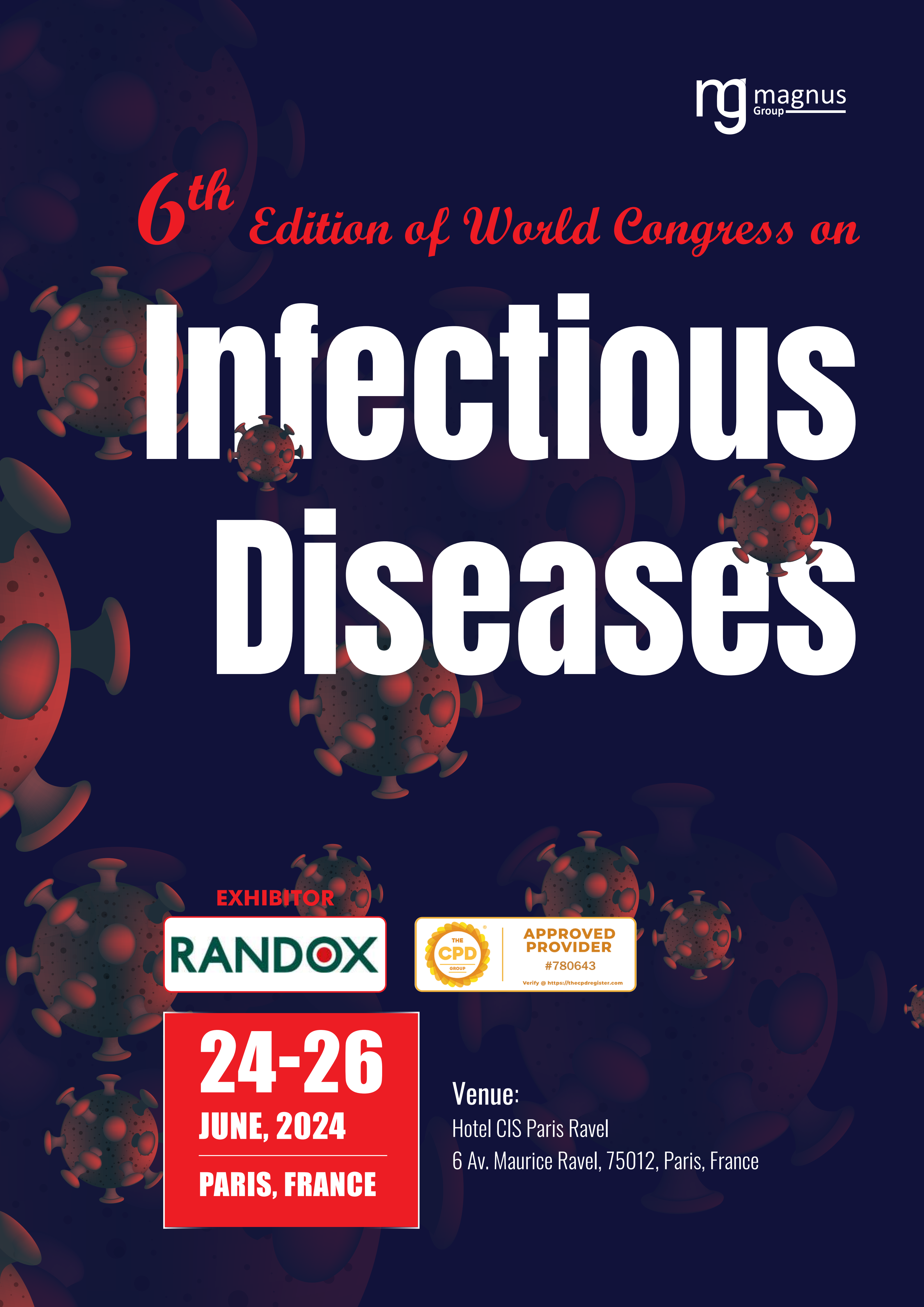

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6th Edition of World Congress on

Infectious Diseases

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24-26
JUNE, 2024

PARIS, FRANCE

Venue:
Hotel CIS Paris Ravel
6 Av. Maurice Ravel, 75012, Paris, France

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JUNE

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Thank You
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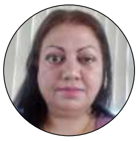

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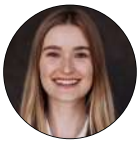

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Thank You
All...

Welcome Message

PROF. DR. Daniel A. Lichtenstein

Ambroise Pare Hospital, France

Dear congress visitors,

It is an honor and pleasure to write a few welcome notes. This conference deals with a wide subject of prime importance in the field I work with (critical care medicine, where sepsis is one of the major concerns). I am impressed so see so many countries involved, making this congress a really international one. Infections concern all countries regardless their income, and this conference is welcome. The topics cover a wide area, with a fine mingling between experts talks and more basic ones. In this perspective, my topic, equivalent so to speak to “how to diagnose pneumonia [using ultrasound]” may appear oversimplistic, so likely, I will learn more than teach. This is all the more true that the topics seem much more clinical than fundamental, with the advanges for the patients one can imagine.

Welcome Message

Stephen Hsu, PhD

Augusta University, GA, USA

Dear Colleagues,

On behalf of the Organizing Committee, we would like to welcome you to participate in the 2nd Edition of World Congress on Infectious Diseases – INFECTION 2022 in Rome, Italy, during June 17-18. I understand it is a very challenging time when we are facing an unprecedented SARS-CoV-2 pandemic. On the other hand, it is also an extraordinary time to witness the collective effort to combat this deadly infectious disease with rapid development of prophylactic and therapeutic methods. The unique theme of this event "Stepping Stones in Infectious Diseases Prevention, Control and Cure" will bring us together to share our discoveries and achievements aiming to improve human health globally. Your participation will certainly contribute to the fight against infectious diseases worldwide.

Welcome Message

Krzysztof Skowron

Nicolaus Copernicus University in Torun, Poland

Dear Conference Attendees,

It is with great pleasure and honor that I extend a warm welcome to all of you participating in the session entitled "Antimicrobials/ Antibiotics/Antibacterial". In the face of the escalating challenge posed by antimicrobial resistance, particularly the growing resistance of bacteria to antibiotics, our collective efforts are crucial to explore innovative solutions.

In recent years, the urgent need for new and effective antimicrobial agents has become apparent. This session aims to delve into the diverse spectrum of problems associated with antimicrobial resistance and present cutting-edge techniques for combatting microorganisms, not limited to traditional antibiotics. Recognizing the gravity of the situation, a multidisciplinary approach is imperative, combining the exploration of novel drugs with both basic and clinical research. The pursuit of groundbreaking interventions is essential to secure therapeutic success, especially in the context of infections caused by multidrug-resistant strains. This session provides a unique platform for participants, ranging from seasoned researchers to budding scholars, scientists, clinicians, and academics, to foster an exchange of ideas and knowledge.

Several key topics will be addressed in our session, including:

1. **Novel Antimicrobial Agents:** Exploring innovative drugs and treatments beyond traditional antibiotics to tackle evolving resistance challenges.
2. **Multidisciplinary Research:** Encouraging collaborative efforts in basic and clinical research to develop a comprehensive understanding of antimicrobial resistance mechanisms.
3. **Alternative Therapies:** Delving into non-antibiotic approaches for combating pathogenic microorganisms and their potential applications in clinical settings.
4. **Global Perspectives on Antimicrobial Resistance:** Discussing the varying degrees of antimicrobial resistance across regions and exploring strategies for global collaboration.
5. **Clinical Implications and Challenges:** Examining the practical implications of antimicrobial resistance in clinical settings and addressing the challenges faced by healthcare professionals.

Our conference serves as a unique opportunity for all participants to not only gain insights into the latest research on antimicrobial drugs but also to engage in meaningful discussions that can shape the future of antimicrobial therapies.

Welcome Message

Masafumi Seki MD, PhD.

Saitama Medical University International Medical Center, Japan

Dear Colleagues and Friends,

It is our great pleasure to invite distinguished researchers to the Infection 2024 on June 24-26, 2024 at Paris, France. Science about infectious diseases field today makes unprecedented progress since the pandemics of novel influenza 2009 and COVID-19. This opens new opportunities to adapt new era to social change, to achieve higher treatment and prevention efficiency, and to introduce intelligent, differentiated methods to works against these infectious diseases. It is obvious that both basic and clinical research could go together, and these studies based of precise microbiological and clinical evidence will be the future basis for success.

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.

ABOUT

Infection 2024

6th Edition of the World Congress on Infectious Diseases is a prestigious global event scheduled to take place in **Paris, France**, from **June 24-26, 2024.** This congress unites scientists, researchers, healthcare professionals, industrialists, and industry experts to exchange knowledge and explore advancements in the field of infectious diseases.

The **Infection 2024** Summit centers around the theme "**Global Strategies in Infectious Disease Control: Challenges and Innovations.**" It emphasizes the critical role of infection control in preventing the spread of infectious agents, improving healthcare outcomes, and promoting overall well-being. The aim of Infection 2024 is to address contemporary challenges faced by societies worldwide and to find innovative solutions.

Attendees can look forward to a comprehensive agenda featuring keynote sessions, workshops, oral and poster presentations, and networking events. The Infection 2024 Conference offers a unique opportunity for meaningful discussions, experience sharing, and establishing professional connections. Renowned speakers from academia, industry, and research institutions will share their expertise on cutting-edge research, emerging trends, and breakthrough technologies in the field of infection. This event brings together like-minded individuals from around the globe, fostering collaboration and interdisciplinary discussions to shape a promising future for humanity through advancements in infectious diseases and related fields.

EXHIBITOR

RANDOX

For over 40 years, Randox has developed an expertise in molecular diagnostics, offering a range of QC solutions for comprehensive infectious disease testing.

Our molecular innovations include the Discovery and Vivalytic analysers, capable of testing for a range of targets ranging from respiratory, genitourinary, and gastrointestinal and hospital-acquired infections. In addition, we are also a leading provider of molecular quality-controls, with Qnostics' expansive molecular IQC portfolio and our world-leading molecular EQA scheme: QCMD with its variety of programmes, Randox is leading the way to meet the needs of today's molecular laboratories.

Contact Information:

Website: https://randoxhealth.com/en-GB/

Email: marketing@randox.com

ABOUT

CPD Credits

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Continuing Professional Development (CPD) credits are valuable for **Infection 2024** attendees as they provide recognition and validation of their ongoing learning and professional development. The number of CPD credits that can be earned is typically based on the number of sessions attended. You have an opportunity to avail 1 CPD credit for each hour of Attendance. Some benefits of CPD credits include:

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

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

Increased knowledge: Attending Infection 2024 and earning CPD credits can help attendees stay current with the latest developments and advancements in their field.

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

Note: Each conference attendee will receive 20+ CPD credits.

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KEYNOTE FORUM

Will the Seine river water jeopardize the athlete's health during the sporting events of the 2024 olympic games in France

After describing the situation in which the athletes of the XXXIII Olympiad in France in 2024 from 26 July to 11 August, will find themselves namely, the city of Paris, the Seine River, the medical infrastructure, the past experience with SARS, and giving data on hygiene, pathogens in rivers, vectors (rats), and briefly presenting the Olympic and paralympic games and their medical organization, the risks to the athletes and parathletes, the authors present diseases that pose a real or potential risk to the competitors and others who will swim in the river.

They start with the transmission of pathogens and broach the following diseases with their mode of transmission, symptoms, and complications: (1) viral diseases, including enteric viruses, hepatitis A and E, the lymphocytic choriomeningitis virus, (2) bacterial diseases, starting with water disease outbreaks due enterococci, escherichia coli, salmonella, including leptospirosis with examples of outbreaks, Escherichia coli 157, salmonellosis, shigellosis, campylobacter, enterococcus faecalis, and parasitic diseases including amebiasis from free amebas, ascariasis, giardiasis, trichuriasis, cryptosporidiosis, and balantidiasis.

In conclusion, they provide recommendations regarding how to eliminate rats with maintenance measures and offer general considerations concerning global health.

The author's goal is to ensure that anyone who swims in the Seine River during the Olympic and paralympic games can do it as safely as possible vis a vis the risk of contracting an infectious or parasitic disease.

Audience Take Away Notes

- The preparation of the Seine River to protect the health of the olympic athletes competing in it may be insufficient
- The data available are too few to be reassuring
- The unknown creates risks to the athletes
- There are ways to do much better
- By informing their colleagues and friends
- By showing the scope of what is needed in such circumstances
- Depending on their subject area, this could be integrated into their teaching
- It provides solution to a problem and make a designer's job more efficient
- This will improve accuracy and assist in design problem

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Biography

Dr. Claudia Ferreira is an MD, PhD, graduated in medicine from the University of Cordoba in Argentina, followed by a fellowship from the Harvard AIDS Institute and the University of Texas Health Science Center in Houston, TX, USA. Dr. Ferreira has dedicated the last 25 years of her career to the fields of infectious diseases, tropical diseases, and gastroenterology. Dr. Ferreira was also a medical editor of a web portal related to community awareness for bioterrorism after 9/11. Dr. Ferreira also worked as an investigator for the National Agency for AIDS Research, a branch of the National Center for Research Science, and for several pharmaceutical laboratories in France. She recently joined Biophytis, a Sorbonne University branch, developing a new drug to against organ damages due to aging related muscular disorders and restauration of pulmonary damage caused by infectious diseases such as Covid-19 and Influenza.

- Other benefits
    - Awareness of the risks
    - General description of the risks
    - Short descriptions of the diseases (mode of transmission, symptoms, complications)
    - Recommendations for solutions
    - Considerations regarding global health

Ultrasound for diagnosing Pneumonia. The place of the BLUE-protocol

The BLUE-protocol is an ultrasound approach of lungs and veins, allowing with fine accuracies an immediate diagnosis of an acute respiratory failure among the six causes which regard 97% of patients seen in critical settings: Hemodynamic pulmonary edema, pulmonary embolism, pneumonia, COPD, asthma and pneumothorax, mainly.

The BLUE-protocol is a fast protocol (less than 3 minutes). It requires a simple unit, uses the ten basic signs of lung ultrasound, and associates signs with locations. Three standardized points per lung are used. BLUE-protocol includes a venous analysis, different from usual habits (we don't detail), done in the case of normal anterior lung surface.

The BLUE-protocol generates eight profiles, half devoted to diagnose pneumonia. The A-profile is a "pre-profile", designing anterior lung sliding with anterior A-lines. It shows normal lung surface, and rules out immediately pneumothorax and hemodynamic pulmonary edema. It generates three profiles. The A-DVT profile means that a DVT was detected, and is 99% specific to pulmonary embolism.

The A-V-PLAPS-profile. The PLAPS (posterior or lateral alveolar and/or pleural syndrome) indicates the presence of alveolar and/or pleural change, uni- or bilateral, at a subposterior point accessible in supine patients with short probes, called PLAPS-point. Alone, a PLAPS has no specificiy. Associated to the A-profile, when the venous network is free, it indicates (posterior) pneumonia with 89% accuracy.

The nude profile, defined by the A-profile, absence of visible DVT and absence of PLAPS. It is usually associated to asthma or COPD (two diseases gathered because therapy is roughly similar). The B-profile, designing anterior lung sliding with anterior lung rockets indicates usually hemodynamic pulmonary edema. It rules out asthma, COPD, pulmonary embolism.

The B-prime profile is a B-profile with abolished lung sliding. It is quite specific to pneumonia (100% in). The A-prime profile is an A-profile with abolished lung sliding. It is highly suggestive of pneumothorax. The detection of a lung point will confirm the diagnosis and indicate the size of the pneumothorax.

The A/B profile is an half A-profile at one lung, and an half B-profile at the other. It is quite specific to pneumonia. The C-profile indicates anterior lung consolidation, regardless size and number. A minima, it can just give the illusion of an irregular pleural line. It is quite specific to pneumonia (98% in).

Daniel A. Lichtenstein

Medical intensive care unit,
Hopital Ambroise Pare, Paris-West University, France

Biography

Daniel Lichtenstein, medical intensivist, Ambroise-Pare Hospital (Paris), created holistic critical ultrasound in 1985 (Intensive Care Med 1993;19:353-355), defined by simple equipments, one universal probe for whole body, emphasis on lung, holistic cardiac sonography, veins, procedures (venous canulation...) extrapolable to multiple disciplines (pediatrics, pulmonology...), settings (ICU, austere areas...). Six hundred conferences. Six textbooks since 1992 (latest "Lung ultrasound in the criticall ill - the BLUE-protocol" - Springer 2016). Original articles including: BLUE-protocol (acute respiratory failure), FALLS-protocol (lung ultrasound in circulatory failure), SESAME-protocol (cardiac arrest), lung ultrasound in neonates. President of CEURF (training center at bedside in I.C.U.).

Many questions are answered. one of the most frequent questions regards the non inclusion of the heart in the decision tree. This analysis is associated, not included, to the BLUE-protocol, which makes a direct analysis of the lung (the suffering organ). A simple cardiac sonography, without Doppler, will provide, at this step, major information, if needed. All these data are gathered in a traditional clinical approach, the aim is to provide quick relief of acute dyspnea, and decrease of use of irradiating tests. The BLUE-protocol is at best taught in authorized centres. It uses simple machines, one whole body probe for lungs, veins, heart, others. The BLUE-protocol is a typical illustration of holistic ultrasound.

Audience Take Away Notes

- By performing critical holistic ultrasound (this term also implies a simplified approach for steep learning curve)
- By finding immediately strong arguments or more for diagnosing pneumonia
- This research that other faculty could use to expand their research or teaching
- This provide a practical solution to a problem that could simplify or make a designer's job more efficient
- It improve the accuracy of a design, or provide new information to assist in a design problem
- Other benefits
    - All the benefits of ultrasound (immediate, bedside, not invasive, repeatable at will, unexpensive, keeps contact with patients and others). Provides visual approach to the lung and most other structural disorders (in abdomen, heart, venous system...). Visual medicine to the point that some call ultrasound the stethoscope of tomorrow (and for us the stethoscope of ever, as we have been using it since 1985)

Antibiotic resistance of enterococcus spp. strains isolated from wild and farm animals - An important non-clinical problem

The increase in the transfer of pathogenic microorganisms between humans, livestock, wildlife and their environment observed in recent years, as well as the irrational use of antibiotics, makes it increasingly difficult to combat the growing multidrug resistance of bacteria such as Enterococcus spp.

The aim of the study was to evaluate the prevalence and antibiotic resistance of Enterococcus Faecalis (EFA) and Enterococcus Faecium (EFM) strains isolated from the environment of pig farms and Enterococcus spp. strains isolated from fecal samples of wild animals. Material for the study was collected in a piggeries and within forested areas and ecotone zones in the Kuyavian-Pomeranian Voivodeship. Samples were inoculated onto selective media, and grown bacteria were identified using the MALDI TOF system. Antibiotic susceptibility was assessed using the disc-diffusion method, according to EUCAST recommendations.

