other conditions in an immunocompromised individual

Biography

Dr. Hussain is an ID fellow at Mayo Clinic Florida. He graduated from Florida State University Medical School. He completed his residency in internal medicine from Rutgers University in Newark, NJ. Prior to starting the ID fellowship Dr. Hussain had a variety of roles which included Medical Director of multiple nursing homes, Hospice Medical Director and Clinical Professor of Medicine at Philadelphia College of Osteopathic Medicine. His future plans are to work in academics as an Infectious Disease Attending. In his spare time he enjoys traveling with his family and three children.

Teri Ngo, Gabrielle Dunn, Nicholas Sammons, Priscilla Krai, George Sigal, Leonid Dzantiev, Yeming Wang, Seth B. Harkins, Matthew Bess, Jocelyn Jakubik* Ph. D, Jacob N. Wohlstadter

Serology Assay Development, Critical Reagents, Quality Control, R&D Meso Scale Diagnostics, LLC., Rockville, MD, USA

Multiplexed serology assays for detection of IgG antibodies against Mpox and vaccinia viruses

Monkey pox (Mpox) Virus (MPXV) spreads through skin-to-skin contact, causing painful lesions. The 2022 outbreak resulted in the Congo's worst surge on record, with the subsequent world-wide spread causing nearly 20, 000 suspected cases and 820 suspected deaths. Effective tools for understand ing MPXV immune responses are needed for developing timely and effective MPXV-specific vaccines, as well as for understand ing the immune correlates of protection from natural infection and /or vaccination. Despite a rapid increase in the number and availability of serology assays that can detect antibodies against MPXV, there is limited information available on their performance and validation status. In addition, most of these assays are low throughput and measure responses to a single antigen, which cannot capture the breadth of antibody responses to MPXV. Here we present a validated, quantitative, multiplexed serology assay to measure antibody responses towards 5 MPXV and 5 Vaccinia Virus (VACV) variant recombinant proteins. Vaccinia is included in the panel due to its common ancestry to MPXV and the prevalence of smallpox vaccination, which is expected to prevent or reduce the severity of MPXV infection. Viral antigens that elicit strong T cell and B cell immune responses were chosen for the panel and include the receptor binding site for MPXV (A29L) and VACV (A27L), outer envelope proteins (MPXV: B6R, A35R and VACV: B5R, A33R) and inner membrane proteins (MPXV: M1R, E8L and VACV: L1R, D8L). The assay uses a 10-spot 96-well plate coated with the 5 MPXV and 5 VACV antigens, along with an Electrochemiluminescent (ECL) detection system. The assay simultaneously detects IgG antibodies to all 10 proteins. Specificity was assessed using purchased serum sample sets that were either collected pre-epidemic from aged smallpox-vaccinated individuals, or during the outbreak from convalescent individuals who recently recovered from MPXV infection. The multiplex MPXV ECL serology assay allows for sensitive, high throughput and simultaneous measurement of IgG levels to multiple antigens in human sera, supporting its use in research, epidemiology and vaccine testing.

Audience Take Away Notes

- A multiplex method for testing at-risk populations to distinguish between vaccinated and /or mpox-infected individuals versus negative individuals
- They can use the V-PLEX Orthopoxvirus Serology Kit for screening a population at risk for MPOX, for surveillance, in high throughput and simultaneously measure IgG levels to multiple MPOX and Vaccinia Orthopoxvirus antigens supporting exploratory R&D to design treatments, assess mechanism of action, for correlate of protection work
- Multiplex sample testing platforms cover a wide range of biomarkers
- Rather than perform singleplex assays, this allows measurement of 10 Orthopoxvirus antigens in 1 well, saving on sample volume, giving more consistent measurement, saving time, money and volume for method development
- It will ensure there is no variability in the measurement due to differences due to variables relating

to using 10 different singleplex assays- which requires higher sample volume, a variety of pipetting days, freeze/thaw cycles and methods. Ten Orthopoxvirus antigens are assessed for functional IgG concentration simultaneously

- The V-PLEX Orthopoxvirus Serology Kit is a validated, quantitative, multiplexed RUO serology kit that accurately and precisely quantifies IgG antibodies against the Mpox and VACV proteins (VACV A27L, VACV A33R, VACV B5R, VACV D8L, VACV L1R, MPXV M1R, MPXV E8L, MPXV B6R, MPXV A35R and MPXV A29L)