In total, 475 and 98 samples were collected from the pig husbandry environment (swabs from troughs, feeding passages and corridors, manure channels, and faeces samples) and from 12 wildlife species (faeces samples), respectively. Of the samples from a pig farm environment, 82 (17.3%) EFA strains and 28 (5.9%) EFM strains were identified. The highest percentage (19.5%) of EFA strains showed resistance to high concentrations of gentamicin (HLGR phenotype), followed by high concentrations of streptomicin (HLSR phenotype) and imipenem (9.8% and 8.5% of strains, respectively). In the case of EFM, an equally high percentage (17.9%) of strains were characterized by the HLGR phenotype and resistance to ampicillin, in addition, 14.3% of strains were resistant to vancomycin (VRE phenotype). In 10.7% of EFM strains was present HLSR phenotype, while 6.1% of EFA was characterized by VRE phenotype. All strains tested showed sensitivity to tigecycline.

Among 92 out of 98 fecal samples from wild animals tested, 118 strains of Enterococcus spp. belonging to 9 species were isolated (EFA, EFM, E. hirae, E. mundtii, E. casseliflavus, E. faecium, E. durans, E. gallinarum, E. avium and E. thailandicus). The most frequently isolated (32.2% of strains) EFA species was detected in 38 collected samples. The remaining species were isolated with a frequency ranging from 1.0% to 22.4%, among which EFM accounted for 7.6% of the isolated strains. The highest percentage of antibiotic-resistant strains from different chemical groups was found among EFA and EFM. The former was most often resistant to eravacycline (50.0% of strains) and linezolid (39.5% of strains), while

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[2]Department of Microbiology and Food Technology, Jan and Jedrzej Sniadecki University of Technology in Bydgoszcz, Poland

Biography

Dr. Hab. Inz. Krzysztof Skowron, prof. UMK, obtained his Ph.D. in agricultural sciences in 2011 from UTP University of Science and Technology in Bydgoszcz, Poland. Since 2011, he has been affiliated with the Department of Microbiology at L. Rydygier Collegium Medicum in Bydgoszcz, Nicolaus Copernicus University in Torun, Poland. In 2019, he earned the habilitated doctor degree in medical sciences, specializing in medical biology. Currently, he holds the position of associate professor. Dr. Hab. Inz. Krzysztof Skowron, prof. UMK, focuses his research on various aspects of antimicrobial

EFM was resistant to quinupristin-dalfopristin (44.4% of strains). VRE, HLGR and HLSR phenotypes were found in 13.2%, 31.6% and 2.6% of EFA strains, respectively. In the case of EFM, only the HLGR phenotype was found (11.1% of strains). The lowest percentage (0.9%) among the Enterococcus spp. strains tested was resistant to ampicillin.

The conducted research has shown that both in the pig faeces and various production sectors of the pigsty, as well as in the feces of wild animals, there are microorganisms potentially pathogenic to humans, which may constitute a reservoir of resistance genes to various antibiotics.

Audience Take Away Notes

- The presentation highlights that the livestock and wildlife environment can also be an important reservoir of multidrug-resistant strains and a pathway for the transmission of antimicrobial resistance genes from commensal zoonotic bacteria to clinical strains
- Wide spread of antibiotic resistance makes therapeutic options for various types of human and animal infections increasingly limited
- Non-clinical monitoring antibiotic resistance in an era of increasing antimicrobial resistance in bacteria is of great importance for public health
- The presentation is intended to draw attention to the rational management of antibiotics in animal production and veterinary medicine, as well as to monitoring antibiotic residues in the environment and the phenomenon of carriage of antibiotic-resistant strains in animals

activities, microbial tolerance to stress factors, antibiotic resistance, and the detection and expression assessment of genes primarily associated with virulence and responses to environmental stress. His interests extend to emerging pathogens, zoonotic pathogens, and the transmission of microorganisms between animals and humans. Dr. hab. inż. Krzysztof Skowron, prof. UMK, has authored 108 full-text publications and contributed to 6 chapters in monographs.

Assay identifies rVSVΔG-ZEBOV-GP vaccination status and correlates ebola virus glycoprotein with vesicular stomatitis Indiana virus nucleoprotein antibodies

In the absence of well-defined correlates of protection, the quantity and duration of the main vaccine-antigen-induced Immunoglobulin G (IgG) antibodies are often used as proxy indicators of vaccine efficacy; IgG responses to vaccine vector antigens are less well-characterized. Here, we describe the concomitant kinetics of IgG responses to the vaccine vector (Vesicular Stomatitis Indiana Virus) Nucleoprotein (VSIV N) and the inserted Ebola virus glycoprotein (EBOV GP1,2) components of the "rVSVΔG-ZEBOV-GP" vaccine. We also evaluate their use as biomarkers to confirm self-reported vaccination status.

Longitudinal samples from 212 participants through one-year post-vaccination from the Partnership for Research on Ebola Virus in Liberia I (PREVAIL I) clinical trial were selected. Anti-EBOV-GP1,2 IgG and anti-VSIV-N IgG titers were measured using the established Filovirus Animal Non-Clinical Group (FANG) Enzyme-Linked Immunosorbent Assay (ELISA) and a newly developed single-molecule array (Simoa) immunoassay, respectively.

Following vaccination, anti-EBOV-GP1,2 IgG and VSIV-N IgG were first detected at 10–14 d. Antibody levels further increased by 28 d and then remained stable through 360 d post-vaccination. Significantly higher antibody titers were measured in samples from female participants compared to those from male participants. Anti-EBOV-GP1,2 and anti-VSIV-N IgG titers were significantly correlated ($p<0.001$) at day 28 ($r=0.47$), day 180 ($r=0.45$), and day 360 ($r=0.59$). At 28 d, the Area Under the Receiver Operating Curve (AUROC) discriminated vaccinated from unvaccinated patients with high accuracy (AUROC=0.965 for anti-VSIV-N IgG; AUROC=0.945 for anti-EBOV-GP1,2 IgG [$p<0.001$]).

We conclude that the newly developed assay reliably measures vector-targeted humoral responses after rVSVΔG-ZEBOV-GP vaccination and can confirm vaccination status in individuals with unknown or self-reported vaccination status. Reliable detection of anti-VSIV IgG may be useful for similar queries of VSIV-vectored vaccine candidates in development for other infectious diseases.

Audience Take Away Notes

- Currently, there are no unambiguous reports of the antibody responses kinetics of vector-induced versus the vector-encoded EBOV GP1,2 antigens. In a Western African population vaccinated with rVSVΔG-ZEBOV-GP, we addressed this gap by determining the IgG response kinetics to VSIV using the Simoa assay in tandem with anti-EBOV GP1,2 IgG in the same study participants. The anti-VSIV-N and anti-EBOV-GP1,2 IgG titers significantly correlated at 28 and

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360 d after vaccination, indicating a coordinated antibody response to the vaccine vector and the antigen of interest

- A novel assay was developed using Simoa Planar Technology to identify rVSVΔG-ZEBOV-GP vaccination status. This assay can be utilized for any vaccine candidate that uses N VSIV as the vector to (a) confirm vaccination status in individuals with unknown or self-reported vaccination status and (b) to understand and clarify the relationship between vaccination and subsequent infection and/or disease
- Sex differences in the rVSVΔG-ZEBOV-GP vaccine IgG responses was observed. Female vaccinees had significantly higher IgG levels than males at earlier time points

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Biography

Dr. Prabha Chandrasekaran, M.Sc., Ph.D., M.P.H., is an Associate Study Director (contractor) at the Integrated Research Facility at Fort Detrick, a National Institute of Allergy and Infectious Diseases biosafety level 4 facility. Dr. Chandrasekaran's role is to support clinical research studies pertaining to high-consequence and emerging pathogens in international settings. She designs and executes the diagnostic/assay countermeasures and develops and deploys high-throughput sequencing and bioinformatics approaches towards outbreak preparedness. Dr. Chandrasekaran is a multidisciplinary scientist with over 40 peer-reviewed research publications and has served as a principal investigator (PI) or co-PI on several projects.

Societal factors constraining the application of advances in biological sciences for controlling COVID-19 and mosquito and tick-borne diseases

While many advances in biological sciences have been applied in medicine, agriculture and industry with great benefit, some recent trends in society, governance structures and communications, appear to be hampering the use of new scientific findings for controlling infectious diseases. These limitations are illustrated with examples related to (i) the adaptation of fresh water mosquito vectors of major arboviral diseases to salinity in coastal areas with consequences for disease transmission, (ii) understanding the implications of reduced dengue transmission during the COVID-19 lockdown for dengue control, (iii) causes underlying the rapid spread of the malaria vector Anopheles stephensi in South Asia and Africa, (iv) the application of serodiagnostic techniques for Lyme disease and tick-borne relapsing fever caused by tick-borne bacteria of the genus Borrelia, and (v) COVID-19 prevention.

Audience Take Away Notes

- Better understand relevance of recent biological 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

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Biography

Ranjan Ramasamy graduated in 1971 and then a PhD in 1974 from the University of Cambridge, UK. He was the Chairman of the National Science Foundation of Sri Lanka, Professor of Life Sciences at the Institute of Fundamental Studies in Kandy in Sri Lanka, Professor of Biochemistry in the University of Jaffna in Jaffna 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.

Clinical significance and global burden of antibiotic resistance

Antibiotic Resistance (AR) is both clinical and global public health concerns. In numerous countries, physicians have very few other options available to treat MDR and XDR infections. The World Health Organization (WHO) acknowledges AR is one of the top global public health and development threats. Indeed, AR is a leading cause of mortality worldwide, with the highest burdens in resource limited countries. Understanding the depth of global AR impact can help identify the current gaps and mitigate measures to control its spread. It's been estimated 12 major infectious syndromes, 23 bacterial pathogens and 18 antibiotic regimens (targeted and empirical) currently contribute to the global AR. Prior to COVID-19 pandemic (2019), it's been reported six additional pathogen-antibiotic combinations each was responsible for nearly 100,000 AR-attributable deaths primarily due to third-generation cephalosporin-resistant E coli, carbapenem-resistant A baumannii, fluoroquinolone-resistant E coli, carbapenem-resistant K pneumoniae, and third-generation cephalosporin-resistant K pneumoniae. Based upon numerous recent studies, nosocomial MDR K. pneumoniae isolates has been recorded from 28 countries in six regions of the world. For example, one study reported the estimates of ESBL- producing K. pneumoniae in Ethiopia were 61.8% and the pooled proportion estimates of MDR isolates for both K. pneumoniae and E. coli were 82.7%. China is another concern due to overuse and abuse of last-resort antibiotics in human medicine, veterinary medicine, and animal husbandry. Currently, there is a prevalence of gram-negative bacteria multidrug resistance in China such as CRAB, carbapenem-resistant P. aeruginosa (CRPA), and CRE. A. baumannii has a higher carbapenem resistance rate than P. aeruginosa and Enterobacter spp. with a proportion of more than 50% among Chinese isolates. The rates of resistance to imipenem and meropenem differ by region in China with Henan Province recorded as highest (78.5%) and Hubei Province recorded as lowest (64.1%). Nosocomial AR in Iran deserved global attention. In a recent study conducted in the southwestern region of the country, the investigators concluded "Considering widespread empirical antibiotic therapy in Iran, the rate of increasing resistance to common antibiotics prescribed for ambulatory and hospitalized patients is concerning." Most commonly antibiotic resistance was seen with cephalexin (100%), cefotaxime (100%), cefazolin (100%), amoxicillin (80%), and all cases of oxacillin were resistant. Vancomycin resistance was higher than 50% in this study. The authors have also reported a widespread resistance for azithromycin (94.4%) and erythromycin (63.6%) in Yasuj metropolitan area which is alarming. To address rapid spread of AR in human and animal communities and their environmental impacts, efforts must be focused on educations healthcare professional for making appropriate therapeutic decisions, improving surveillance and laboratory infrastructure particularly molecular epidemiological methods and genetic analysis of resistant pathogens as an urgent priority to combat global AR. In the meantime, the current clinical protocol vis-à-vis principles of antimicrobial stewardship adherence is a practical approach for minimizing the incidence of AR in outpatient and inpatient settings.

Prof. Dr. Reza Nassiri

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Biography

Prof. Dr. Nassiri is a former dean of global health at MSU, East Lansing, Michigan, USA. He is a French-trained hematologist with expertise in global health, infectious diseases, and antibiotic resistance. He is currently a professor of clinical pharmacology at MSU. He is on the editorial board of 4 medical journals and has written extensively (viewpoint) about COVID-19 and emerging variants.

Clinical features of adult, hospitalized, non-vaccinated COVID-19 patients during the omicron variant surge in Japan

Background: The mortality of SARS-CoV-2 infection in non-vaccinated patients is still thought to be high despite the appearance of the omicron subvariant. A total of 36 adult, non-vaccinated patients who were hospitalized with SARS-CoV-2 infection during the omicron variant surge were included in this study.

Case Series: Severity of illness at admission was mild, moderate, and severe in 0 (0%), 29 (80.6%), and 7 (19.4%) patients, respectively, and three (3/36=9.1%) patients died. The patients who died were as follows. (Case 1) A 64-year-old man on hemodialysis developed severe pneumonia caused by SARS-CoV-2 infection. His pneumonia did not worsen, but he developed septic shock on Day 5 with a catheter-related blood stream infection due to Methicillin-Resistant Staphylococcus Aureus (MRSA) and Extended Spectrum Beta-Lactamase (ESBL)-producing Escherichia coli. (Case 2) An 87-year-old man with a history of esophageal cancer had moderate pneumonia at admission, but suddenly developed massive brain hemorrhage on Day 6. (Case 3) A 94-year-old man with a history of brain infarction and atrial fibrillation had moderate pneumonia on admission. His pneumonia was improving, but he died on Day 7 of acute renal failure and suspected recurrent brain infarction.

Conclusions: These data and cases suggest that non-vaccinated patients showed high mortality, especially elderly male patients with underlying diseases. They died due to reasons other than respiratory failure and/or pneumonia, and impairment of blood vessels, especially in the brain, heart, and kidneys, by SARS-CoV-2 infection was thought to have occurred, though the omicron variant has generally low pathogenicity.

Audience Take Away Notes

- We need more vaccination for COVID-19
- Vascular diseases, including heart attack, stroke, and acute renal dysfunction should be carefully managed in unvaccinated and/or less vaccinated persons for COVID-19
- Early diagnosis and start treatment by antiviral agents is critical
- In addition, not only COVID-19, but also the other viral and bacterial diseases, including influenza, respiratory syncytial virus diseases, and pneumococcal diseases should be prevented by vaccine

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Biography

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

Carbapenemase-producing multidrug resistance of gram negative bacilli causing bacteremia at the general hospital of Mexico

Bloodstream infections due to Gram-negative bacilli is a highly consequential nosocomial infection with serious consequences and even more so because the organisms are usually highly resistant to antimicrobials. The aims of this study were to describe incidence of bacteremia caused by Gram-negative ESKAPE bacteria during COVID-19 pandemic, the clinical and microbiological characteristics, and the Antimicrobial Resistance (AMR). A total of 115 Gram-negative ESKAPE isolates were collected from patients with nosocomial bacteremia in a tertiary care center in Mexico between January – December 2020. A. baumannii (34%) and K. pneumoniae (28%) were the most frequent followed by P. aeruginosa (23%) and Enterobacter spp (16%). A. baumannii showed the highest levels of AMR (100%), followed by K. pneumoniae (87%), Enterobacter spp (34%) and P. aeruginosa (20%). Furthermore, the 27 K. pneumoniae isolates resistant to beta-lactams carried the blaCTX-M-15 and blaTEM-1 genes, while 33/39 A. baumannii isolates were carriers of the blaTEM-1 gene. In isolates resistant to carbapenems, 29/39 A. baumannii were carriers of blaOXA-398 and 4 of blaOXA-24. In P. aeruginosa, only one isolate was a carrier of the blaVIM-2 gene, while the 2 K. pneumoniae and 1 Enterobacter spp carried the blaNDM gene. Among colistin-resistant isolates mcr-1 gene was not detected. The clonal relatedness assessed by Pulsed-Field Gel Electrophoresis (PFGE) and by Multi-Locus Sequence Typing (MLST) demonstrated two outbreaks caused by A. baumannii ST208 and ST369 and a genetic diversity for K. pneumoniae, P. aeruginosa and Enterobacter spp. Remarkably, the ST136 and ST208 belonged to the clonal complex CC92 and IC2. A. baumannii was associated with a high mortality rate of 72%, mainly in patients with COVID-19 75% cared for in the Respiratory Ward. There was no statistically significant association between MDR profile of Gram-negative bacteria and in COVID-19 and non-COVID-19 patients. In summary, the results points to the important role of Gram-negative MDR causing bacteremia in nosocomial settings before and during the COVID-19 epidemic. In addition, the COVID-19 pandemic had no local impact on antimicrobial resistance rates in the short term. Already publish Gram-negative ESKAPE bacteria bloodstream infections in patients during the COVID-19 pandemic.

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Biography

Dr. Silvia Giono Cerezo PHD National School of Biological Sciences Instituto Politecnico Nacional- IPN Chemist Bacteriologist Parasitologist Doctor of Science Member of the National Academy of Medicine Member of the Mexican Association of Infectious Diseases Collegiate Member of the Postgraduate Studies Professor of Medical Bacteriology and Host-Parasite Relationship Theory and laboratory also Problems of Medical Bacteriology Tutor, Director Advisor of Bachelor's, Master's and Doctorate students Lines of research: Diagnostic Medical Microbiology and Antimicrobial Resistance of the ESKAPE group diagnosis and analysis of the genome of Helicobacter pylori MLST of Stenotrophomonas spp several publications.

Efficacy and safety studies of EC16 nanoformulations against human coronavirus

Background: Severe Acute Respiratory Syndrome (SARS) coronavirus 2 (SARS-CoV-2) is responsible for the 2019 coronavirus epidemic (COVID-19). SARS-CoV-2 infection is associated with high mortality and morbidity worldwide. A common sequela is chronic neurologic diseases, which severely impact the quality of life and increase the burden on healthcare systems. The Post-COVID, or Long COVID neurologic symptoms are due to the robust replication of SARS-CoV-2 in the nasal neuroepithelial cells, leading to neuroinvasion and inflammation of the Central Nerve System (CNS). Currently used medications and vaccines are not targeting the neuroinvasion of SARS-CoV-2, and these methods do not inhibit the robust SARS-CoV-2 replication in the nasal epithelial cells. Therefore, a significant gap in treatment/preventive strategies that needs to be filled is to rapidly inhibit SARS-CoV-2 replication in the nasal cavity to block viral invasion to CNS, in order to minimize neurologic damages. We recently invented a method to facilitate self-assembling of EGCG-palmitate (EC16) nanoparticles. This technology allows us to utilize the antiviral, anti-inflammatory, antioxidant and neuroprotective properties of EC16 as a nasal drug to be formulated in aqueous nanoformulations to treat Long COVID symptoms.

Method: Formulations suitable for intranasal applications were developed and tested in vitro against human □ coronavirus 229E (CoV-229E) and □ coronavirus OC43 (CoV-OC43) using TCID50 assay. Formulations met the FDA standard with the highest antiviral activity were selected for further improvement in stability and homogeneity. The final formulation (F18D) suitable for animal and human tests was selected and tested in comparison to vehicles in cell culture infection systems following two test protocols (with or without direct contact with the virus). The cytotoxicity was performed in MRC-5 cells and primary human nasal epithelial cells. In addition, nasal nanoformulations were evaluated on the tissue integrity, cytotoxicity, and cilia beat frequency in a 3-D human nasal epithelia model.

Results: The initial results demonstrate that EC16 formulations in normal saline, phosphate buffered saline, and cell culture medium effectively inhibited human coronavirus infection (>99%) after a single application, with or without direct contact with the virus. The final formulation F18D was able to inhibit viral infectivity by >99.9999%. Viral replication was reduced by 99% after a single 10-min application in a post-infection assay in human primary nasal epithelial cells. Cytotoxicity and 3-D human nasal epithelia model study demonstrate the nanoformulations are suitable for human use. To the best of our knowledge, this result represents the first approach using EC16-containing nasal nanoformulations to rapidly

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Biography

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

inhibit human coronavirus without toxicity. Future studies are planned to determine product suitability for clinical trials toward new drug application.

Conclusion: With its antiviral, antioxidant, anti-inflammatory, and neuroprotective properties, EC16 in nasal nanoformulations could be further developed for clinical applications to patients for minimizing Long COVID neurologic symptoms such as anosmia.

Audience Take Away Notes

- Understand the “facilitated self-assembled” nanoparticles and their advantage over conventional nanoparticles
- Disadvantages in current interventions for Long COVID patients
- Learn the unique beneficial properties of EGCG, a catechin-derivative found in green tea
- Understand the advantage to use nasal application to deliver a drug vs. oral application
- Learn the potential mechanisms of “persistent viral infection” is association with Long COVID

Clinical characteristics analysis of Bordetella Psertussis infection in adult cough patients

Purpose: In contemporary epochs, the prevalence of pertussis has been progressively on the rise, persisting as a formidable health concern. The manifestations following pertussis infection lean towards the atypical, making them easily disregarded or subject to misdiagnosis. Our aim is to ascertain the pertussis infection rate among individuals presenting with a cough and scrutinize the clinical attributes of the infected.

Materials and Methods: Screening transpired between July 1, 2023, and September 20, 2023, at Tianjin Chest Hospital and the Second People's Hospital of Tianjin. It focused on individuals seeking medical attention due to cough symptoms or those in contact with presumed pertussis cases. A cohort of 1025 patients was assembled, and nasopharyngeal swabs were procured for polymerase chain reaction (PCR) analysis.

Results: 1. In accordance with the pertussis case definition, 417 cases (40.7%) were diagnosed as clinically suspected, and 145 cases (14.1%) exhibited epidemiological correlations. The median duration of symptoms before hospitalization was 15 days. Following PCR testing, 163 individuals tested positive for pertussis, comprising 38 adults (≥18 years old) and 125 infants and children (0~17 years old). Within our study cohort, the pertussis infection rate stood at 15.9%. The infants and children included in our investigation were all suspected pertussis cases, yielding a pertussis infection rate of 45% among this demographic. Among the enrolled adult cases, 139 cases (18.6%) were deemed suspected, resulting in a pertussis infection rate of 5.1% among adults presenting with cough symptoms.

2. Primary Clinical Manifestations: Among children, all presented with paroxysmal coughing; 94 cases (75.2%) experienced post-cough vomiting, 115 cases (92%) had nocturnal coughing, 57 cases (45.6%) manifested a whooping cough-like sound, 103 cases (82.4%) had a cough duration of ≥2 weeks, 64 cases (51.2%) exhibited inspiratory pause after coughing, 115 cases (92%) had nocturnal coughing, 21 cases (16.8%) had low-grade fever, 7 cases (5.6%) had pneumonia, and 25 cases (20.0%) experienced weight loss. In adults, 33 cases (86.8%) had paroxysmal coughing, 20 patients had a cough duration of ≥2 weeks (52.6%), 25 cases (65.8%) had nocturnal coughing, 1 case (2.6%) experienced post-cough vomiting, 2 cases (5.3%) had a whooping cough-like sound, 1 case (4%) exhibited inspiratory pause after coughing, and additional observations included 1 case (4%) with syncope after coughing, 3 cases (7.9%) with perspiration after coughing, 1 case (2.6%) with low-grade fever, and 3 cases (7.9%) with pneumonia.

3. Comparative Analysis of Hematological Parameters Across Various Age Groups and Immune States: White blood cell counts exhibit elevation in the non-immune cohort, with a statistically significant difference observed between distinct immune groups (P<0.01); Neutrophil levels progressively rise with advancing age, demonstrating statistical significance across different age brackets (P<0.01);

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Biography

Dr. Xiaoyun Zhao studied Clinical Medicine at the Nankai University and got his MM degree in 2004, and then received his MD degree at the Tianjin Medical University. His fellowship was supervised by Dr. Richard Castriotta at the Texas University Health Science Center at Huston. Now he serve as the chief doctor and the discipline leader of National Respiratory Medicine Clinical Key Specialty at Tianjin University Chest Hospital. Also he serve as a professor of Clinical Medicine and Biomedical Engineering at the Tianjin University, Tianjin Medical University, Tiangong University, China. He has published more than 70 research articles in journals.

Lymphocytes display a marked elevation in the non-immune group ($P < 0.01$), with a statistically significant variance noted among diverse age groups ($P<0.05$); Monocytes exhibit elevated values in the non-immune group, showcasing a statistically significant difference across various immune statuses ($P<0.01$); Platelet counts show heightened values in the non-immune group, with statistically significant disparities apparent between distinct immune statuses and age groups ($P<0.01$).

Conclusions: Pertussis, identified as a causative agent of persistent coughing, affects both immunized children and adults, presenting with atypical clinical symptoms. Our study suggests a potential overestimation of the diagnostic efficacy of blood routine tests in infants aged 0-3 months. Furthermore, the existing vaccine immunization strategy proves inadequate in preventing pertussis, emphasizing the imperative for the development of novel diagnostic criteria and a comprehensive immunization approach.

Key Words: Bordetella Pertussis, Adults, Clinical Features, Polymerase Chain Reaction, Hemogram.

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6th Edition of World Congress on

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SPEAKERS

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Immune transcriptomic analysis of COVID-19 patients with varying clinical presentations

Background: Coronavirus disease (COVID-19) is an infectious disease with a heterogeneous clinical presentation caused by the novel coronavirus, the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). The distinctive features of COVID-19 infection encompass a clinical spectrum ranging from asymptomatic forms to severe illness involving diverse underlying pathophysiological processes such as dysregulated inflammation, endothelial dysfunction, thrombotic pulmonary microangiopathies, and multiple organ failure. However, the underlying molecular mechanisms of host responses to this infection, particularly systemic inflammation and the host immunity against SARS-CoV-2, remain largely undefined.

Methods: In this prospective study, Ribonucleic Acid (RNA) sequence analysis from venous blood of 228 COVID-19 patients (comprising 188 males, aged 21-87 years), was performed using a shotgun sequencing pipeline and subsequently clustered using an unsupervised algorithm. Differential gene expression was assessed, integrated pathway and network data, along with clinical information between clusters, as well as estimating circulating cell populations from the sequencing data and investigating its correlation with disease severity and mortality.

Results: This research identified various transcriptomic clusters and globally dysregulated immune-related pathways, leading to distinct host inflammatory cytokine profiles in severe and critical SARS-CoV-2 infected patients. This underscores the association between COVID-19 pathogenesis and excessive cytokine release. Additionally, our results reveal variances in circulating cell populations and the activation of apoptosis and the P53 signaling pathway in lymphocytes induced by SARS-CoV-2 infection.

Conclusions: The transcriptomic dataset of COVID-19 patients with diverse clinical presentations holds promise as a valuable resource for guiding clinical decisions regarding anti-inflammatory intervention, offering potential insights into the molecular underpinnings of the disease.

Biography

Dr. Abdallah received his PhD in Molecular Biology from the VU University Amsterdam, in 2008. His dissertation work focused on several aspects of protein secretion mechanisms in mycobacteria. Following postdoctoral appointments at the VU medical Centre and The Netherlands Cancer Institute, he started his academic career at the King Abdullah University of Science and Technology, KSA. Dr. Abdallah is an expert Molecular biologist and his research interests are in the area of Microbial Genetics, host-pathogen interaction and molecular pathogenesis of infectious agents. Dr. Abdallah joined the Qatar University, College of Medicine as an Assistant Professor of Genetics on August 2019.

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The impact of SARS-CoV2 pandemic on the prevalence and the outcome of candida auris infections, admitted to a tertiary hospital in United Arab Emirates (UAE), in 2022

In 2016, according to the United States Centers for Disease Control and prevention (CDC), and Public Health England, Candida auris, has been labeled as an emerging Multidrug-Resistant (MDR) yeast. Despite causing significant mortality, there are still no available Minimum Inhibitory Concentration (MIC) breakpoints for C. auris. When breakpoints of other candida species were applied, almost all C. auris isolates were noted to have high resistance to fluconazole. A substantial number of isolates were resistant to voriconazole and amphotericin B. Thus, leaving echinocandins as the empirical treatment of choice. Since its discovery, C. auris has caused hospital outbreaks in multiple countries in all continents. Interestingly, significant genetic variability of isolates has been identified depending on geographic location. Besides causing bloodstream, and wound infections, C. auris has also been isolated from cultures from urine and respiratory tract.

In terms of the UAE, C. auris was first reported in 2018, in the blood of an elderly lady requiring prolonged ICU stay due to septic shock from multiple sources with persistent fungemia. Therefore, aggressive infection control measures should be implemented for early identification and to avoid any potential transmission given the vulnerable status of the patients at risk of invasive C. auris infection.

The United Arab Emirates (UAE) has borne the devastation of COVID-19 in terms of the number of infections in the population. It is important to emphasize the impact of the SARAS COV2 pandemic on Candida auris infection in the United Arab Emirates, and Al-Qassimi Hospital is an example of this. As a result, other health centers will be encouraged to do the same.

The main aim of our research is to determine the prevalence and the outcome of Candida auris infections in patients admitted to our tertiary hospital during the year 2022. While also, identifying the body sources/ sites from which Candida auris infection was isolated, and assessing the risk factors related to poor outcomes in patients with isolated C. auris.

The statistical process of this research also seeks to evaluate the burden of candidemia cases on the health and social care system in terms of epidemiological findings. This is through evaluating the length of stay and ICU admissions of patients from confirming the diagnosis and identifying the Mortality Rate at 7 days from confirming the diagnosis of candidemia.

This retrospective study reviewed medical files for a total of almost 100 patients. Sampling was done on the basis of all adults/adolescents who were admitted to the Hospital and confirmed to have candida auris isolated from a body site.

Audience Take Away Notes

- Identify potential co-infections. Besides understanding Co-Infections and Complications
- Achieving more effective patient care and infection control measures
- A better understanding of the outcomes of patients with both infections regarding the impact on mortality rates and long-term morbidity
- Our data would encourage more research opportunities such as exploring the immunological, molecular, and clinical interactions between SARS-CoV-2 and Candida auris for potential therapeutic targets or preventive strategies

Biography

Ahmad Subhi is a graduate of the University of Baghdad, College of Medicine, in 1997. He finished his training in internal medicine at Hahnemann hospital- Drexel University in Philadelphia-Pennsylvania, and he completed his fellowship in Infectious Diseases at Cooper University Hospital in New Jersey State. He has more than eleven years of experience as a licensed physician in the USA. His background was in Internal Medicine and Infectious diseases, with a particular interest in the Hepatitis C virus, HIV, and infectious diseases in immune-compromised patients. He is a member of the Infection Control and Central antibiotic stewardship committee, the Emirates Infectious Diseases Society and the American College of Physicians. He is board certified by the American Board of Internal Medicine & Infectious Disease.

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Sever adenovirus infection in an immunocopemtment host

Adenovirus is a frequent cause of mild respiratory tract infection and gastroenteritis in children, it can cause severe respiratory illness in immunocompromised patients. Outbreaks and aggressive respiratory symptoms have been reported in military camps. Epidemics are well known to occur in close or crowded settings.

We report a case of severe adenovirus pneumonia in a young 38 year old immunocompetent female who lives in a refugee camp in Co. Wexford. Ireland. She presented with fever associated with mild respiratory symptoms that progressed rapidly to severe pneumonia with bilateral consolidation on chest x ray and ground glass opacities on high resolution Computed tomography.

On admission, she was febrile at 40oC, other vital signs were normal, she did not require oxygen support. Initial bloods showed high C – reactive protein with normal White Cell counts and differential and Chest X ray showed patchy right lower lobe infiltration. Full cultures, throat swab, Pneumococcal and legionella urinary antigen in addition to viral serology and immunoglobulin levels were requested, and she was started on broad spectrum antibiotics. 48 hours later, she deteriorated clinically and required oxygen support, she was continuously spiking fever and her chest x ray showed worsening of the pneumonic patches to multilobar pneumonia. By day 4 of admission, she required high flow oxygen with Fi02 up to 80 % to maintain her partial pressure of oxygen around 10. High resolution CT thorax showed multiple ground glass opacities. Echocardiography excluded any cardiogenic causes for her respiratory deterioration. Adenovirus was detected in the nasopharyngeal swab with adenovirus PCR DNA of 1.31x10^7 in serum. Sputum culture and serial blood cultures were negative. Tuberculosis cultures and B-D glucan level / galactomannan level were negative. Serum immunoglobulins and HIV test were negative. HBA1c was normal. Our patient improved successfully, she recovered by day 15 with supportive management, no antiviral was given.

Severe adenovirus infection is rare in immunocompetent adults. This case demonstrates a rapidly progressive respiratory course. Specific groups including refugee camps, military recruits etc, should be evaluated and assessed cautiously to prevent outbreak and poor outcomes. Signs of mild viral illness in the population should be handled carefully with a high index of suspicion and early isolation of specific groups including immunocompromised patients is advisable.

Audience Take Away Notes

- Be open to different kind of viral illness
- Close assessment for viral illness should be taken in acute viral illness in specific group of people

Biography

Abdalla Ahmed, a dedicated physician, embarked on his journey in the field of medicine after graduating from the prestigious University of Khartoum in 2011. His passion for serving others led him to Saudi Arabia, where he worked tirelessly for six years, gaining invaluable experience and honing his skills. Driven by a desire to expand his knowledge and make a difference in the field of infectious diseases, Abdalla set his sights on Ireland. With unwavering determination, he pursued his dream of becoming a proficient clinician Dr. Ahmed's commitment to excellence is evidenced by his attainment of full membership in the Royal College of Physicians UK and certification by the Educational Commission for Foreign Medical Graduates (ECFMG). Currently serving as a medical registrar at Wexford General Hospital in Ireland, Dr. Ahmed continues to make significant contributions to the medical community. Abdalla Ahmed's journey serves as an inspiration to aspiring physicians and researchers alike, illustrating the profound impact that dedication, perseverance, and a genuine passion for healing can have on the lives of others.

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HHV6 encephalitis in an immunocompetent host

Introduction: A previously healthy and a fully vaccinated 5-year-old pre-schooler-aged male who presented to the ER with an insidious onset of decreasing level of consciousness and headaches before developing Status Epilepticus, and requiring admission to the PICU; with a final diagnosis of HHV6 Encephalitis based on the BioFire CSF testing.

HHV6 is known to cause CNS infections in immunocompromised individuals, particularly oncology patients; thus, its diagnosis in a previously healthy and an immunocompetent host sheds light on the suspicion, diagnosis, and treatment options for the aforementioned individuals.

Case Description: Presented was initially seen on the same day of the symptoms' onset in a PHC, where he was prescribed Augmentin treating a throat infection.

Throughout the illness's course, he was becoming progressively more tired, confused, had developed decreasing eye-to-eye contact, and sleepiness.

He was later referred to our facility for further evaluation, when he started to have convulsions, and later on, Status Epilepticus.

Subsequently, he was transferred to the PICU, loaded with Phenytoin, and started on Midazolam IV. A Brain MRI showed diffuse cortical/deep cortical changes along with DWI restriction and ADC changes, and was suggestive of Hypoxic-Ischemic changes.

His initial CSF studies (analysis, culture, and viral panel were normal); however, based on his greatly worrying symptom progression, repeated CSF samples were taken, which came to be positive for HHV6.

He was started on Foscarnet and Ganciclovir; and started to show great improvement and return to his neurological baseline, with a repeated CSF study being negative for the virus.

Followed later on in the clinic, where he was on Keppra prophylaxis and on regular follow-up with Occupational Therapy and Speech-Language Pathology.

Discussion: Viral encephalitis is a medical emergency. It is an aseptic inflammatory process of the brain parenchyma associated with clinical evidence of brain dysfunction, significant morbidity, and mortality (Michael and Solomon 2012).

HHV6 is usually associated with Roseola, which manifests with high fever, URTI symptoms and the development of a rash after the fever subsides.

In immunocompromised patients (haematological malignancies and transplantation), reactivation of roseoloviruses may cause severe, lethal organ dysfunctions, including damage to the limbic system, brain stem, and hippocampus; thus, it could potentially lead to life-long disability.

Moreover, an HHV6 infection may lead to a chromosomally integrated human herpesvirus 6 status, in which the HHV-6 genome is integrated into the host's genome and is vertically transmitted in a Mendelian manner;

that itself may cast doubt on the recently utilized BioFire technology as it could lead to misdiagnose the causation of the illness, and the unnecessary initiation of antiviral therapy that requires strict monitoring and might lead to serious side effects.

The main purpose of presenting the case is to highlight the unique presentation of HHV6 Encephalitis in an immunocompetent host, and to discuss the challenges associated with suspecting the diagnosis, reliability of testing for the infection with a recently utilized technology, and the decision to proceed for, and types of management.

Biography

Dr. Ahmed Mahboub is a dedicated Pediatric Resident and Chief of Interns and External Learners at Tawam Hospital in Al Ain, United Arab Emirates. He graduated from United Arab Emirates University's College of Medicine & Health Sciences (CMHS) in Al Ain, where he obtained his medical degree in 2019. After completing his primary medical education, Dr. Mahboub pursued an internship at Tawam Hospital, where he gained valuable clinical experience and developed a deep understanding of patient care. He then went on to specialize in Pediatrics and is currently in the residency program at Tawam Hospital, where he continues to enhance his skills and knowledge in the field. Dr. Mahboub is passionate about providing personalized and holistic care to the pediatric community. He firmly believes in the significance of nurturing and supporting the well-being of children as they are the future generations of humanity. Through his dedication, he strives to make a positive impact on the lives of his young patients and their families. In addition to his medical pursuits, Dr. Mahboub has diverse interests outside of medicine. He is an avid writer of poetry in both Arabic and English, allowing him to express his creativity and emotional depth. He also keeps himself updated on the latest developments in Information Technology, Artificial Intelligence, and Virtual Reality, recognizing their potential to revolutionize healthcare and improve patient outcomes. Furthermore, Dr. Mahboub takes pleasure in the art of hospitality, appreciating the importance of creating a warm and welcoming environment for patients and their families. Looking ahead, Dr. Ahmed Mahboub has ambitious goals for his career. He aspires to pursue a fellowship in Pediatric Infectious Disease, aiming to specialize further in this critical area of pediatric medicine. By acquiring specialized knowledge and expertise, he aims to contribute to the field and make a significant impact on the prevention, diagnosis, and treatment of infectious diseases in children. Dr. Ahmed Mahboub's commitment to pediatric care, his pursuit of knowledge, and his diverse interests make him a valuable asset to the medical community. His dedication to providing holistic care, combined with his passion for innovation and personal interests, sets him apart as a well-rounded and compassionate healthcare professional.