Biography

Dr. Jakubik studied Immunology and Microbiology with a focus on HIV immune complex pathogenesis at Rush University Medical Center, Chicago, IL. Her career began at Millipore Corporation (Bedford, MA) and then she held scientific positions at pharmaceutical companies (Genetics Institute, Wyeth, Pfizer, Idenix) prior to leading teams developing and performing biofunctional assays for clinical trials at CROs (PPD, Precision for Medicine). This high-throughput infectious disease vaccine work led to a transition into a non-profit, Sabin Vaccine Institute (Washington D. C.), to delve into BSL-4 virus targets and vaccine development with USA government (BARDA) funding. Currently, Jocelyn is leading Serology Assay Development at Meso Scale Diagnostics, Rockville, MD and using her vast history in infectious disease to launch new products on MSD's multiplex platform to address global disease surveillance, vaccine development and outbreak response.

Julianna Pieknik, Loretta Nimoh, Nicholas Sammons, Seth Harkins, George Sigal, Jocelyn Jakubik* Ph. D, Jacob N. Wohlstadter
Serology Assay Development, Critical Reagents, Quality Control, R&DMeso Scale Diagnostics, LLC., Rockville, MD, USA

A novel multiplex serology assay to evaluate immune response to RSV, SARS CoV-2 and influenza

Respiratory Syncytial Virus (RSV), Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) and influenza are prominent respiratory pathogens that significantly impact global public health. Each of these viruses poses distinct challenges and complexities, contributing to respiratory infections that range from mild illnesses to severe, life-threatening conditions. Understand ing the immune responses elicited by RSV, SARS-CoV-2 and influenza is crucial for effective disease management, preventive strategies and the development of targeted interventions. Often called a “tripledemic” due to their seasonal coincidence, there are now vaccines for all three to prevent severe disease and limit transmission. In light of the emergence of novel SARS-CoV-2 variants, the need for surveillance data on new RSV vaccines and the unpredictability of the influenza virus caused by circulating strains that vary from year to year, the imperative for a reliable and sensitive tool to concurrently monitor all three infections has become increasingly evident.

In this study, we present an innovative tool designed for monitoring serological responses to RSV, SARS-CoV-2 and influenza. This multiplex serological assay offers quantitative measurements of antibodies targeting diverse strains of influenza, different variants of SARS-CoV-2 and the common virus/vaccine component associated with RSV. The development and validation of such a comprehensive tool are essential steps toward enhancing our capacity to assess and manage the evolving land scape of these respiratory infections. Intra- and inter-plate precision and accuracy, calibrator performance and control measurements were assessed as part of the validation of these assays. Quantitation spans multiple logs of dynamic range, reducing the need to test multiple sample dilutions. This tool holds promise for enhancing our understand ing, assessment and management of the dynamic serological land scape presented by RSV, SARS-CoV-2 and influenza infections and vaccinations.

Audience Take Away Notes

- A multiplex method for testing and monitoring serological responses to RSV, SARS-CoV-2 and influenza
- They can use the V-PLEX Respiratory Panel 4 (IgG) Kit for at-risk populations to distinguish between vaccinated and /or infected individuals versus negative individuals, for surveillance, in high throughput and simultaneously measure IgG levels to multiple respiratory antigens supporting exploratory R&D to design treatments, assess mechanism of action, for correlate of protection work
- The MSD multiplex sample testing platforms cover a wide range of biomarkers
- It rather than perform singleplex assays, this allows measurement of 9 Respiratory antigens in 1 well, saving on sample volume, giving more consistent measurement, saving time, money and volume for method development
- It will ensure there is no variability in the measurement due to differences due to variables relating to

using 9 singleplex assays- which requires higher sample volume, a variety of pipetting days, freeze/thaw cycles and methods. Nine respiratory antigens are assessed for functional IgG concentration simultaneously

- The V-PLEX Respiratory Panel 4 is a validated, quantitative, multiplexed RUO serology kit that accurately and precisely quantifies IgG antibodies against proteins: CoV-2 Spike (wild-type), CoV-2 Nucleocapsid Spike (XBB. 1. 5), Flu A/Wisconsin/588/2019 (H1N1), Flu A/H7/Shanghai/2013, Flu A/Darwin/6/2021 HA (H3N2), Flu B/Austria/1359417/2021 (B/Victoria-like), Flu B/Phuket/3073/2013 (B/Yamagata-like) and RSV pre-fusion F