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A case of disseminated histoplasmosis presenting as fever of unknown origin in a patient with diabetes mellitus

Background: Histoplasmosis is an endemic mycosis that is usually asymptomatic but occasionally results in severe illness. While it is endemic in some regions of the world, including America, Africa, and parts of Asia, it is considered rare in India. Most patients who develop disseminated histoplasmosis are immunosuppressed (eg, AIDS, solid organ transplantation, treatment with tumor necrosis factor-alpha inhibitors) or are at the extremes of age. Here, we present a case of disseminated histoplasmosis in patient with diabetes mellitus.

Case Presentation: A man in his 40s presented with fever and cough for one month duration. The fever was high grade, predominantly in the evening hours and not associated with any periodicity or rhythmicity. He also had minimally productive cough with a mucoid sputum and occasional hemoptysis. His past medical history is notable for Alcoholic Chronic liver disease (Child Pugh grade B) and Type 2 diabetes mellitus. He also had history of treated pulmonary tuberculosis in his childhood. He frequently visits a nearby forest and had significant exposure to bird droppings. Physical examination revealed pallor and features of volume overload. Examination of the respiratory system showed coarse inspiratory crepts in the right mammary, infraaxillary and infrascapular areas. Patient was clinical diagnosed with Fever of unknown origin with a respiratory focus. His lab reports showed pancytopenia with a high Erythocyte Sedimentation Rate (ESR). HRCT thorax revealed minimal bronchiectasis in right lower lobe and subpleural fibrotic nodule. Bone marrow biopsy showed non caseating granulomas and yeast forms of fungi, as evidenced by positive Grocott's methenamine silver staining. Meanwhile his urine histoplasma antigen turned positive. The patient was diagnosed with disseminated Histoplasmosis and received a 14 day course of Amphotericin B, followed by a plan for oral itraconazole for one year. He became afebrile of Day 5 of antifungal treatment and is currently doing well.

Discussion: Histoplasmosis is a disease usually seen in immunocompromised individuals in endemic areas. The incidence of the disease is increasing in India, mainly due to better recognition of the disease. In a place where tuberculosis is endemic, the diagnosis of Histoplasmosis which has overlapping clinical features remains challenging. Hence early suspicion and prompt investigations help in the recognition of this deadly disease. Moreover there are increasing case reports, where diabetes has been the sole risk factor for the disease. Our patient too, didn’t have the classical risk factors associated with Histoplasmosis. Hence further research into the possible relationship between diabetes and incidence of Histoplasmosis is also warranted.

Audience Take Away Notes

- This case shows the diagnostic difficulties in histoplasmosis especially in a non endemic area. This will help in the better awareness and recognition of the disease
- The case also opens novel research opportunities like the role of diabetes as a risk factor for histoplasmosis and the need for better non invasive markers for early diagnosis

- This case may also create new avenues in the recognition of fungal infections in cases of prolonged fever

Biography

Dr. Aji Antony studied his MBBS from Coimbatore Medical College, Tamilnadu and is currently doing his Internal Medicine residency in Government Medical College Kozhikode. He has attended and presented papers in numerous international and national conferences. He has published three papers in renowned journals and has an excellent academic record.

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HIV associated vasculopathy presenting as cerebrovascular accident in a young girl with HIV

Introduction: Stroke in a case of HIV, occurs by various mechanisms. The mechanisms include vasculitis secondary to opportunistic infections, HIV associated vasculopathy, cardioembolic stroke and HIV associated coagulopathy. Of these, the HIV associated vasculopathy is a diagnosis of exclusion. Here we present a case of HIV associated vasculopathy in a young girl with HIV.

Case Presentation: The patient is a 14-year-old HIV infected girl, diagnosed at the age of 1 and has been drug default for the past 3 years. 1 month back, she was diagnosed with Ileocecal Tuberculosis and was started on Antitubercular Therapy (ATT). 1 week later, patient developed ATT-induced hepatitis and modified ATT regimen was started. The next week, patient presented to us with acute onset weakness of right upper and lower limbs. Patient was clinically diagnosed with cerebrovascular accident. MRI head showed an acute infarct in the left corona radiata and fusiform ectasia of Left terminal Internal carotid artery, left middle cerebral artery and left anterior communicating artery. Cerebrospinal fluid analysis revealed a lymphocytic pleocytosis (cells = 70, lymphocytes – 70%) and elevated protein (70 mg/dl). Workup for tuberculosis, varicella zoster, toxoplasmosis and neurosyphilis turned out negative. Echocardiogram of the patient was also normal. Since the secondary causes were considerably ruled out, patient was diagnosed with HIV vasculopathy. The role of antiplatelets in HIV vasculopathy remains controversial. The patient was started on Anti-retroviral therapy. Her general condition improved, but she had residual weakness of her limbs.

Discussion: The incidence of stroke in HIV varies from 1-5%. Stroke in HIV patients were seen in younger individuals compared to those in normal population. Ischemic stroke appears to be the predominant type comprising around 90% of individuals. HIV vasculopathy is a rare cause of stroke in HIV patients. The diagnosis requires significant vessel wall changes after ruling out opportunistic infections. Effective ART plays a significant role in the prevention of HIV vasculopathy.

Keywords: HIV, Vasculopathy, Cerebrovascular Stroke.

Audience Take Away Notes

- HIV vasculopathy is rare neurological complication of HIV. This case describes the presentation and management of the condition
- The management of HIV vasculopathy remains challenging. This case may provide novel
- research opportunities for the various treatment options in this condition
- This case also highlights the need for early diagnosis of HIV and good drug compliance to prevent such complications

Biography

Dr. Aji Antony studied his MBBS from Coimbatore Medical College, Tamilnadu and is currently doing his Internal Medicine residency in Government Medical College Kozhikode. He has attended and presented papers in numerous international and national conferences. He has published three papers in renowned journals and has an excellent academic record.

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Abrupt and lethal rare complication: A case report of a 32- year-old male who suffered from pyogenic ventriculitis

Introduction: Pyogenic ventriculitis is characterized by ependymal lining inflammation of the cerebral ventricular system and presence of suppurative fluid in the ventricles. Risk factors include a compromised immunity such as human immunodeficiency virus, diabetes, and cancer. This infection could arise as a complication from deep-seated cerebral abscesses, carrying a higher mortality rate, ranging from 30% to 85%, and leaving 60% of survivors with lasting neurological sequelae. Early recognition is crucial but data on clinical and neuroimaging features are scarce. Our case report sheds light on specific clinical and neuroimaging aspects for pyogenic ventriculitis in a young male adult, at in-hospital setting and, as a complication of extensive multiloculated cerebral abscesses involving atypical locations.

Case Presentation: We present a case of a 32-year-old male with a history of intravenous drug abuse and homelessness who arrived at the Emergency Department for muscle aches, sore throat, and multiple infected ulcers. Participating in a methadone rehabilitation program, they were concerned for noticing episodes of hypoactivity. Initial examination revealed a mildly hypoactive, afebrile patient with a Glasgow Coma Scale (GCS) of 14/15, stable vital signs, and no meningeal irritation or focal neurological findings. Multiple infected ulcers were noted on his upper extremities. General laboratories were mostly unremarkable, except for mild elevated erythrocyte sedimentation rate. Head Computer Tomography (CT) reported no intracranial abnormalities. Therefore, the patient was admitted for infected ulcers management and further workup investigations.

On day ten, the patient experienced a sudden clinical deterioration that was remarkable for peaks fever, decreased alertness, apathy, withdrawal, and a reduced GCS of 10/15. Focal neurological deficits were noted, including horizontal nystagmus, leftward eyes deviation, vertical gaze palsy, and right nasolabial fold flattening. A new head CT with and without contrast revealed ill-defined lesions in the right frontal and occipital lobes surrounded by edema and communicating hydrocephalus. A subsequent Magnetic Resonance Imaging (MRI) diagnosed multiple intraparenchymal brain abscesses and ventriculitis. Unusual features included abnormally enhancing patterns involving the fourth ventricle and left frontal periventricular region. Lesions were identified in both infra and supratentorial regions, including the midbrain and prepontine cistern. The largest lesion was located at the right side of the genu and splenium affecting the corpus callosum. Moreover, serial blood culture results remained negative, and transthoracic and transesophageal echocardiogram reported no vegetations. The patient's cognitive decline abruptly got worsened by the third week of admission leading to comma.

Conclusion: Pyogenic ventriculitis might present lethally as a severe complication of extensive multiloculated abscesses and it requires early recognition and timely intervention. Additionally, it can present with diverse infectious origins or unknow primary sources. MRI of the brain is essential for a comprehensive evaluation of this complication and known as the most reliable neuroimaging study for establishing diagnosis, management guidance, and prognosis. Furthermore, this life-threatening infection often requires prolonged antibiotic treatment combined with external ventricular drainage and intraventricular antibiotics for the most favorable outcomes.

Audience Take Away Notes

- The audience would be able to use the discussion of this case to expand their clinical knowledge and skills, specifically on early recognition, prognosis, and management strategies of pyogenic ventriculitis in a setting of multiloculated brain abscesses. They would benefit from my presentation not only in their jobs for a better making decision capacity but on gaining special skills and getting specialized knowledge about the Magnetic Resonance Imaging study on this specific setting and when it comes to specific unusual findings presenting on this complication. To our knowledge, this is the only case of Pyogenic Ventriculitis in a young male adult with these specific clinical settings. Therefore, this case report would offer an investigational window for future collaborations and new study designs. There are other academic benefits that would be offer during my presentation, including previous research analysis, most common pathogens involved, and discussion of scientific limitations

Biography

Dr. Alexis Torres studied Biology at the University of Puerto Rico, in 2002-2007. He then received his medical degree in 2014 at the Autonomous University of Guadalajara in Jalisco, Mexico. Has a diverse experience in multiple clinical settings, serving patients from all socioeconomic backgrounds. About to complete his post-graduate medical training in Internal Medicine, at the Universidad Central del Caribe in Puerto Rico, United States of America. Has prepared and presented several seminars regarding high-yield topics in medicine and public health. He is currently focused on clinical research, Infectious Disease, and debuting as a youth speaker of the medical community.

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Sustainable soap bars delivering skin health and hygiene benefits for infection protection

Background: As the world returns to pre-pandemic behavior patterns, surges in infections caused by antibiotic-resistant bacterial strains and seasonal viruses are a cause of serious concern. Persistent circulating infections exert socio-economic burdens on public health systems and affect all age groups, with a higher risk of complications in children and elderly. Frequent handwashing has been recommended by global health authorities as the most effective way to reduce transmission of pathogens in a community setting and a bar of soap offers one of the most affordable mass hygiene interventions for frequent use. However, the carbon footprint of a soap bar is high due to elevated usage of natural oils in formulations. In alignment with multiple United Nation's Sustainable Development Goals, it is a global imperative to develop and implement technologies for manufacturing soap bars with uncompromised efficacy against germs along with skin benefits that will serve public health at large, whilst reducing their environmental impact.

Objective: Conventional soap bar formulation comprises of high percentages of oils (termed Total Fatty Matter -TFM) where approximately 70-80% of soaps are fatty acids derived primarily from oils. A large percentage of this oil is derived from palm and this usage is a large contributor to the non-edible global palm oil/fat usage footprint. The soap industry needs to innovate for reduced palm oil consumption by lowering TFM in bars, creating more environmentally sustainable cleansing solutions. Our research offers a soap bar technology with lower TFM without compromising hygiene and skin benefits.

Methodology: The novel low TFM soap bars were evaluated against higher TFM soap bars on cleansing efficiency, hygiene efficacy, skin barrier health, and skin mildness with industry wide accepted methods of testing. Further, Zein test for mildness and in-vitro and ex-vivo 2D and 3D bioassays to evaluate skin bio-markers relevant to skin barrier health were also conducted.

Results: The results demonstrated that the novel low TFM technology-based soap bars deliver superior cleansing, superior antibacterial efficacy, and advanced skin benefits compared to higher TFM soaps. Through in-vitro assays on skin 3D models, the low TFM soap bars were found to significantly upregulate skin barrier markers, these low TFM technologies are calculated to have upto ~ 40% lower greenhouse gas footprint (due to reduced palm oil usage).

Conclusion: The results challenge existing regulatory frameworks that mandate high TFM levels in a soap bar as means of classification rather than functional properties. We would like to argue that low TFM soap bars which utilize significantly a lower amount of palm oil will continue to contribute to public health as an accessible and affordable preventative intervention for regular infections and outbreaks while being more sustainable as a technology.

Key words: Low TFM Soap bar, Germ efficacy, Sustainable, Hygiene, Skin Mildness

Audience Take Away Notes

- Soaps have been known for centuries by man for their cleansing ability. Dating back to almost 2500 BC soaps are natural cleansing products used for personal hygiene
- Hand washing with soap is mandated by WHO as one of the key interventions for protection against infections
- Design of soap bars with a lower TFM (total oil) content allows efficient incorporation of several skin benefit agents leading to milder formula which is proven to deliver superior skin hygiene benefits
- Low TFM bars thus present a dual advantage - they improve skin hygiene & health while significantly reducing environmental impact

Biography

Dr. Amitabha Majumdar received his PhD from the Department of Biochemistry in the University of Calcutta on Molecular Virology. After finishing his PhD, he joined the Department of Biochemistry at the Weill Medical College of Cornell University in New York and worked there as a Post Doctoral Associate. Following his post doc, Dr. Majumdar joined Unilever R&D and he has been working on various aspects of infection biology, hygiene, and skin health and immunity

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Initial SARS-COV-2 infection in a group of individuals with their social behavior

COVID-19 type virus infection in a group of individuals results from the uptake by the lungs of these individuals of virions from the local atmosphere created by infected members of the group. The concentration of virions is determined by the social activity of group members and the stage of disease development in infected members. For example, in the case of panic, increased numbers of people near exits can significantly elevate the concentration of virus microparticles in the atmosphere and lead to infection of a significant number of group members. The presence of socially attractive areas or localized areas within a room that are dangerous to visit also contributes to the active spread of infections. It is important to be able to predict the dynamics of primary infection in order to evaluate different scenarios of disease development after evacuation of people from the danger zone.

Scientific Objective: Creation of a simulation model that predicts the evolution of viral infection in the human body during the period of movement in a group taking into account social behavior and after leaving an area with polluted atmosphere. Estimation of the probability of serious disease progression after evacuation from a danger zone or natural degeneration of the virus in the organism depending on the level of initial immunity. Predicting health care need and vaccination efficacy based on disease stage.

Research Methods: Mathematical cellular microbiological models of pathogen dynamics in the organism, a macromodel simulating the behavior of a group of individuals in different social conditions and a model of virus microparticle spreading in a turbulent atmosphere. The modified SARS-CoV-2 microbiologic model takes into account the level of baseline immunity and the flux of virions into the body from the local atmosphere. The modified cell model is validated against experimental data from the literature. The macromodel of the movement of a group of individuals uses modern methods of the theory of random processes and computer modeling technologies. The results of modeling the social dynamics of a group in an obstacle course room under different conditions are compared with empirical observations from the literature.

Research Results: The results of simulation modeling and analysis of different infection scenarios of a group of individuals including infected and susceptible individuals to COVID-19 are presented. It has been established that the crucial factor, on which the dynamics of the disease after leaving the zone with polluted atmosphere depends, is the level of pathogen concentration in the organism at the moment of evacuation. If the concentration of pathogen in the body is less than the critical level, the virus in the body will degenerate after leaving the danger zone, if the concentration of pathogen is higher than the critical level, the disease will be passed in a severe form. The intensity of virus microparticle absorption by the lungs of an individual depends on the scenario of movement of individuals in a group under different conditions. For example, during a panic, an increased concentration of individuals near an exit from a room significantly enhances the probability of absorbing virions with concentrations above a critical value. The probability of active infection is also much higher if the room has socially attractive or dangerous areas for people to be in. A methodology has been developed to estimate the proportion of infected individuals who will have natural viral degeneration or severe disease. The results of simulation modeling of vaccine administration that reduces the probability of the virus microparticles damage to the target cells of the organism are presented.

Audience Take Away Notes

- The presentation will demonstrate the practical importance of simulation modeling for predicting the probability of SARS-CoV-2 infection in a group of individuals in different social situations
- The results of the study can be used in the development of restrictive measures to reduce the risk of infection of groups of individuals in places of entertainment, supermarkets, educational institutions, etc
- The methodology of a unified mathematical description of microprocesses occurring at the cellular level and macro-processes of movement of groups of individuals in different social conditions can serve as a new element of education in the course of bioinformatics
- Estimating the fraction of infected people who are more likely to develop the disease after evacuation from an infected area will enable estimates to be made of the number of vaccines, the medical care necessary, and the required police response
- The results of simulation modeling of the movement of a group of people in a room with internal obstacles will allow to evaluate design specifics and recommendations during evacuation to reduce the possible proportion of infected people with a severe course of the disease after leaving the danger zone
- Other benefits

o If mathematical models of other viral infections are available, the proposed modeling methods can be used to predict the dynamics of disease dynamics in persons who have left the territory with polluted atmosphere. In addition, the proposed approach can be used in assessing the risks of terrorist acts using biologically active substances

Biography

Panova A. A. studied Applied Mathematics at the Bauman Moscow State Technical University and graduated as MS in 2019. Now she is postgraduate student of BMSTU and currently preparing to defend her PhD on the topic “Mathematical modeling of the spread of viral infections in groups of people taking into account their social behavior”. During her scientific career, more than 20 articles were published, included in the RSCI, WoS, Scopus. Also Panova took part in 10 international conferences held in Moscow, Novosibirsk, Saratov, as well as in Greece, Spain and the Republic of Belarus.

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Evaluation of two minicircle DNA vaccines encapsulated in peptide nanoparticles against HPV-16

Infection with the Human Papilloma Virus (HPV) is known as the main cause of the development of several types of cancer, especially cervical cancer. Due to the presence of oncoproteins, mainly E6 and E7, in HPV-16 and HPV-18 strains, this virus has a great capacity to suppress apoptosis and stimulate abnormal cell proliferation and angiogenesis, which contributes to the malignant transformation of cervical epithelium cells.

Until now, the only available option to avoid cervical cancer is the prevention of the HPV infection, but commercial prophylactic vaccines cannot treat an established cancer. DNA vaccines encoding HPV oncoproteins genes have been promising approach, due to numerous advantages such as stability, cost-effectiveness and mainly the potential to activate immune system pathways that can lead not only to the prevention of infection but also to the specific elimination of cancer cells as a therapy.

Therefore, the aim of this work is to evaluate the delivery of two nanovaccines against HPV-16 formulated with peptides nanoparticles to Antigen Presenting Cells (APCs). This work explored two different delivery systems based on RALA (a cell-penetrating peptide), functionalized with octa-arginine mannose (R8M) to encapsulate two minicircle DNA (mcDNA) vectors: one encoding the E6 mutated oncoprotein alone (mcDNA/E6mut), and a multigenic vector with both E7 and E6 mutated oncoproteins (mcDNA/E7-E6mut) of HPV-16. For comparative purposes, two different systems were evaluated: RALA and RALA-R8M. The systems were prepared at various Nitrogen-to-Phosphate group (N/P) ratios and characterized in terms of size, Polydispersity Index (PDI), surface charge, morphology and encapsulation efficiency. Moreover, the systems stability was evaluated after incubation in 10% FBS and MEM-α medium. In vitro transfection studies of dendritic cells (JAWS II) were performed, along with viability studies for 24 and 48h to ensure the biocompatibility of all nanocarriers.

Delivery systems encapsulating mcDNA/E6mut presented sizes of 87.05 nm (± 8.16) and 101.79 nm (± 17.94), PDI of 0.234 (± 0.03) and 0.253 (± 0.04) and surface charge of -7.49 (± 0.19) and -12.35 (± 0.42) for RALA and RALA/R8M, respectively. For the multigenic vector, the results were in the same order 106.73 (± 12.07) and 132.77 (± 20.54), 0.294 (± 0.03) and 0.292 (± 0.05), -13.25 (± 2.88) and -12.71 (± 3.09). RALA systems have a spherical shape, with a smoother morphology due to the addition of R8M. Encapsulation efficiencies for all nanovaccines were above 99%.

The systems showed stability in the presence of 10% FBS and MEM-α medium and biocompatibility after transfection of JAWS II cells. Regarding the E6 expression, both vectors encapsulated with RALA/R8M demonstrated the highest levels of transcripts in JAWS II cells, with no statistical differences between them. Mannosylated systems have shown promise in delivering mcDNA to APC cells, but with a multigenic vector is expected to induce a stronger and more complete immune response against HPV-16 virus. At this moment, the RALA mannosylated system containing mcDNA/E7-E6mut is under studies to convert the nanovaccine into a dry-powder by the Thin-Film Freezing (TFF) technique, aerosol performance and intranasal administration in animals.

Audience Take Away Notes

- The audience will learn about the advantages of using minicircle DNA vaccines as a preventive and therapeutical approach against HPV-16
- The advantages of exploring the use of cell-penetrating peptides, such as RALA, in DNA vaccines
- The applications of mannosylated delivery systems to improve the targeted distribution of these vaccines to APCs
- This work can clarify some of the techniques used in the production of DNA vaccines on a small scale, but with cost-benefit and easy reproducibility
- The advantages of converting a liquid vaccine into dry powder using the Thin-film freezing technique

Biography

Andressa Giusti graduated in biology from the University of Vale do Itajai, Brazil in 2020 and is currently a master's student of Biomedical Sciences at the University of Beira Interior, Portugal. Before moving to Portugal, she worked in research and clinical practice in the area of Assisted Reproduction and taught Biology in secondary education. During her master, she joined the research group of Prof. Angela Sousa at CICS-UBI at the Faculty of Health Sciences and is currently a research fellow within the Research Project DryVac, which is currently being carried out at the University of Texas at Austin (USA).

Ludena Angelica*, MD; Negron Merliz, MD; Cruz Kattya, MD; Colon Melba, MD; FACP, FIDSA

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Is plasmapheresis the future treatment for leptospirosis? Case report of a 75-year-old patient with complete recovery after plasmapheresis therapy

Leptospirosis is a zoonotic disease produced by spirochetes of Leptospira, with an incidence ten times higher in tropical regions like Puerto Rico, in comparison to the rest of the world. The principal reservoir are rats, dogs, cats and farm animals with excreted infected urine, contaminated soil or water that produces the disease through direct contact of broken skin, mucosa or conjunctivas. During the first infective phase, Leptospira are found in blood and cerebrospinal fluid and the course is asymptomatic, followed by an immune phase where Leptospira are excreted in the urine. Ten percent or less progress to septic shock and multi-organ dysfunction (Weil's Disease) presenting with acute kidney injury, pulmonary hemorrhage, Acute Respiratory Distress Syndrome (ARDS), bleeding diathesis, impaired hepatic functions, jaundice, thrombocytopenia, circulatory collapse or even death.

This is the case of 75-year-old female with major depressive disorder with psychotic features, who arrived with fever of 400 C, decreased appetite and lower extremities myositis, who practiced daily farming and rose gardening and had direct contact with horses, cats, dogs and recently found dead animals. Upon admission, the patient was acutely ill, awake, alert, oriented and was tachycardic, with a blood pressure of 84/50 mm Hg, and a negative Tourniquet test. Within 24 hours, marked deterioration was noted and she was admitted to intensive care unit (ICU) for suspected leptospirosis and viral syndrome. Acute Kidney Injury (AKI), sepsis, leukocytosis of 14,500 10^3/uL, moderate thrombocytopenia, elevated transaminases, hyperbilirubinemia, severe dehydration, and moderate hyponatremia developed, therefore empiric intravenous antibiotic was started. After four hours in the ICU, she was intubated and thirty six hours later developed ARDS and pulmonary hemorrhage. Jaundice, increased leukocytosis of 24.5K, severe thrombocytopenia of 29K, elevated liver enzymes and AKI stage 3 were present, therefore hemodialysis was started. By day eleven Leptospira DNA PCR was confirmed. During hospitalization, a total of seven plasmapheresis, six hemodialysis, one fresh frozen plasma, seven platelet transfusions, and three packed red blood cell transfusions were given. By day ten, after clinical and renal improvement the patient was extubated successfully.

Plasma exchange may interrupt the mechanisms causing tissue damage in severe sepsis. Renal injury in leptospirosis might be caused by activation of Toll-Like Receptors (TLR) 2 and 4 by Lipopolysaccharides (LPS) causing interstitial edema and a tubulointerstitial nephritis with cellular infiltrate. Also, lung injury is thought to be induced by deposition of IgM, IgA, IgG and C3 in the alveolus. The outer membrane of Leptospira shares characteristics of both Gram-positive and Gram-negative bacteria and the binding of LPS to TLR4 on the surface of B lymphocytes results in the activation of B-cells and the production of IgM against the LPS of Leptospira. Activation of B-cells and T-cells, which promote the killing of Leptospira, also produces pro-inflammatory cytokines and tissue inflammation. Plasma exchange may prevent immune complex-mediated tissue injury.

As a result, anytime a patient with septic shock and multi-organ failure with a history of dead animals or suspected infected water contact is revealed, leptospirosis should be considered, and plasma exchange could be the preferred therapy.

Biography

Angelica M. Ludena De Freitas, Medical Doctor PGY-1 at Internal Medicine Residency, ACGME accredited program Universidad Central del Caribe, Puerto Rico. She is graduated from Universidad Autonoma of Guadalajara Jalisco Mexico and did her Internship at Hospital Auxilio Mutuo San Juan, Puerto Rico and she is originally from Lima, Peru. Angelica M. Ludena De Freitas recently won 1st place at American College of Physicians Annual Oral Presentation Puerto Rico.

Dr. Anil Budania[1]*, Dr. Kumar S Abhishek[2], Dr. Sarika Kombade[2], Dr. Naveen K H[3], Dr. Gautam Ram Chaudhary[4], Dr. Charu Sharma[5], Dr. Akriti Agrawal[6]

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A new insight in the clinical profile of Indian patients of urethritis and cervicitis with the help of molecular characterization of the causative organisms

Introduction: Urethritis and cervicitis, in the majority of cases, are caused by sexually transmitted agents. They presents as discharge, pain, burning sensation but sometimes the patient may remain asymptomatic. Neisseria gonorrhoeae (Gono-coccal) and chlamydia trachomatis (Non-gonococcal) are considered classical causative organisms of urethritis and cervicitis in developed and developing world respectively. Other causes are Mycoplasma genitalium, Ureaplasma Urealyticum, Trichomonas vaginalis and Herpes simplex etc. Number of newly diagnosed urethritis and cervicitis cases are increasing worldwide leading to many complications like prostatitis, epididymitis, pelvic inflammatory disease and infertility. Non-gonococcal urethritis and cervicitis cases are difficult to diagnose because of minimal visible discharge. Treatment is done with empirical antibiotics when the causative organism cannot be isolated. So basically urethritis and cervicitis are difficult to diagnose and treat which may lead to significant morbidity specially in the developing countries.

Objectives: To study the profile of patients presenting with symptoms of urethritis and cervicitis and to elucidate the various etiologic agents.

Methodology: Patients within 15-45 years (both sexes) with history of urethral or cervical discharge, dysuria and dyspareunia were included in the study. Urethral or cervical samples were collected with the help of dacron swabs for multiplex real time polymerase chain reaction analysis of Neisseria Gonorrhoeae, Chlamydia Trachomatis, Mycoplasma Hominis & Ureaplasma Urealyticum.(TRUPCR□ STD Panel kit 3B BlackBio Biotech India Ltd.

Results: A total of 70 patients were included and analyzed. Analysis was done using the SPSS version 21 for Windows (Chicago, Illinois, USA). Out of 70 patients, 64.3 % were female and 35.7% were male. Around 59% patients were in the age group of 18-30. Around 15.7 % had history of multiple sexual partners. PCR showed positivity for Ureaplasma urealyticum in 37.7%, Neisseria gonorrhoea in 15.9%, Chlamydia trachomatis in 10.1 %, Trichomonas vaginalis in 5.8 % cases. Rest of the samples showed mixed growth of multiple organism including Gardnerella Vaginalis and HSV 2.

Discussion: Prevalence of urethritis/cervicitis is increasing worldwide and it varies around the globe. Especially the drug resistance strains of various gono-coccal and non-gonococcal pathogens are growing. Empirical treatment without knowing the exact pathogen can lead to persistent infection and complications. NAAT and species specific PCR test are recommended to decide etiology based treatment.

We found Ureaplasma urealyticum as the major pathogen causing urethritis and cervicitis. This is in contrast to western data where we see chlamydia as the major pathogen Though initially considered as commensal, Ureaplasma urealyticum is considered a significant pathogen causing persistent urethritis and cervicitis after 1950 AD. This is in contrast to western data where we see chlamydia as the major pathogen. Significant numbers (40%) had mixed infections also. So we wish to emphasize the role of PCR and etiology based regimen in the management of urethritis and cervicitis.

Audience Take Away Notes

- Urethritis and cervicitis cases are increasing worldwide and causing significant morbidity
- Microbiological profile of urethritis and cervicitis is changing and non-gonococcal organisms are leading in developing world (India) also where we usually follow syndromic management
- PCR and then etiology based management can help in reducing the number as well as complications of urethritis and cervicitis
- This study can help to plan further research not just in the field of Dermatologuy but also in Microbiology, HIV medicine, Urology, Gynaecology and obstetrics etc
- More simplified, user friendly and cost effective PCR kits to diagnose multiple organism can be devised

Biography

Dr. Anil Budania studied Dermatology and Sexually transmitted infections at PGIMER Chandigarh and received his post-graduation degree in Dermatology, Venereology & Leprology. Then he joined VMMC & Safdarjung Hospital which is a premier institute for STI and HIV medicine in India. He joined AIIMS Jodhpur in 2017 as Assistant Professor and promoted to the post of Additional Professor in July 2023. This study is the product of an intramural institute funded project on sexually transmitted infections. Apart from STI, his area of interests is superficial cutaneous fungal infection. He has published more than 40 research articles in pubmed indexed journals.

Anju Kaushal, PhD
Auckland, New Zealand

RNA interference, its applications and benefits

The activation of double stranded interference RNA occurring in the host cell is a natural phenomenon to control the over transcriptional effects of genes that could suppress the translational patterns. This genetic ability is currently being exploited in making the medicines to suppress the lethal post-translational effects as an outcome of aberrant or disease related genes. This revelation has been made to treat those inherent diseases were rendered untreatable in the past. RNAi therapeutics silence the lethal/adverse effects of a gene function. The modulation of siRNA can be brought by changing some chemical patterns in RNA chains. The phosphorylation and off target effects are greatly reduced during phosphonate modifications, ribose sugar effects and base substitutions. Additionally, these modifications are likely to control the immune stimulation and hyper activation of the innate response. The universal pattern and advanced patterns have been used in various therapeutics. The heavy modifications in the anti-sense & sense strands are used using 2-OMe, L-DNA, UNA, N-acetyl glucosamine etc. Innate immune regulations can be established through TLR receptors' signaling, but PKR and RIG are also capable to carry out the IFN induction in the absence of TLR sensors. This presentation will walk us through the immune modulation of siRNAs to reduce toxicity and regulate the innate and adaptive immune response to produce the favorable effects.

Audience Take Away Notes

- The audience will learn about siRNA medicines and how this mechanism can be explored for various medicines
- This presentation will provide the insights of novel therapeutics and their involvement to establish the protective immune response.
- It is evidence-based research, thus, providing a practical solution to a problem that could simplify or make a designer's job more efficient
- It improve the accuracy of a design, or provide new information to assist in a design problem
- Other benefits
    - o This is an advanced novel field of research
    - o These medicines can be utilized to treat various gene related diseases and other infectious diseases
    - o These therapeutics give hope to people who suffer from untreatable diseases
    - o Besides, this emerging field open the door for many other opportunities to use these modalities to make medicines and diagnostics

Biography

Dr. Anju Kaushal is PhD in Science from Panjab University. She is a current-member of NZOQ and a Research Topic Coordinator–Frontiers in Antibiotics. She worked on Rabies, Aspergillus, Candida, HIV, enzymes, fermentation technologies etc. Her areas of interest include vaccines, sera, diagnostics and novel therapeutics. Her expertise is in R&D, Productions and Quality in biologicals, diagnostics and academia, including marketing, information and communications, and small business management. She has assisted many scientists in their careers. She has authored 15 articles in peer reviewed journals, published >40 articles on LinkedIn, and peer reviewed a variety of research around the globe.

Ilhem Berrou[1], Laura Hobbs[2], Sue Jones[3], Sian Hughes[4], Anne Morris[5]*, Thomas Manning[6], Hannah Bailey[3]

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Implementing the COVID-19 vaccination programme in the Southwest of England: Lessons from a normalisation process theory perspective

Background: Vaccination remains one of the most successful public health interventions in preventing severe disease and death. The roll-out of Covid-19 vaccination programmes has helped protect billions of people around the world against Covid-19. Most of these programmes have been unprecedented in terms of scale and resources, and have been implemented at times of significant humanitarian crisis. This study aims to outline the lessons learnt from the implementation of a regional Covid-19 vaccination programme. These will help inform emergency preparedness and future crisis management.

Methods: This qualitative study sought to explore the key drivers to the successful implementation of the Covid-19 vaccination programme in a region in the Southwest of England, applying the Normalisation Process Theory lens (NPT) to examine multi-stakeholder perspectives. Data collection involved semi-structured interviews with 75 participants. Document analysis was also used to corroborate the findings emerging from the interviews. Inductive thematic analysis of the data was used to identify the key drivers for the successful implementation of the programme. The NPT lens was then applied to map the themes identified to the domains and constructs of the framework.

Results: Ten key drivers to the successful implementation of the Covid-19 vaccination programme locally were identified. These include the clarity and consistency of the programme's goal; the diverse representation of stakeholders within the programme leadership team and the mechanisms created by this team to ensure psychological safety, autonomy, operational flexibility and staff empowerment; Communication and data specialists' input, and collaboration with local communities to maximise the reach of the programme; and allocating funding to tackle health inequalities.

Conclusions: This study highlights the lessons learnt from the implementation of the Covid-19 vaccination programme at a local level, and the mechanisms that can be used in future crises to respond efficiently to the needs of individuals, communities and governments.

Audience Take Away Notes

- This paper provides a blueprint for responding to a crisis and how to achieve the necessary goals
- The study provides information which will enable colleagues to develop emergency preparedness and organizational resilience
- Audience will be informed of the key drivers to success and how this can be transferable
- The study provides practical solutions describing how data was used extensively to reinforce targeting of activity and the roles played by communications and insight in support of this
- The study also describes the importance of creating a skilled team and how asset based community development was used to tackle health inequalitie

Biography

Anne Morris is an experienced senior nurse and leader who has worked in many roles within the local health system. She qualified as a registered general nurse in 1984 and then went on to study renal nursing and gained an MSc in Leadership and Management at Bath Spa University in 2010. Anne has presented papers at national and international conferences.

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Awareness of antimicrobial resistance evaluating the impact of a foldscope based workshop

Background: Antimicrobial Resistance (AMR) is a global public health concern that threatens the effectiveness of antibiotics and other antimicrobial drugs. As a result of drug resistance, antibiotics and other antimicrobial medicines become ineffective and infections become difficult or impossible to treat, increasing the risk of disease spread, severe illness, disability and death. It is imperative to address this issue by increasing awareness and knowledge among young adults, as they are a crucial demographic in shaping future healthcare practices.

Purpose: This study aims to evaluate the effectiveness of a hands on workshop on spreading awareness of antimicrobial resistance. The workshop aimed to educate the students about the importance of understanding different types of cells and microorganisms, their interactions and co-existence. Thus assess the impact of the workshop on participants' knowledge related to microbes, infections caused by microbes, and antimicrobial resistance.

Methodology/Approach: A portable paper folding microscope, Foldscope was used to enable the students explore the microflora around them. Using the tool, students gained a better understanding of different types of cells by making observations. The samples included the onion cell, potato cell, pollen grains, squamous epithelia and more. These observations helped them explain various sources of fever, that include bacteria, viruses, fungi, and parasites. An online survey link was sent to all the participants to assess changes in self-reported knowledge and behavior (outcomes) following the workshop, that included questions about the causative agents of fever, the remediation of fever, consuming antimicrobials without a prescription, and having leftover formulations. Of the 400 students who attended the workshop 60 % responded, 93.58 % participants' felt confident in using a microscope effectively, 82% responded that the experience bettered their understanding of microbes and their knowledge about antimicrobial resistance. A significant number 82.57% felt their likelihood of incorporating the workshop's content into their life as caregivers.

Findings: The dataset incorporates responses from individuals across various demographics, providing insights into the level of understanding and perception regarding AMR. The analysis of survey responses, aims to identify key factors influencing awareness, such as educational background, geographic location, and access to healthcare resources. The findings reveal varying degrees of awareness among the surveyed population, highlighting potential gaps in knowledge that need attention. Additionally, the study investigates the impact of media, educational campaigns, and healthcare professionals in shaping public awareness and understanding of AMR. The results of this research contribute valuable information for policymakers, healthcare professionals, and public health organizations to design effective strategies aimed at enhancing awareness and promoting responsible antimicrobial use. Addressing gaps in knowledge is crucial in the global effort to combat the growing threat of antimicrobial resistance and preserve the effectiveness of existing antibiotics.

Conclusion: This study contributes to the literature by evaluating the effectiveness of these workshops on spreading awareness of antimicrobial resistance among young adults. The findings highlight the workshop's positive impact on participants' knowledge and skills, indicating its potential value in promoting awareness and understanding of antimicrobial resistance. It emphasizes the importance of incorporating hands-on activities and interactive sessions to enhance participants' learning experience and skills development.