Biography

Dr. Jakubik studied Immunology and Microbiology with a focus on HIV immune complex pathogenesis at Rush University Medical Center, Chicago, IL. Her career began at Millipore Corporation (Bedford, MA) and then she held scientific positions at pharmaceutical companies (Genetics Institute, Wyeth, Pfizer, Idenix) prior to leading teams developing and performing bio functional assays for clinical trials at CROs (PPD, Precision for Medicine). This high-throughput infectious disease vaccine work led to a transition into a non-profit, Sabin Vaccine Institute (Washington D. C.), to delve into BSL-4 virus targets and vaccine development with USA government (BARDA) funding. Currently, Jocelyn is leading Serology Assay Development at Meso Scale Diagnostics, Rockville, MD and using her vast history in infectious disease to launch new products on MSD's multiplex platform to address global disease surveillance, vaccine development and outbreak response.

Katherine R Sommers MD
Department of Internal Medicine, Wake Forest University School of Medicine, Winston-Salem, North Carolina, United States

Reactivated disseminated tuberculosis in pregnancy despite repeated negative AFB testing

Disseminated Tuberculosis (TB) is a life-threatening condition resulting from massive hematogenous spread of Mycobacterium tuberculosis leading to infection of various organ systems. It can occur in the setting of primary infection or reactivation of latent infection. Patients often present with nonspecific symptoms and confirmatory lab testing can be time-consuming, making diagnosis difficult. Therefore, maintaining a high clinical suspicion is imperative for early diagnosis and treatment. We discuss a 29-year-old pregnant female who initially presented to the hospital with several weeks of vaginal bleeding in the setting of PPROM (pre-term premature rupture of membranes). She was found to be febrile, tachycardic and hypotensive requiring vasopressor support prior to undergoing D&E in the setting of maternal sepsis with nonviable pregnancy. Her course was complicated by persistent headache and fever with unclear cause. Initial MRI at another hospital revealed multifocal areas of signal abnormality in bilateral hemispheres, cerebrum and brainstem. Repeat MRI with flair showed ring-enhancing lesions within these areas as well as parenchymal edema and nodular leptomeningeal enhancement of the right parietal lobe. Lumbar puncture showed elevated WBC with neutrophil predominance (248), low glucose (20) and elevated protein (90). Despite treatment with broad spectrum antibiotics, the patient continued to fever and intracranial biopsy was pursed which revealed gliosis without evidence of inflammation or malignancy. She began experiencing respiratory symptoms with CT chest demonstrating diffuse bilateral disease with reticular pattern. Bronchoscopy was performed with BAL and cultures were negative. Notably bacterial DNA, fungal DNA, MTB DNA, non-tuberculosis mycobacterial DNA and BAL AFB smears were negative. She developed neurological symptoms for which MRI of the spine was obtained and showed enhancing foci at multiple locations within the spinal cord. Infectious disease was consulted to assist with management. During broad infectious workup, patient was found to have positive QuantiFERON gold and history revealed her to be from a known endemic region. Given above findings, there was high suspicion for disseminated tuberculosis in setting of immunocompromised state secondary to recent pregnancy and septic abortion. RIPE therapy along with steroids was initiated, intermittently held due to elevated liver enzyme and resumed in a stepwise fashion. She was discharge with plan for Directly Observed Therapy (DOT) and close outpatient ID follow up. This case illustrates the importance of maintaining high clinical suspicion for tuberculosis infection despite negative culture data. In unclear cases, a broad workup and detailed history is imperative to ascertain risk factors. By considering the overall clinical picture, imaging and laboratory testing, appropriate treatment can be initiated quickly to prevent further life-threatening complications.

Audience Take Away Notes

- Report a clinical case in which negative testing does not equal absence of disease
- Review diagnostic process involved in latent and /or disseminated tuberculosis
- Discuss an often-overlooked cause of immunocompromise

Biography

Katherine Rose Sommers is a second-year internal medicine resident at Wake Forest University School of Medicine in Winston-Salem. She completed medical school at Indiana University School of Medicine in Indianapolis, IN graduating in 2023. Her clinical interests include infectious disease, immunocompromised patient care, medical education and point of care ultrasound.