Audience Take Away Notes

- The audience will be able to plan hands-on training sessions for young adults using a low cost tool (Foldscope), if we want to augment the outreach/impact of AMR to young adults. They will learn practical skills in microscopy, sample preparation, and data interpretation. Participants will understand the relevance of anti-microbial resistance (AMR) and how microscopic analysis can contribute to identifying potential microbial threats
- Understanding AMR through practical applications will empower healthcare workers to make informed decisions on antibiotic usage, contributing to more effective treatment strategies
- The hands-on approach fosters an engaging learning environment that can be adapted for different educational levels, from high schools to universities
- The Foldscope, being a cost-effective and portable tool, can simplify the process of microbial analysis, making it accessible in various settings
- The workshop can enhance the accuracy of designs related to medical diagnostics, environmental monitoring, and other fields where microbial analysis is crucial
- Other benefits
    - **Increased Awareness**: Participants will gain a deeper understanding of the global issue of antimicrobial resistance and its implications
    - **Community Engagement:** The workshop fosters community involvement and awareness, potentially leading to collaborative efforts in addressing AMR
    - **Skill Development:** Attendees acquire valuable skills in microscopy, sample preparation, and data interpretation, which can be applied in diverse professional settings
    - **Interdisciplinary Collaboration:** The workshop encourages collaboration between professionals from different fields, fostering a holistic approach to addressing AMR
    - **Cost-effectiveness:** The use of Foldscopes makes microscopy more affordable and accessible, especially in resource-limited settings

Biography

Dr. Anupma Harshal W. is a high-achieving teacher, mentor who has steered Under Graduate Research, engaging students in research projects. She has a Ph.D. in BIochemistry from Mumbai University, a collaboration between Hindustan Unilever Research Centre, National Centre for Cell Science and B.Y. Nair Hospital & Topiwala Medical College. As a woman in STEM she has 28 research projects with Undergraduate students at Kishinchand Chellaram College, Mumbai University of which 11 have received funding from the Ministry of Science & Technology, Mumbai University, U.G.C., and other private labs. She is a certified trainer for STEM teachers training on Research-Based Pedagogy and an avid Foldscoper. She uses the tool to explore the microscopic world conducting Awareness of Antimicrobial Resistance workshops in schools pan India. Have been a reviewer for several International Journals and have also reviewed a few books on Pedagogy. She has contributed to the coursework for M.B.A. program in Sanitation & Hygiene, Waste Management, WASH & Nutrition by MGNCRE, MHRD, and two books on Foldscope and its applications. She has contributed to several Govt. of India Projects as a Consultant on Biocuration, Scholarships, Public engagement and Science Communication. She travels pan India and conducts Awareness of Anti-Microbial Resistance workshops, raising funds for the same.

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Unraveling a case of tubercular thyroiditis presenting as thyrotoxicosis

Introduction: Tuberculosis is chronic infection caused by mycobacterium tuberculosis and primarily attacks the lung. Tuberculosis of thyroid gland is an uncommon entity as the gland is resistant to infection due to bactericidal property of colloid high iodine content and extensive vascularity.

We hereby present the case of 34 year old male who presented to us with fever, loss of weight and tremors of both upper limbs for past 2 months. Fever was intermittent with one to two spikes per day associated with evening rise of temperature and night sweats. He gave history of significant weight loss of around 7kg loss over past 2 months which was associated with loss of appetite. He also had tremors of both the hands which aggrevated on activity that affected his daily routine life. His past history was unremarkable. On examination he had pallor cervical and axillary lymphadenopathy and anterior neck swelling moving with deglutition and had tachycardia. Systemic examination revealed hepato-splenomegaly. On investigating he had anaemia with elevated ESR. Thyroid function test revealed low tsh and elevated ft4 suggestive of hyperthyroidism, ultrasonography of neck was suggestive of thyroiditis and initial FNAC showed Bethesda category 2. Whole body Pet-Ct scan revealed bulky right lobe of thyroid gland and increased metabolically activity in axillary, gastrohepatic, perigastric, paratracheal lymphnodes and segment 6 and 8 of liver. Histopathological examination of axillary lymph node revealed sinus histiocytosis and thyroid gland revealed multiple caseating granulomas consistent with tuberculosis. Patient was hence diagnosed as case of tubercular thyroiditis presenting as thyrotoxicosis with disseminated tuberculosis and was initiated on antitubercular drugs.

Discussion: Tuberculosis is endemic in India and can affect any organ of the body Tubercular involvement of thyroid gland maybe either primary or as a part disseminated disease process in immunocompromised individuals and most cases are euthyroid. Tuberculosis of thyroid gland should be considered in differential diagnosis when evaluating a thyroid nodule especially in presence of lymphadenopathy organomegaly and anemia with elevated ESR and should be extensively evaluated.

Biography

Dr. Aparna M Menon, completed her MBBS from MVJ Medical College Karnataka and is currently doing Internal Medicine Residency in Government Medical College Kozhikode.

Arjun Chadha*, Anthony Ognjan
Michigan State University, United States

Ocular syphilis with concomitant neurosyphilis and tuberculosis: A case report

Syphilis is a venereal or vertically transmitted infectious disease caused by Treponema pallidum, a corkscrew shaped, motile spirochete. It generally progresses via stages and, if left untreated, can result in devastating cardiovascular and neurological sequelae.

Ocular syphilis refers to infectious inflammation within any portion of the eye. It typically results in uveitis, but can also cause optic neuropathy, retinal vasculitis and interstitial keratitis. It presents as diminished visual acuity and delayed treatment may result in permanent vision loss. Similar to neurosyphilis, ocular syphilis can occur during any infectious stage.

Towards the end of the 20th century, significant progress in syphilis prevention resulted in an all time low prevalence in high income countries, such as the United States. This rare complication only had an annual incidence of 0.3 cases per million adults between 2009 to 2011. However, there have been concerns of increased prevalence in syphilis in the past decade. The prevalence of syphilis complications has also increased during this time span, including ocular syphilis. This trend is consistent globally, with noteworthy data arising from Europe, North America, and South America. In 2016, the World Health Assembly adopted a strategy with the intention to reduce the incidence of global syphilis by 90% from 2018 to 2030.

We present a rare case of ocular syphilis in a 61 year old, immunocompetent male. The patient's ocular syphilis manifested as left chorioretinitis, resulting in progressive monocular vision loss. The patient cited concerns for memory loss, and lumbar puncture confirmed concomitant neurosyphilis. His condition was complicated with latent tuberculosis. Administration of penicillin resulted in improvement of symptoms.

This report highlights the reemergence of ocular and neurosyphilis. Emphasis should be placed on appropriate identification of ocular syphilis in a timely manner. In doing so, swift antibiotic management can subsequently prevent morbid visual and neurological sequelae.

Audience Take Away Notes

- Recognize the increasing prevalence of Syphilis on the global scale and its feared complications
- Understand the management of Ocular Syphilis and Neurosyphilis to facilitate early treatment
- Emphasize the importance of documenting cases of Syphilis to facilitate its proper surveillance
- Increase visibility on the lack of research revolving syphilis complications

Biography

Dr. Arjun Chadha graduated with Honors distinction from Wayne State University with a B.S. in Biological Sciences. During this time, he worked meticulously on basic biophysics research. He received his M.D. at Michigan State University College of Human Medicine (MSU-CHM). He pursued a residency program with Michigan State University College of Osteopathic Medicine (MSU-COM) at McLaren Macomb, allowing him to focus on clinical medicine by accessing a wide array of pathologies. His professional passions include medical education and personal interests include dancing.

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An unusual case of multidrug-resistant Klebsiella pneumoniae and vancomycin-resistant enterococcus faecium skin and soft tissue infection in an immunocompromised host

Skin and Soft Tissue Infections (SSTI) represent an uncommon source of infection (<10%) in patients with persistent or recurring fever and neutropenia. Worldwide, the prevalence of immunocompromised hosts is increasing even as the incidence of gram-negative and of Multidrug-Resistant (MDR) SSTI are also increasing, exacerbating existing challenges in treating infection in neutropenic patients.

A 43-year-old male with B-cell Acute Lymphoblastic Leukemia (B-ALL) (on treatment with R-hyper-CVAD [rituximab, cyclophosphamide, vincristine, doxorubicin, dexamethasone] with intrathecal cytarabine) and schizophrenia (on multiple psychiatric medications) presented with neutropenic fever. He had a history of three MDR Klebsiella pneumoniae bloodstream infections within the last six months alone. Indeed, his blood cultures were positive for Klebsiella pneumoniae again and meropenem was started, with therapeutic drug monitoring used to optimize dosing. The source, however, remained unclear. CT of the chest, abdomen, and pelvis was unremarkable. An echocardiogram performed to evaluate for endocarditis revealed neither vegetations nor valvular changes. He continued to be febrile and vancomycin therapy was added empirically.

Then, the left gluteal lesion that had been present on admission ruptured and began draining purulent material. The abscess itself had an unusual appearance with dark purple coloring, initially suggestive of ecthyma gangrenosum. Bedside incision and drainage was performed. However, the surrounding erythema and induration continued to progress even after presumed source control. Empiric antifungal therapy was considered but deferred given the potential interactions with both his chemotherapy and antipsychotic medications. Vancomycin was switched to daptomycin, and he was taken to the operating room for surgical exploration of the abscess. Intraoperative deep tissue cultures ultimately grew both MDR Klebsiella pneumoniae and vancomycin-resistant Enterococcus faecium. Both meropenem and daptomycin were continued and he improved clinically. For the management of his B-ALL, in order to avoid future neutropenia, he was switched from chemotherapy to bispecific T-cell engager therapy.

We present a case of a mixed MDR SSTI in an immunocompromised host, with SSTI as a presumed source of recurrent gram-negative bloodstream infection. Both Klebsiella pneumoniae and Enterococcus faecium are uncommon culprits in SSTI. Broad-spectrum antibiotics, source control, and species identification were critical in managing infection in an already vulnerable host.

Audience Take Away Notes

- We present a case of a mixed multidrug-resistant skin and Soft Tissue Infection (SSTI) in an immunocompromised host causing recurrent gram-negative bloodstream infection. Both Klebsiella pneumoniae and Enterococcus faecium are uncommon culprits in SSTI
- Therapeutic drug monitoring is a useful tool, with antimicrobials such as meropenem, to optimize drug dosing

- Skin and Soft Tissue Infections (SSTI) represent an uncommon source of infection (<10%) in patients with persistent or recurring fever and neutropenia. However, given the increase in immunocompromised hosts worldwide and the increase in co-morbidities such as obesity and diabetes, consider SSTIs as a source in a patient with persistent or recurring fever

Biography

Ashley Zhou, M.D. studied Neuroscience at Duke University for her undergraduate degree and graduated with a B.S. in 2019. She went on to study at the Johns Hopkins University School of Medicine for her medical training and received her M.D. in 2023. She is currently undergoing residency training in the Department of Ophthalmology at the Mayo Clinic in Rochester, Minnesota.

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An unexpected twist under the microscope: Schistosomiasis masquerading as endometriosis

Introduction: Schistosomiasis is a parasitic infection endemic to Asia, Africa, and South America, and can be an unusual cause of pelvic pain in women. Due to similar symptoms with endometriosis, the diagnosis is often missed in regions of the world where Schistosomiasis is uncommon. We present a rare situation with longstanding schistosomiasis due to a misdiagnosis and delayed treatment.

Case Presentation: A 24-year-old woman presented with chronic pelvic pain, dysmenorrhea, and dyspareunia. She had no prior history of sexually transmitted infections. She had no fever, urinary symptoms, irregular menstrual cycles, vaginal bleeding or discharge. Her pelvic exam was notable for tenderness on the right uterosacral ligament with a 1-2 cm nodule. Diagnostic laparoscopy revealed a small amount of endometrial implants on the anterior cul-de-sac, which was cauterized. She was then prescribed oral contraceptives. However, her pelvic pain persisted for several months. Pelvic MRI was normal without any findings of endometriosis. A second laparoscopy demonstrated an enlarged uterus and endometriotic tissues on the colonic serosa associated with surrounding fibrosis and scarring. Excised tissues were sent for pathology. Light microscopy of the specimen did not show endometriotic characteristics but a background of granulomatous inflammation interspersed with calcified Schistosoma eggs, later identified as Schistosoma mansoni. Upon reviewing her exposure history, she reported spending two months in Uganda and Rwanda, during which she participated in baptisms in Lake Victoria, about 2 years prior to the onset of symptoms. Notably, she never had eosinophilia but had an elevated Schistosoma IgG level. She was started on a 60mg/kg dose of praziquantel over 24 hours together with a course of oral prednisone. She completed a second dose of praziquantel 4 weeks later. She had two subsequent stool studies which were negative for ova and parasites. Unfortunately, her pelvic pain did not improve.

Discussion: Schistosomiasis is a chronic parasite infection that is not common in the United States. Schistosoma mansoni enters the host via the skin, migrates through blood and settles in mesenteric vessels. It can present as an acute hypersensitivity reaction or a chronic granulomatous inflammation. The prolonged inflammation and fibrotic changes on laparoscopy due to delay in treatment explain why this patient did not improve after laparoscopy and anthelminthic therapy. The diagnosis of schistosomiasis can be made through various approaches including parasite egg-microscopy in urine or stool samples, parasite antigen, or antibody assays. Praziquantel is the preferred treatment option for Schistosomiasis with relatively few adverse effects. A second dose is often recommended to kill juvenile worms 3-6 weeks after the initial treatment. Steroids are sometimes added to reduce the risk of complications related to the host inflammatory response.

Conclusion: Due to varying clinical manifestations of the disease, diagnosing schistosomiasis can be difficult or even mistaken for another pathology when it is encountered outside of endemic regions. This case emphasizes the importance of obtaining a comprehensive exposure history in patients with long-standing unexplained pelvic pain.

Audience Take Away Notes

- To increase recognition of untreated Schistosoma mansoni as a potential source of chronic pelvic pain
- To highlight the pathogen's transmissibility, clinical presentation, and identification on tissue pathology
- To emphasize the potential result of chronicity of pain in cases of delayed treatment

Biography

Dr. Naing finished his medical studies at the University of Medicine, 1, Yangon, Myanmar and graduated in 2019. He worked as a small group teacher for USMLE Step 1 and Step 2 CK at Kaplan Medical Center, New York and as a clinical assistance at Essen Healthcare, New York, in 2020. Then, he started his internal medicine residency at Eastern Virginia Medical School, Norfolk, Virginia, in 2021, and he is in the last year of residency training.

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Uncharted territory in mycobacterial world: The second reported case of mycobacterium shimoidei in the United States

Introduction: Mycobacterium shimoidei is a rare, slow-growing nontuberculous mycobacterium, first isolated in Japan in 1968. Only one case was reported in the United States, out of a total of fifteen cases reported worldwide. Due to its rarity and the current understanding of its pathogenicity, identifying predisposing risk factors and providing effective treatment is limited. We present a case of macrolide-resistant Mycobacterium shimoidei infection causing a cavitary lung requiring surgical resection.

Case Presentation: A 68-year-old male with a history of heavy cigarette smoking and COPD presented with a six-month-long hacking cough with sputum production, night sweats, weight loss, and malaise. He was treated with multiple courses of azithromycin for community-acquired pneumonia without improvement. He had a history of asbestos exposure as a shipyard worker. He did not travel outside of the US and had no known exposure to TB. Imaging of the chest revealed a complex left upper lobe cavitary lesion with surrounding consolidation and nodular densities in the left upper and lower lobes with background emphysematous changes. He underwent a bronchoscopy due to concerns for lung cancer. Bronchoalveolar lavage cultures later grew Mycobacterium shimoidei, identified based on gene sequence analysis. Sputum was positive for acid-fast-bacilli and cultures also grew Mycobacterium shimoidei. He was started on clarithromycin, rifabutin, and ethambutol. He had mild side effects of treatment, including nausea, fatigue, hair loss, and dry skin, but he managed to continue therapy. Cultures showed sensitivity to ethambutol and rifabutin but resistance to clarithromycin. On a 6-month follow-up, he continued to have a persistent low-grade fever and cough with purulent sputum speckled with black particulate matter. COPD symptoms had worsened, causing persistent wheezing and shortness of breath. Repeat CT of the chest showed progression in the size of the cavitary lesion with surrounding ground glass opacities. It was deemed that the antibiotic treatment had failed. After a multidisciplinary discussion with pulmonary, infectious disease, and cardiothoracic surgery teams, a decision was made to proceed with left upper lobectomy. The patient's recovery was without any complications, and his symptoms improved significantly. Pathology of the resected specimen showed non-caseating granulomatous inflammation. On follow-up visits over the next 5 years, he remained symptom-free, and repeat sputum AFB tests continued to be negative. CT scans of the chest showed no recurrence of the disease.

Discussion: Mycobacterium shimoidei predominately affects middle-aged men with immunosuppression, preexisting pulmonary disease, previous tuberculosis, and lung cancer. The mycobacterium has been reported in Japan, Germany, Australia, Canada, Croatia, and Italy with only one case reported in the US. There is no evidence of human-to-human transmission or clear environmental sources. The infectious presentation is similar to tuberculosis, and it predominantly causes pulmonary disease. However, renal complications have also been reported. There is no current consensus on established therapy, but the triple-drug regimen, including clarithromycin, rifabutin, and ethambutol, has been effective in most reported cases. Additionally, Moxifloxacin and Levofloxacin, Sulfamethoxazole, Pyrazinamide, as well as Clofazimine have been reported to be potentially useful. There is limited experience with cases of macrolide resistance and therapeutic failure. There have never been any case reports requiring surgical resection which might be a potentially curative option for appropriately screened patients.

Conclusion: There are limited guidelines for treating Mycobacterium shimoidei infection with drug resistance. Due to their extreme rarity, our knowledge on surgical options for such cases with antibiotic failure is limited. Our case highlights that surgical resection might be a curative option after a careful joint decision-making process among patients and multidisciplinary teams.

Audience Take Away Notes

- To actively contribute to the advancement of medical knowledge on a rare case of Mycobacterium shimoidei
- To enhance practice-based learning by sharing the natural history of drug-resistant Mycobacterium shimoidei
- To emphasize the potential curative treatment with surgical resection

Biography

Dr. Naing finished his medical studies at the University of Medicine, 1, Yangon, Myanmar and graduated in 2019. He worked as a small group teacher for USMLE Step 1 and Step 2 CK at Kaplan Medical Center, New York and as a clinical assistance at Essen Healthcare, New York, in 2020. Then, he started his internal medicine residency at Eastern Virginia Medical School, Norfolk, Virginia, in 2021, and he is in the last year of residency training.