Mehwish Zeb
Garden city Hospital, United States

Right thalamic abscess in a caucasian man with rheumatoid arthritis, an intriguing case report

Brain abscess is a localized collection of pus within the brain tissue. It is a rare condition and approximately 1500-2000 cases are presented annually in the United States. The patients with immunocompromised state have a higher incidence of acquiring brain abscess. The most frequent pathogens are streptococcus, staphylococcus, candida, cladophialophora. Most of the brain abscess are spread from contiguous sites, foreign bodies or surgical procedures. Common odontogenic sources include streptococcus, prevotella, haemophilus, fusobacterium. The most common presentation of brain abscess is headache, nuchal rigidity, seizures, cranial nerve deficits, altered mentation, fever, vomiting and focal neurological deficit such as hemiparesis or aphasia.

Herein, we present the case of 57-year-old male patient with two-year history of rheumatoid arthritissince one and half year under treatment with methotrexate and etanercept, presented to our hospital with sudden onset headache, nausea, vomiting and fever for 5 days. Brain Magnetic Resonance Imaging (MRI) illustrated right thalamic intracranial abscess. The right stereotactic brain biopsy was performed and cultures were obtained which detected streptococcus intermedius. He was treated successfully with ceftriaxone and metronidazole forthe course of eight weeks with noneurological sequalae.

To the best of our knowledge, thalamic intracranial abscess of dental origin in an immunocompromised patient is a rare presentation. A clinician should be aware of such patients and early recognition as wellasearly intervention are important to prevent long term sequalae.

Biography

Mehwish Zeb is an Internal medicine resident in Garden city hospital Michigan. She received my MRCP from UK and She is graduated from National University of Sciences and Technology, Pakistan. Her special interest includes travelling and She feels greatest joy from spending time with her husband and her children. She is a doting mother to a beautiful daughter and she keeps her sanity with regular exercise.

Nzolameso Makaya Jennifer
Hopital General De Reference De Kimbanseke Pierre Pokom, 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 rand omized 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

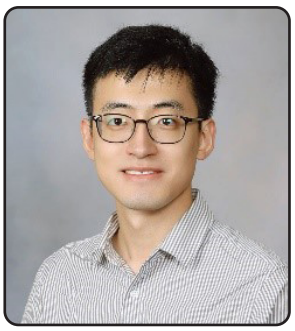
- Proposed treatment is discussed with the patient's family: basal insulin therapy 1-2*/day
- Teaching on the prevention and treatment of hypoglycaemia.
- Home supervision: nursing visit 2*/day for injection and blood sugar control, meals delivered, blood sugar targets: *10mmol

- 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:

Nzolame Somakaya 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.



Qingxiang Liu* and Rew Mercer, Ruipeng Wang, Nate Sallada, Amol Karwa, Vedita Singh, Lucy Gordon, Romel Rosales, Ignacio Mena, Cheyne Kurokawa, Yueh-Ming Loo, Wade Blair
IntegerBio Inc., Gaithersburg, Maryland, United States

Synthetic interferon exhibits potent antiviral activity across both DNA and RNA viruses with reduced pro-inflammatory gene induction

The type I Interferon (IFN) system is a potent host innate defense mechanism against viral pathogens. Activation of this pathway occurs upon engagement of IFN with the host IFN Alpha Receptors 1 and 2 (IFNAR1/2), resulting in activation of > 300 Interferon Stimulated Genes (ISGs). While type I IFN and its derivatives have been utilized in patients as antiviral drugs, toxicity has limited widespread therapeutic use. Here, we describe the generation of synthetic proteins that compete with natural IFNs, comprised of bispecific antibody binding domains with one domain targeting IFNAR1 and the second domain targeting IFNAR2, that were selected to maintain the antiviral properties of IFNs while reducing the pro-inflammatory properties. We show that these molecules activate the IFN pathway as measured by monitoring the phosphorylation of STAT transcription factors in cell lines and primary cells. In addition, we demonstrate significant activation of antiviral ISGs while showing reduced activation of pro-inflammatory and pro-apoptotic ISGs and retention of potent antiviral activity comparable to natural IFN against a broad panel of viruses, including Hepatitis B Virus (HBV), human Cytomegalovirus (CMV), Respiratory Syncytial Virus (RSV), influenza, SARS-CoV-2 as well as other viruses. Our data demonstrate potent antiviral activity with the potential for a meaningful improvement in therapeutic index for improved tolerability and safety in the clinic. In addition to progressing towards therapeutic cand idate, the panel of molecules we have engineered allow for greater interrogation of the underlying biology of the type I interferon pathway and mechanisms of ISG stimulation.

Audience Take Away Notes

- We have generated synthetic proteins that bind to IFNAR1/2 and activate the IFN pathway
- These synthetic interferonsdemonstrateantiviral properties equivalent to natural IFNs against a broad panel of DNA and RNA viruseswith reduced activation of pro-inflammatory and pro-apoptotic ISGs
- Synthetic interferons demonstrate the potential to provide meaningful improvement in therapeutic index for improved tolerability and safety in the clinic
- Synthetic interferons can confer greater understand ing of the biology of the type I interferon pathway and mechanisms of signaling that lead to ISG expression

Biography
Dr. Qingxiang Liu is currently a Senior Scientist at IntegerBio Inc. Dr. Liu studied biochemistry and molecular biology in the context of innate immune signaling transduction and antiviral response and received his PhD from the Sun Yat-sen University, China in 2019. He pursued his postdoctoral training with Professor Chris Garcia (Stanford University) studying interferon and cytokine engineering. Dr. Liu pursueda second postdoctoral fellowship with Professor Jorg Goronzy (Mayo Clinic) studying T cell immunityand autoimmunity.

Shivani Aluru, MD* and Rone Chun Lin, MD
Internal Medicine, University of Illinois College of Medicine, Peoria, IL, USA

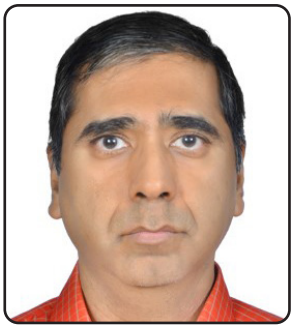
Miliary histoplasmosis in a recently transplanted patient

Miliary histoplasmosis is an unusual presentation of pulmonary histoplasmosis and may also represent disseminated disease at onset. Immunocompromised patients remain at high risk for this rare infection - with solid organ transplant patients specifically having an incidence of <0. 5%, even in endemic areas. This case study follows a 29-year-old male with a complex medical history, including factor 5 deficiency, end-stage renal disease secondary to glomerulonephritis and a recent living donor renal transplant. Initially presenting with respiratory symptoms, he was diagnosed with atypical community-acquired pneumonia, later identified as histoplasmosis. Despite initial treatment, including ceftriaxone and azithromycin, the patient's condition deteriorated due to immunocompromise from anti-rejection medications. Further testing confirmed histoplasmosis, leading to treatment with voriconazole and subsequent complications, including a drug reaction and relapse of infection. The case highlights challenges in managing fungal infections in immunocompromised hosts and the importance of adjusting treatment based on radiographic findings and laboratory tests. Additionally, it raises questions about the optimal duration of antifungal therapy in solid organ transplant recipients, suggesting the need for longer courses compared to guidelines for other patient populations.

Audience Take Away Notes

- How to use urine antigen testing to guide ongoing antifungal therapy
- Assessing ongoing multidisciplinary guided therapy for both ongoing antifungal use with immunosuppressants to avoid graft rejection
- Consider how imaging intervals can be further optimized to assess for disease progression/ regression when symptoms are atypical

Biography
Dr. Aluru is an internal medicine resident with an interest in pulmonary medicine. After graduating from American University of the Caribbean, Aluru gone on to train in Illinois at UICOMP/OSF.



Dr. Arun Agarwal[2], Director Internal Medicine, Dr. Sunit Mathur[1]*, Consultant & In charge Adult Vaccination Centre, Dr. Mudit Agarwal[3], Resident

[1, 2]Department of Internal Medicine, Fortis Escorts Hospital, Jaipur, Rajasthan, India

[3]Resident, All India Institute of Medical Sciences, New Delhi, India

Incidence of influenza A in COVID-19 patients admitted during COVID-19 global pand emic in a multispecialty hospital in Rajasthan, India

Introduction: The Coronavirus disease COVID-19 pand emic stretched the global health care system to its maximum limits. There is significant overlap between Coronavirus disease and Influenza A with similar modes of transmission and symptoms. This study was undertaken to estimate the incidence of coinfection of Influenza A in patients of Corona virus disease and the interaction of both the viruses.