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Repercussions of pasteurella multocida infection in humans: A case report

Pasteurella multocida is a gram-negative bacterium commonly found in the respiratory and gastrointestinal tracts of animals, such as cats, dogs and birds. This bacterium is known to cause a variety of infections in animals and can occasionally be transmitted to humans, resulting in infections known as pasteurellosis. In humans, it generally occurs after direct contact with infected animals, such as bites, scratches or licks. Some of the manifestations caused by this bacteria include skin, respiratory and/or systemic infections. Patient, 14 years old, male, mixed race, student, presented to the emergency room, accompanied by his mother, presenting with tachycardia, tachypnea, hypotension, polyarthralgia with edema on the right upper limb and lower limbs that started a week ago, after dog bite to the second finger on the right and fall followed by injury to the right knee. On physical examination, retroauricular and cervical lymph node enlargement, jaundice (Kramer zone 3), calf enlargement, board-like abdomen and significant hepatomegaly. The patient was taken to the Intensive Care Unit, where imaging tests such as Joint and Abdomen Computed Tomography were requested. Furthermore, his laboratory tests showed significant leukocytosis and a slight change in bilirubin. His serologies for HIV, syphilis and hepatitis B and C were non- reactive. Joint puncture was performed and purulent secretion was drained. Vigorous hydration and empirical broad-spectrum antibiotic therapy (ceftriaxone with metronidazole) were initiated until the test results were obtained. The patient improved after three days of treatment. There was a case of sepsis, with a focus on the skin, which was unusual, which presented a favorable outcome at first, however, after 6 months, the patient returned to the office for follow-up, with a characteristic picture of osteomyelitis, on imaging examination, which was possibly disseminated hematogenously.

Audience Take Away Notes

- With the presentation of the case report, the public will be able to learn more about Pasteurella multocida, which is rare in humans; about the evolution of the condition and possible complications. This way, they will be able to early diagnose similar cases that they may encounter in clinical practice and intervene accurately in order to prevent complications. As it was a rare case, it was shown as a case report, however in the future it is possible to expand the research and carry out an intervention with a larger sample, in order to promote greater accuracy in the treatment

Biography

Dr. Camila is a physiotherapist, a business administrator and studied Medicine at the Faculdade Pitagoras de Medicina de Eunapolis, Brazil and graduated as a doctor in 2024. She then joined the research group of Prof. Guilherme Bonfim at the Faculdade Pitagoras de Eunapolis. She has published more than 50 research articles in different journals and congress.

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Repercussions of monkeypox infection in humans: A case report

Monkeypox (Mpox) is an emerging viral zoonosis that has gained increasing attention due to its clinical similarity to smallpox and its ability to cause sporadic outbreaks in human communities. This condition, caused by the Monkeypox virus (MPXV), belonging to the Poxviridae family and Orthopoxvirus genus, is characterized as an acute febrile disease with skin rashes. The infection has a restricted geographical distribution, mainly in Central and West Africa, but global concern has increased due to the possibility of its spread beyond these borders. Thus, it poses a significant threat to public health, especially in regions where the interaction between humans and wild animals is common, particularly rodents, which serve as natural reservoirs for the virus. This report is about a 35-year-old male patient, black, freelancer, with a diagnosis of B24 since 2012 under outpatient follow-up at ICOM. He presented to the emergency room reporting that in October 2023, he started developing vesicular skin lesions initially around the anus, progressing to the entire body, raising suspicion of Monkeypox. A PCR test for Monkeypox was collected. He complained of intense pain in the anal region, with lesions already in the crusting phase throughout the body, painful to the touch, with no evidence of local purulent discharge, associated with constipation. The patient also had yellowish discharge from the anus and crusted lesions in the perianal region. He reported a history of herpes in the anal region. He mentioned using Ibuprofen and Paracetamol/Codeine for pain control, but significant anal pain persisted. He had taken Ceftriaxone 500mg and Azithromycin 1000mg prescribed in a previous consultation. He reported unprotected sexual intercourse at the end of September and continued to experience pain, worse in the perianal region. Therefore, this zoonosis represents a significant threat to public health, especially in regions where there is frequent interaction between humans and wild animals, such as rodents, acting as natural reservoirs of the virus. Although initially restricted to the regions of Central and West Africa, global concern has increased due to the possibility of its spread beyond these borders. The presented case highlights the importance of monitoring and controlling this disease, emphasizing the need for preventive strategies and interventions in communities prone to outbreaks, especially when there are risk factors such as unprotected sexual relations and a history of anal herpes. Additionally, it illustrates the clinical complexity of the infection, emphasizing the importance of epidemiological surveillance and preventive measures to contain the spread of Monkeypox.

Audience Take Away Notes

- With the presentation of the case report, the public will be able to learn more about the monkeypox virus and its associated symptoms, about the evolution of the condition, even when the fetus is removed and possible consequences. This way, you can early diagnose similar cases that may be encountered in clinical practice and intervene with results to prevent complications. As this is a rare case, it was presented as a case report, but in the future it is possible to expand the research and carry out an intervention with a larger sample, in order to promote greater precision in the treatment

Biography

Dr. Camila is a physiotherapist, a business administrator and studied Medicine at the Faculdade Pitagoras de Medicina de Eunapolis, Brazil and graduated as a doctor in 2024. She then joined the research group of Prof. Guilherme Bonfim at the Faculdade Pitagoras de Eunápolis. She has published more than 50 research articles in different journals and congress.

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Shiver: A syphilis/HIV 'test and treat' poct intervention trial to reach rural/remote and underserved populations in Saskatchewan, Canada

Context: An alarming increase of infectious and congenital syphilis rates is being seen in Saskatchewan and the prairie provinces of Canada. According to the Public Health Agency of Canada, the national rate of infectious syphilis increased from 5.1 per 100,000 population in 2011 to 30 per 100,000 population in 2021, with the prairie provinces reporting the greatest relative increases from 2017 to 2021 (1346% in Saskatchewan and more than 400% in Alberta and Manitoba). Confirmed early congenital syphilis cases in Canada have considerably increased from prior years, with 50 cases reported in 2020 and 96 cases in 2021, compared with 7 cases in 2017. In 2020, Saskatchewan reported 10 confirmed cases of congenital syphilis, and two stillborn babies. In 2022, 67 congenital cases were reported. Syphilis carries serious life-threatening complications for the individual and the unborn child, if left untreated.

In March 2023, Wellness Wheel Clinic launched the Syphilis HIV Early Rapid Test (SHIVER) project, with the support of the REACH Nexus, collaborating First Nations communities and participating provincial sites, aimed to address the urgent need for faster testing and treatment, and reduce access barriers to treatment for rural/remote areas and underserved inner city groups.

Objective: To understand how Point of Care Testing (POCT) options, along with culturally responsive care interventions, offer opportunities for immediate treatment and linkage to care for syphilis for undiagnosed individuals in inner city, remote, rural and underserved populations in Saskatchewan.

Research Question: How does the implementation of a "test and treat" model of POCT, delivered as a culturally informed and responsive interventional team approach, offer immediate treatment and linkage to care for syphilis, and reach those undiagnosed in sites across Saskatchewan?

Method: This project is a multiplex point-of-care "test and treat" intervention study based on a successful 2020 study in Alberta, Canada. The program demonstrated the clinical utility in diagnosing and linking underserved and hard to reach individuals into care. The SHIVER approach offers 3 rapid finger prick test options (syphilis only, HIV only, or syphilis and HIV) with education and participant experience survey. Additional blood is drawn for confirmatory results and screen for false positive/negative. In the event of a positive diagnosis, treatment, and linkage to care for follow-up is immediately carried out. The POCT device was found to be >98 per cent accurate in detecting active syphilis. Test kits provide a test result in under five minutes using a fingerstick blood specimen. Acting on the device's instantaneous nature, connecting participants to care and early treatment was a key priority of the study. This initiative aims to enroll 1,500 individuals for testing of HIV and/or syphilis.

Results: As of November 2023, SHIVER has recruited 20 sites, including 10 First Nations on-reserve communities, 1 northern community health centre, 8 community organizations providing harm reduction care and support services to people living in inner-city settings, and the Saskatchewan Federal Penitentiary. Preliminary numbers report 443 participants have taken part in the project across the 9/10 participating sites. 71/443 participants testing positive for syphilis, and 14/71 also receiving a positive HIV diagnosis (co-infection). Within those testing positive, 35/71 were of male biological sex and 36/71 were female biological sex. Among those women with a positive syphilis result, 2 were pregnant. Biological sexed women, aged 18 to 39, had the highest diagnosis rate with 29/36 individuals being between ages of 18 and 39. Biological sexed men were older with 29/35 of the positive diagnoses being among those aged 30-49. No one over the age of 59 years had a positive result for either disease. 12 women and 12 men (total n=24) had a positive HIV result along with a negative syphilis result. Most POCT and positive results were among inner city harm reduction community organization cohorts. Efforts are underway to increase testing rate in communities through testing events and culturally tailored public awareness campaigns. Data reporting is ongoing and additional sites will be onboarded throughout 2024 to expand the POCT program.

Audience Take Away Notes

- Gain insight on the utility and efficacy of POCT rapid blood tests to improve quick treatment starts and linkage to care, especially for groups that are harder to reach or not engage in care
- Rapid test and treat care intervention can be done by nursing and frontline community provider staff quickly and with ease, reducing the time and blood quantity required by conventional testing methods
- Rapid results enable care providers to link a patient to care and treatment immediately, improving the engagement of care along the continuum and reducing transmission
- Closing the time gap between testing/diagnosis and treatment reduces the challenges care providers may face in following up or contacting the patient once they have left the facility
- Other faculty will be able to use this research in their own research or teaching by
- Undertaking a similar type of project to reach street involved and rural/remote groups who are at highest risk for STBBI-related infections and/or hardest to reach or not engage in care
- Understanding how to integrate and tailor health interventions to be more culturally appropriate for populations they wish to reach
- Facilitate easier access to a proven simplified testing that requires fewer resources with improved reach, especially during times of health crisis
- This provide a practical solution to a problem that could simplify or make a designer's job more efficient
- This project was established in response to the syphilis and STBBI-related health crisis emerging in Saskatchewan and the prairie Canadian provinces. Prior to 2017, syphilis rates were low in Saskatchewan and resources were focused on other priorities, such as HIV and HCV. Saskatchewan is also sparsely populated with First Nations communities spread across the province in rural and remote locations. This presents a barrier to accessing timely resources, care and treatment for any illness. The SHIVER project brings testing, rapid start treatment and linkage to care to these communities
- It improve the accuracy of a design, or provide new information to assist in a design problem
- This project will inform on the efficacy of rapid HIV/Syphilis testing and allow others to tailor and implement similar interventions to reduce access barriers, facilitating broader uptake of STBBI screening, education, and treatment among hard to reach and underserved locations
- This project will also glean insight into how to improve treatment adherence among cohort populations that are street-involved or experience resistance to screening and seeking medical care
- Finally, a portion of this project will develop a robust portfolio of culturally tailored educational resources for frontline providers and the target population through a collaborative integrated knowledge mobilization initiative

Biography

Dr. Cara Spence received her Ph.D. in Global Health at the University of Saskatchewan in Saskatoon, Saskatchewan, Canada in 2020. She has worked in the field of infectious diseases since 2012, and completed her post-doctoral research at McGill University, faculty of medicine. Dr. Spence conducts both community-based and clinical research, and is the Research Director for infectious diseases for Wellness Wheel Clinic – a non-profit health organization providing comprehensive culturally responsive STBBI care in rural/remote and on-reserve First Nations communities. She currently holds an Associate Researcher position at the College of Medicine at the University of Saskatchewan.

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Equine polyclonal F(ab)'2 as a rapid and strong therapeutic answer against potential new SARS-CoV-2 surge

Successive sub-lineages of Omicron have spread since the occurrence of BA.1 in November 2021. Identified in July 2022, BQ.1 and BQ.1.1 expanded dramatically in Europe and North America. XBB and XBB.1 were first identified in India in mid-August 2022 and quickly spread to become predominant worldwide. The XBB lineage originated from a recombination of two BA.2-derived variants (BJ.1 and BM.1.1.1) and progressively replaced most of previous Omicron strains. Members of this lineage are characterized by enhanced transmissibility rates and immune evasion properties. The rapid rise of these subvariants and their extensive array of spike mutations raised concerns that they will further compromise the efficacy of current COVID-19 vaccines and monoclonal antibody (mAb) based therapeutics. This was confirmed by many publications showing that human convalescent plasma from patient having received 3 shots of Wuhan-based vaccines were not able to efficiently seroneutralize XBB.1, XBB, BQ.1.1 and BQ.1 variants. Confirming this continuous drift in SARS-CoV-2 mutants, the BA.2.86 lineage first detected in August 2023 has rapidly evolved and led to the emergence of the JN.1 sublineage in September 2023. As of December 2023, JN.1 was sharply increasing in frequency in Europe and USA.

Both BQ and XBB sublineages are now completely resistant to bebtelovimab, leaving us with no authorized antibody for treatment use.

Leveraging its equine polyclonal F(ab')2 platform, Fabentech has developed FBR-002 product, purified from Immunoglobulins obtained after horse immunization with SARS-Co2 Wuhan spike protein. FBR-002 represents a pertinent therapy candidate for treating patients hospitalized with COVID-19 because of its polyclonality, which enables the targeting of multiple epitopes of the spike protein, limiting the risk of viral escape if new strains emerge.

Although FBR-002 showed a decreased activity level for the seroneutralization of D614G mutant-related strains compared to the last variants, the Fab'entech developed polyclonal F'(ab)'2 was still able to neutralize BQ.1.1, XBB.1.5 and XBB.1.16 strains with strong potency. In comparison, Sotrovimab seroneutralisation was barely detectable.

Fabentech is currently evaluating the seroneutralisation activity of FBR-002 against the latest variant JN.1 derived from BA.2.86.1 in comparison to the activity of various human convalescent plasmas.

In a context of rapid evolution and adaptation of emerging Covid-19 variants, and a lack of activity of mAbs, the polyclonal antibody approach should be considered as a particularly relevant therapeutic product for the treatment of high-risk populations such as immunocompromised patients.

Audience Take Away Notes

- Covid-19 sub-lineages are still arising and remain of major concerns in case of new surge. Vaccination with the original strain is poorly efficient against last variants and there are no more monoclonal antibodies in the market, leaving people at high risk with very few therapeutic solutions in case of emergence of a new highly pathogenic strain

- Contrary to mAbs, Fab'entech Equine polyclonal F(ab)'2 FBR-002 still cross-neutralizes with high potency newly emergent Covid-19 variants and offers an unprecedent treatment of emergency against Covid-19
- A better understanding of immune mechanisms at stake during the horse immunisation process would foster the design of horse immunisation protocols to reinforce the specific immune response to targets of interest
- Research to characterize the polyclonal antibody response would allow the design of innovative "broad spectrum" treatments

Biography

Dr. Caroline Ballet has studied Cellular Biology at the University of Nantes. After 3 years fellowship supervised by Pr. Jean-Paul Soulillou, she was graduated as PhD in 2008. She joined biotechnology companies as project leader in the field of Infectious diseases, Oncology and transplantation. Since 2022, she coordiantes National and European programs in the field of Emergent Infectious diseases at Fab'entech.

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Hemophagocytic lymphohistiocytosis syndrome and syndrome of inappropriate antidiuretic hormone ADH release: Keep in mind visceral leishmaniasis. Case report and literature review

Introduction: Visceral leishmaniasis is an potentially fatal and neglected tropical disease, according to the World Health Organization's: mortality is still very high (95%) when untreated. This disease presents a broad spectrum of symptoms (oligosymptomatic infection, but also life-threatening chronic condition). Shorter (≤30 days) diagnostic delay and treatment completion are associated with less mortality.

Case report and Literature review: We present the case of a 72-year-old woman came to our observation for asthenia, episodes of confusion, fever, liver function derangement, hyperferritinemia, biological inflammation syndrome, pancytopenia resulted secondary to hemophagocytic lymphohistiocytosis and severe hyponatremia. HS score 141. Anamnesis was positive just for dysmetabolic syndrome (overweight, diabetes mellitus II, hypertensive heart disease). Abdominal ultrasound showed hepatosplenomegaly. Our diagnostic hypotheses were: a dysmetabolic liver disease with secondary splenomegaly due to portal hypertension, a splenomegaly due to haematological aetiology (rare blasts in peripheral blood), an infectious hepatosplenomegaly. An hypercortisolism was present.

The case was characterized by two points:

- A severe hyponatremia associated to hypo-osmolality in normovolemic patient, resulted secondary to Syndrome of inappropriate ADH secretion (SIADH). A sensitive search on Pubmed (Mesh term 'Hyponatremia' and 'visceral leishmaniasis') shows only 6 analogous cases.
- A Hemophagocytic lymphohistiocytosis syndrome. In this context, the Leishmania PCR from peripheral blood and bone marrow was positive, negative serology for toxoplasma, HIV, CMV, EBV, Parvovirus, HZV, HHV 6-8. A sensitive search on Pubmed (Key-words 'Hyponatremia' and 'visceral leishmaniasis') shows other 43 anlaogous cases (limits: 'adults'). The patient was treated with Amphotericin with progressive clinical remission.

Conclusions: The pathogenesis of hyponatremia in Leishmaniasis is very complex and is associated to several hemodynamic and hormonal factors (reduced body water, especially if present vomiting, diarrhea and dehydration associated to vasopressin release, as well as renin-angiotensin-aldosterone system activation, renal Na+ loss, tubular dysfunction, polyclonal activation of B lymphocytes with secondary pseudo hyponatremia). SIADH in Leihsmaniasis most likely derives from the intense inflammatory response associated to activation of hypothalamic-pituitary axis and antidiuretic hormone release. -Hemophagocytic lymphohistiocytosis syndrome is more common associated to malignancy and infection. Mortality is 29% in study cohort and so it should be considered a lethal disease. It is important to keep in mind a leismaniasis etiology in the presence of these 2 conditions, to clearly improve the prognosis of patients.

Audience Take Away Notes

- The audience will be able to think early about the diagnosis of Leishmaniasis in the presence of the two points (hyponatremia and Hemophagocytic lymphohistiocytosis syndrome)
- The description of the case can help doctors to treat these patients early, with a marked improvement in the prognosis
- This case and the literature review could be a starting points for cohort studies related to the evaluation of hyponatremia and the syndrome in the prognosis of visceral Leismaniasis

Biography

Dr. Daniela Tirotta studied Internal Medicine at the Ancona University, Italy. He worked as an internist in the Rimini AUSL, then in the Forlì AUSL. He attended the Clinical Governance master's degree in Internal Medicine, at the Carlo Cattaneo University, Milan. She has published more than 22 research articles in SCI (E) journals, HI 22.

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Viral profile of respiratory infections according to age in hospitals in Brazzaville, Republic of Congo

Context: Respiratory Tract Infections (RTIs) are one of the most common infectious diseases in children and represent a major cause of morbidity, hospital admission and mortality worldwide, with an estimated 3-5 million deaths per year. Although children are most at risk, adults are also vulnerable to RTIs. There are multiple etiologies of RTIs, with viruses accounting for almost 80%. The most common viruses are HRV, HRSV, HAdV, HCoV, HBoV, HPIV, and FluA/B. In Africa, little is known about respiratory infections in adults and the prevalence of these infections is often underestimated in hospitals due to the small amount of data available. The aim of this study was to determine the viral profile of respiratory infections and its correlations with age in hospitals in Brazzaville, Republic of Congo.

Method: The study was conducted between March 2022 and April 2023 in Brazzaville. Nasopharyngeal samples were collected from patients with respiratory syndrome and enrolled in the study at the Hôpital de Référence de Talangai and the Hopital de Référence de Makelekele. These samples were analyzed for detection of respiratory pathogens using the FTD-21 panel, a commercial multiplex Real-Time Polymerase Chain Reaction (RT-PCRm) kit targeting 21 pathogens. As the kit does not targets SARS-CoV-2, the TaqPath kit was used specifically for its identification, following the manufacturer's instructions.