Material and Methods: A cross sectional study was conducted in Department of Internal Medicine at Fortis Escorts Hospital, Jaipur, Rajasthan, India. We estimated the incidence of Influenza A coinfection in 101 COVID-19 patients from 1, August, 2020 to 31, December, 2020. This study was approved by the Institutional Ethical Board of Fortis Escorts Hospital, Jaipur, Rajasthan, India.

Observation/Result: We analyzed the data of 101 COVID-19 patients admitted from 1, August, 2020 to 31, December, 2020 and found that out of 101 COVID-19 patients 9 were coinfected with Influenza virus with an incidence of 8. 9%. All the 9 coinfected patients had raised total leucocyte count (TLC) range (10. 65-18. 4) and Neutrophil/Lymphocyte ratio range (7. 75-18. 0). The duration of stay in hospital was also prolonged in co infected patient than isolated COVID-19 patients.

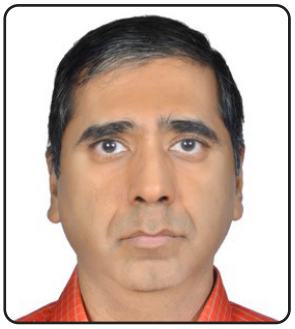
Conclusion: Incidence of Influenza A with Coronavirus disease is variable in different parts of the world. The coinfected patients have a significantly higher inflammatory response with more severe form of disease as compared to isolated coronavirus disease. The duration of stay in hospital was also prolonged with more risk of complications. High risk patients like pregnant females, elderly, Type2 DM, malignancy and or with multiple co-morbidity must be screened for Influenza A virus. This study has some limitations like small sample size, short duration and the confinement to single geographical location. More extensive studies are required to understand the interaction between Influenza A and Coronavirus disease.

Audience Take Away Notes

- The study highlights the need to screen Coronavirus disease patient with Influenza A
- The audience will understand the need to screen the Corona virus disease patients with high risk like elderly, comorbidity patient for Influenza A
- The study highlights the need for more extensive study to understand the interaction between Influenza A and Coronavirus Disease
- This study also highlights the need for more extensive seasonal flu vaccination drive for community at risk as a preventive measure
- The coinfected patients had hyperinflammatory response, are at increased risk of complications, prolonged hospitalization

Biography

Dr. Mathur is Geriatrician, Public Health Specialist and Health Educator who has done medical graduation from Jawahar Lal Nehru Medical College, Ajmer. Mathur done Masters from University of Wollongong, Australia. Mathur also done European accredited one-year Diploma of International Association of Gerontology and Geriatrics IAG e-TRIGGER ASIA Oceanic course awarded by Swiss Health Sciences e training Foundation in 2024. Mathur worked for World Health Organization on Study on Global Ageing and Adult Health. Mathur also participated in Virtual Toronto International Training Program to Strengthen Family Medicine and Primary Care in 2021 and 2022 conducted by DFCM, University of Toronto, Canada. Mathur trained in HIV Medicine from University of Medicine and Dentistry, New Jersey, USA. Mathur been certified by AHA as Instructor for Basic and Advanced Cardiac Life Support provider course.



Dr. Neeraj Nagaich[1], Dr. Sunit Mathur[2*], Dr. Radha Sharma[3]
[1, 2]Department of Gastroenterology, Fortis Escorts Hospital, Jaipur
[3] Department of Pathology RUHS CMS Jaipur

Profile of patient with acute viral hepatitis: An 8-year observational study from a tertiary care centre

Hepatitis A virus (HAV) and hepatitis E virus (HEV) are important causes of acute viral hepatitis (AVH) and acute liver failure (ALF). Due to the paucity of data, the exact burden of the disease is not established.

Objective: Considering this background, the present study aims to determine the prevalence, epidemiology and biochemical correlation in AVH due to HAV and HEV.

Setting and Design: It was a retrospective observational study conducted over 8 years from August 2016 to September 2024 in a tertiary care hospital.

Material and Methods: The study population included 907 patients (outdoor and hospitalized) having clinical features of AVH. All serum samples from these patients were tested in duplicate for immunoglobulin M (IgM) anti-HAV and IgM anti-HEV antibodies using commercially available enzyme-linked immunosorbent assay (ELISA) kits. The liver function tests (LFTs) were also monitored.

Results: Of the 907 specimens processed from the patients with AVH, 60 (6. 50%) were positive for IgM anti-HAV antibodies and 77 (7. 5%) were positive for IgM HEV antibodies. A total of 5 patients (0. 60%) were positive for both anti-HAV IgM and anti-HEV IgM antibodies indicating HAV-HEV confection. Our study shows that the HAV infection was more prevalent in the pediatric age group. The HEV infection was seen in all age groups and more prevalent in the age group of 20–30 years. The infection was more prevalent between the month of June to October, that is, during monsoon and post-monsoon seasons. Total serum bilirubin, serum glutamic oxaloacetic transaminase (SGOT), serum glutamic pyruvic transaminase (SGPT) and alkaline phosphatase (ALP) were elevated at 85. 84, 86. 79, 91. 5 and 83. 96%, respectively, in HAV-infected and elevated at 78. 12, 93. 75, 67. 18 and 57. 03%, respectively, in HEV-infected patients. The patients with HAV-HEV coinfection had all deranged LFTs indicating more severe form of disease.

Conclusion: The present study emphasizes the importance of screening all hepatitis viral markers (A, B, C, E) for early diagnosis and curtailment of outbreaks and epidemics by the public health sector reducing morbidity and mortality.

Biography

Dr. Mathur is Geriatrician, Public Health Specialist and Health Educator who has done medical graduation from Jawahar Lal Nehru Medical College, Ajmer. Mathur done Masters from University of Wollongong, Australia. Mathur also done European accredited one-year Diploma of International Association of Gerontology and Geriatrics IAG e-TRIGGER ASIA Oceanic course awarded by Swiss Health Sciences e training Foundation in 2024. Mathur worked for World Health Organization on Study on Global Ageing and Adult Health. Mathur also participated in Virtual Toronto International Training Program to Strengthen Family Medicine and Primary Care in 2021 and 2022 conducted by DFCM, University of Toronto, Canada. Mathur trained in HIV Medicine from University of Medicine and Dentistry, New Jersey, USA. Mathur been certified by AHA as Instructor for Basic and Advanced Cardiac Life Support provider course.

Xinxin Wang*, Yunliang Tu
ICU of Peking University Shenzhen Hospital, Shenzhen, China

Pulmonary vascular endothelial injury and acute pulmonary hypertension caused by COVID-19: The fundamental cause of refractory hypoxemia?

Coronavirus disease (COVID- 19) is a severe infectious disease caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) that binds to the cells; Angiotensin Converting Enzyme 2 (ACE2) receptor. In the first severe case of COVID- 19 in Shenzhen city, we found that in addition to the typical clinical manifestations, our patient presented hemoptysis, refractory hypoxemia and pulmonary fibrosis- like changes on Computed Tomography (CT) involving alveoli and pulmonary interstitium in the early stage and acute pulmonary hypertension and right heart failure in the later stage, which were not completely justified by myocarditis, Acute Respiratory Distress Syndrome (ARDS), pulmonary fibrosis and high PEEP level. The lung compliance deteriation of this patient was not as serious as we expected, indicating classic ARDS was not existed. Simultaneously, the first autopsy report of COVID- 19 in China showed normal- structured alveoli and massive thick excretion in the airway. Then, we speculated that the virus not only attacked alveolar epithelial cells, but also affected pulmonary vascular endothelial cells. Imbalance in the ACE2-RAAS-bradykinin axis and the cytokine storm could be an important mechanism leading to pathophysiological changes in pulmonary vascular and secondary refractory hypoxemia. Pulmonary vasculitis or capillaritis associated to immune damage and an inflammatory storm could exist in COVID- 19 because of ground-glass opacities in the subpleural area, which are similar to Connective Tissue Disease associated Interstitial Lung Disease (CTD-ILD). Thus, this case elucidates new treatment measures for COVID- 19.

Audience Take Away Notes

- The reasonfor acute pulmonary hypertension
- Whether the right heart failure induced by high PEEP besides pulmonary hypertension
- The role of autoimmune responses in the case
- The result of imbalance among the ACE2- RAAS-bradykinin axis
- What message had been transmitted by autopsy
- Whether the case show classic ARDS

Biography

Dr. Wang Xinxin obtained his clinical medical degree from Southern Medical University in 2011. She then undertook stand ardized training at Peking Union Medical College Hospital from 2011 to 2014 and successfully graduated. Since 2014, she has been dedicated to the field of critical care medicine and has earned a master's degree. Dr. Wang has long been committed to the clinical work of critical care medicine.

BOOK OF ABSTRACTS

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