Results: A total of 643 patients were enrolled and tested, and 461 of them were found to be infected with at least one respiratory pathogen. Out of these positive patients, 300 (300/461; 65%) were under 5 years old (0-4), 53 (53/461; 11%) were 5-15 years old and 108 (108/461; 23%) were 16-87 years old. Viral diversity was highest in the under 5 years, with the most prevalent and statistically significant pathogens being HRV (120/384; 31.2%), HAdV (83/384; 21.6%), HBoV (57/384; 14.8%) and HRSV (38/384; 9.8%). HPIV-3 (36/384; 9.3%), FluA (34/384; 8.8%) and SARS-CoV-2 (26/384; 6.7%) and many other viruses (with very low proportions) were not significant. For 5-15 years, the most prevalent viruses were FluA (15/70; 21.4%), HRV (12/70; 17.1%), HAdV (10/70; 14.2%), HBoV and SARS-CoV-2 (8/70; 11.4% each). In the oldest age group (16-87 years), the most prevalent viruses were HRV (32/189; 16%), FluA (23/189; 12.1%), HAdV (18/189; 9.5%) and SARS-CoV-2 (11/189; 5.8%). We found 199 cases of co-infection, including 146 (146/199; 73%) in children under 5 years of age (0-4), 20 (20/199; 10%) in those aged 5 to 15, and 33 (33/199; 17%) in older children (16-87).

Conclusion: Respiratory infections were more prevalent in children under 5, with a more varied viral profile. However, adults were found to be as vulnerables as children. The most prevalent viruses in all age groups were HRV, FluA, HAdV and SARS-CoV-2.

Key Word: Respiratory Infections, Viruses, Age, Hospital, Brazzaville.

HRSV: Human Respiratory Syncytial Virus ; **HRV:** Human Rhinovirus ; **HAdV:** Human Adenovirus ; **Flu A/B:** Influenza viruses A/B type; **HPIV 1-4:** Human Parainfluenza viruses 1-4 types; **HCoV:** Human Coronavirus; **HBoV:** Human Bocavirus; **SARS-CoV-2:** Severe Acute Respiratory Syndrome Coronavirus-2 ; **FTD:** Fast Track Diagnostics ; **RTIs:** Respiratory Tract Infections (RTIs).

Biography

Jordy Exauce Demboux is a PhD student at the Marien Ngouabi University in Brazzaville, Republic of Congo, and obtained a Master's degree in Biology and Applied Microbiology in 2020. He joined the technical team at the National public health laboratory, set up by the Congolese government as part of the response to COVID-19. He then joined the JEAI project (Jeune Equipe Associee a IRD) to complete his doctoral thesis on respiratory infections under the supervision of Professor Pembe Issamou Mayengue and Doctor Becquart Pierre.

Dian Wulandaru Sukmaning Pertiwi[1]*, Fatima Safira Alatas[1], Rosalina Dewi Roeslani[1], Novie Amelia Chozie[1], Tri Hening Rahayatri[2], Amanda Soebadi[1], Ari Prayitno[1]

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Risk factors for bacterial infection in children following liver transplantation in Indonesia: A preliminary study

Objective: Survival rate and quality of life of children with chronic hepatobiliary disease has improved since the development of liver transplantation. Incidence of bacterial infection is 36– 79% at 6 months post-transplantation and mortality of 3.0–10.6% at 3 months post- transplantation. Adequate prevention of bacterial infection will reduce morbidity and mortality and increase survival. This study aimed to determine the risk factors for bacterial infection in children who underwent liver transplantation in Indonesia.

Methods: This retrospective cohort study includes pediatric recipients who underwent liver transplantation in Cipto Mangunkusumo Hospital (CMH) during December 2010 – April 2023 with total sampling method. Subjects were classified into groups with and without bacterial infection.

Results: Prevalence of bacterial infection of the 63 subjects was 84.13%. A majority of the bacterial infection cases were healthcare-associated infections (HAIs), comprising of surgical site infections (29.63%), ventilator-associated pneumonia (14.81%), and catheter-related urinary tract infections (13.58%). Multivariate analysis showed ICU length of stay ≥20 days (RR 1.212; CI 95% 1.028–1.426; p = 0.022) and volume of blood loss during surgery ≥70 mL/kg (RR 1.283; CI 95% 1.009 –1.631; p = 0.042) were risk factors for bacterial infection following liver transplantation. Subgroup analysis presented ICU length of stay ≥20 days increased risk of multi- drug resistance bacterial infection by 2.479 times (CI 95% 1.185 – 5.187; p = 0.016).

Conclusion: Bacterial infection prevalence at six-months post-liver transplantation of children in CMH was 84.13% with ICU length of stay ≥20 days and volume of blood loss during surgery ≥70 mL/kg as risk factors. Further studies with better design and larger samples are needed.

Keywords: Bacterial infection, risk factor, post-liver transplantation, children, pediatric.

Audience Take Away Notes

- Adding information about risk factors of bacterial infection at 6 months following liver transplantation in children from liver transplantation centers in developing countries, especially in Southeast Asia
- The first study from Indonesia regarding this topic
- Prevention of bacterial infection post-liver transplantation in children
- Baseline study for future prospective researches regarding this topic

Biography

Dian Wulandaru Sukmaning Pertiwi, MD. studied Medicine at the Brawijaya University, Indonesia and graduated as MD in 2015. She then studied at Department of Child Health, University of Indonesia, Indonesia and graduated as Pediatrician in 2023. She has experienced being in 4 researches so far, and presented study and case reports in national and international conferences. She currently works as Pediatrician in a Public Hospital in West Java, Indonesia.

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Korea seroprevalence study of monitoring of SARS-CoV-2 antibody retention and transmission (K-Serosmart): A community-based longitudinal seroprevalence survey

The primary objective of this investigation is to estimate the population prevalence of SARS-CoV-2 antibodies, monitor the waning pattern of seroprevalence, and develop forthcoming vaccination strategies through a longitudinal study using a population-representative sample over time in Korea.

In August 2022, the initial survey targeted 10,000 individuals aged 5 and above, selected through two-stage probability random sampling. Subsequently, a follow-up was conducted on participants from the first wave. The third survey involved a cross-sectional study of 10,000 new household members. Lastly, the fourth survey conducted longitudinal follow-up on Wave 2 and 3 participants. Various methods such as mobile web, telephone, and face-to-face surveys were employed to collect data on health status, COVID-19 history, and demographic information. Blood samples were collected and analyzed for anti-S and anti-N antibodies using electrochemiluminescence immunoassay. Population prevalence was estimated using PROC SURVEYMEANS with weighting reflecting demographic data at each survey time point.

The first survey involved 9,945 individuals in 258 communities. 74.9% follow-up rate from Wave 1 in the second survey. The third survey involved 9,798 individuals. Subsequent surveys involved 11,271 in the fourth, with follow-up rates of 74.4% and 57.8% from Waves 2 and 3 participants, respectively. The overall population-adjusted prevalence rates of anti-S antibodies from 97.5% in the first to 99.8% in the fourth survey. Anti-N antibodies increased gradually from 57% in the first survey to reaching 84.9% in the final survey. Unreported rates of antibodies remained relatively stable at approximately 20%-25%, with the highest rates observed in the 50s and 60s age groups. Furthermore, the titers of anti-S antibodies tended to decline over time following the last immunological event, particularly noticeable after a span of six months.

This study provides estimates of population seroprevalence and highlights the decline in antibodies against SARS-CoV-2 over time in a nationally representative sample. It furnishes essential epidemiological evidence for formulating national COVID-19 vaccine policies and underlines the necessity of continuous surveillance for COVID-19.

Audience Take Away Notes

- The methodology employed in estimating the population prevalence of SARS-CoV-2 antibodies, including the use of longitudinal studies and representative sampling
- The waning pattern of seroprevalence over time, including insights into how antibody levels change following immunological events and the duration of their persistence
- The development of vaccination strategies informed by longitudinal data, offering insights into the effectiveness and longevity of immune responses
- The demographic patterns of COVID-19 antibodies, including prevalence rates across different age groups and any disparities observed

- The implications of the study findings for national COVID-19 vaccine policies and the importance of continuous surveillance for monitoring the pandemic's trajectory

Biography

Dr. Dong-Hyun Kim has served as the Dean of Hallym University Graduate School of Health Sciences, and professor at the Department of Social and Preventive Medicine at Hallym University since 1995. He received his M.D. from the Seoul National University College of Medicine. He was also a visiting scholar at the Department of Epidemiology at Harvard School of Public Health for two years, from 1999 to 2001. He was the past president of the ‘Korean Society of Epidemiology’ during 2018~2020. He is a principal investigator of Korea Seroprevalence Study of Monitoring of SARS-COV-2 Antibody Retention and Transmission (K-SEROSMART).

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1 + 1 = 0: Challenges in managing early lyme disease with anaplasmosis co-infection

Lyme disease, the leading vector-borne illness in the United States, impacts roughly 476,000 individuals each year. As its geographical reach expands, healthcare providers face increasing hurdles in diagnosing and treating the disease, especially in its early stages. Despite being nationally notifiable since 1991, Lyme disease presents ongoing challenges, highlighting the imperative for more effective management strategies. This clinical case underscores some of these challenges and offers practical insights for improving the management of early Lyme disease with concurrent anaplasmosis infection. Tickborne Rickettsial Diseases (TBRD) can result in severe illness and fatalities in otherwise healthy individuals, despite the wide availability of effective and affordable treatments. The primary barrier lies in promptly diagnosing these diseases and administering appropriate treatment. Given the rising prevalence of LD and other tick-borne illnesses, alongside the potential for significant long-term health consequences, healthcare providers require better guidelines for diagnosis and treatment. Existing clinical reference tools often lack the necessary depth or efficiency to address this growing demand, leaving primary care providers grappling with these challenges. This paper aims to illuminate some of the obstacles and crucial considerations in the management of early Lyme disease, particularly when co-infection with anaplasmosis is suspected.

Audience Take Away Notes

- Current issues in Lyme disease diagnosis and treatment
- Its co-infection makes the already complicated disease more difficult to manage
- Issues with guidelines
- Some practical insights on Lyme disease and co-infection management

Biography

Dongsheng Jiang, M.D. Trained and board certified in family medicine, Dr. Jiang works as family physician and an associate professor at department of family and community medicine, Penn State Health, Milton S Hershey Medical Center, College of Medicine, Pennsylvania State University, State College, PA, USA.

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An iPSC-derived organoid-based model of intestinal filovirus infection

Affected Ebola Virus Disease (EVD) patients lose copious amounts of fluids in a matter of days, rapidly deteriorating into hypovolemic shock and death. Similar intestinal manifestations were also reported for Marburg Virus (MARV) disease, another filovirus. At present, available animal models insufficiently recapitulate the gastrointestinal symptoms of EVD patients. To fill this gap, we have established an induced Pluripotent Stem Cell (iPSC)-derived Human Intestinal Organoid (HIO) model that can be primed towards proximal (small intestine) or distal (colonic) intestinal lineages. Three-dimensional tissue-specific organoids recapitulate the heterogeneity, architecture and cellular functions of the primary tissue, thus representing a powerful tool to study development and disease. The generation of a hiPSC CDX2-GFP reporter line highlights the role of CDX2 as a marker for the emergence of hindgut intestinal progenitors during our differentiation protocol. This platform can facilitate the study of late-stage EVD gastrointestinal symptoms, including diarrhea. Single-cell RNA sequencing characterization of the HIOs revealed a significant number of CDX2 and Villin 1 expressing cells as well as separate clusters indicating the major transcriptional changes in cell identity that are known to occur during the stages of intestinal differentiation. The HIOs exhibit a distribution of the different cell types that physiologically resemble the human intestinal epithelium. We employed the generation of these organoids to study the effects of filovirus infection on intestinal epithelial integrity. Successful robust EBOV and MARV infections of hiPSC-derived HIOs, affecting mostly epithelial CDX2+ enterocytes was achieved. The infected cells showed signs of cell damage. Transcriptomics analysis indicated the modulation of cell junction pathways and a set of ion transporters known to play a role in the induction of diarrhea. Taken together, these data suggest that EBOV and MARV compromise barrier integrity of the intestinal epithelium and cause abnormal ion flux as the basis for gastrointestinal dysfunction and diarrhea.

Audience Take Away Notes

- Novel induced pluripotent stem cell (iPSC)-derived human intestinal organoid (HIO) three-dimensional models to study filoviruses or other viral infections of the gastrointestinal tract
- Established methods and also some exciting novel perspectives on organoids in the fields of gastroenterology and infectious diseases, specifically how these models may be used address questions that are not feasible in other cellular models
- A 3D model has the potential to recapitulate the physiology of the desired organ of study, offering novel avenues for experimental design and exploration

Biography

Elizabeth Yvonne Flores is a fourth year PhD candidate at Boston University School of Medicine in Boston, MA, USA. She is currently a National Institute of Health F31 fellow and is conducting her dissertation project in the laboratories of Dr. Gustavo Mostoslavsky at the Center of Regenerative Medicine and Dr. Elke Muhlberger at the National Emerging and Infectious Diseases Laboratories, specifically in the Biosafety Level 4 (BSL-4) laboratories.

Eric Takashi Kamakura de Carvalho Mesquita[1], Washington Carlos Agostinho[2], Ana Karoline Sousa Mendes Simas[1], Lidio Lima Neto[3], Enio Mouri[4], Paulo Eduardo Brandao[2], Francisco Borges Costa[1]*, MV, PhD

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Epidemiological aspects of rabies in an Amazon-Cerrado transition region of Northeastern Brazil

Rabies is an acute viral disease that affects mammals, caused by an RNA virus belonging to the family Rhabdoviridae and the genus Lyssavirus. The disease is transmitted through bites or scratches from an infected animal. Rabies was one of the first infectious diseases to be scientifically studied, with a detailed description of symptoms and clinical course. The global incidence of rabies varies among different regions, and it is estimated that it causes around 60,000 deaths worldwide each year, with a higher prevalence where there are no effective control measures. Most cases occur in developing countries where animal vaccination and proper post-exposure prophylaxis are less accessible. The rabies virus has several variants that are specific to each animal reservoir, and in Brazil, five of these variants have already been identified. This study aimed to better understand the epidemiological aspects of the rabies virus variants circulating in the Amazon-Cerrado transition region through immunological and molecular assays, as well as their reservoirs and distribution in the biomes. To achieve this, 62 biological samples sent to reference laboratories in the state of Maranhão between 2015 and 2022 were analyzed using the Fluorescent Antibody Test (FAT) and Reverse Transcriptase Polymerase Chain Reaction (RT-PCR) techniques. Primers 504 (sense) and 304 (reverse) were used for the N gene in the RT-PCR reactions, amplifying 240 bp, and the positive samples were submitted to Sanger sequencing to identify the antigenic variant. Of all the samples, 74% tested positive in FAT and 63% tested positive in RT-PCR. Among FAT-negative samples, 19% were detectable for the rabies virus by the RT-PCR. Of all samples that tested positive in both tests, only 28% were successfully sequenced, revealing antigenic variants of Desmodus rotundus and Cerdocyon thous. It was observed that these variants circulate in both the Amazon and Cerrado biomes, with the bat variant being more prevalent in the Amazon biome with human cases of rabies in the early 21st century, while the wild canid variant was more prevalent in the Cerrado, as there are reports of this variant in domestic dogs and humans in this Amazon-Cerrado transition region northeastern Brazil. Thus, these results guide epidemiological surveillance procedures that can be used in each specific case with a one health approach.

Audience Take Away Notes

- They will be able to carry out more precise epidemiological surveillance according to the variant circulating in each biome
- They will learn a little about the dynamics of the variant mediated by wild canids and bats that circulates in the Amazon-Cerrado biomes
- They will learn the importance of One Health in these cases
- Optimize financial resources for more specific epidemiological surveillance work
- Understand the dynamics of the virus in its regional ecological niche, especially in Latin America
- Once you understand the dynamics of the disease, it will be easier to plan future actions within the scope of “One Health”

- The information provided so far addresses new directions in future on the surveillance system projects
- Other benefits
    - It will bring together professionals from other areas of knowledge with a focus on the One Health approach

Biography

Dr. Francisco Borges Costa graduated in Veterinary Medicine from the State University of Maranhao, Sao Luis, Maranhao - Brazil, and pos-graduated as Master Science in 2009. He then joined the research group of Prof. Marcelo Bahia Labruna at the Department of Preventive Veterinary Medicine and Animal Health of the School of Veterinary Medicine and Animal Science of the University of Sao Paulo, where he obtained his Ph.D degree in 2014. After two years postdoctoral fellowship supervised by Dr. Labruna in the Program in Experimental Epidemiology Applied to Zoonoses, he obtained the position of Professor at the PPGCA/UEMA. He has published more than 80 research articles in various areas.

Eric Takashi Kamakura de Carvalho Mesquita[1], Washington Carlos Agostinho[2], Ana Karoline Sousa Mendes Simas[1], Lidio Lima Neto[3], Enio Mouri[4], Paulo Eduardo Brandao[2], Francisco Borges Costa[1]*, MV, PhD

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Investigation of wild canid-mediated human rabies death, Brazil, 2021

Rabies is an acute viral disease with extremely high lethality, still causing approximately 59,000 human deaths worldwide every year. Despite being a disease studied for many years and having a very efficient prophylaxis, a high incidence rate is observed in developing countries. Because the rabies virus has various reservoirs (all mammals), controlling viral circulation is not an easy task for health surveillance teams, especially in rural areas, as domestic animals (dogs and cats) actively participate in the virus's infectious cycle, and wild animals such as bats and foxes also enter in this ecological niche. And right now, we report a case of a 2-year-old boy who tragically succumbed to human rabies in northeastern Brazil. Initially, the child had a history of being attacked on the legs by a cat, according to the family`s report. Some nervous symptoms appeared 35 days after the aggression by the animal, but there was an association with an allergy to the polio vaccine two days before the onset of symptoms, and the cat was still alive. Through Sanger sequencing and on-site epidemiological investigation, we have confirmed, for the first time, this case of human rabies linked to the wild canid variant in an area of the Amazon-Cerrado transition. Despite attempts at treatment following the Recife protocol, the child passed away on November 3, 2021. Our findings highlight the interrelationship between humans, the variant virus, and animals, focusing on the importance of thorough medical history-taking by medical services in these rural areas. This highlights the impact on global public health in the Amazon-Cerrado transition region of northeastern Brazil, due to the re-emergence of wild canid-mediated human rabies, sounding a significant alert for health surveillance services in remote areas away from urban centers.

Audience Take Away Notes

- They will be able to apply the experience reported in future clinical cases
- They will learn a bit about the dynamics of attacks by rabies-infected foxes
- They will learn the epidemiological surveillance procedures used in this specific case
- They will learn the importance of One Health in these types of cases
- The listeners' perception to conduct a more careful medical history taking in children will improve
- They will learn the importance of One Health in cases of rabies
- The perception of an in situ epidemiological investigation will improve
- This could use to expand their research or teaching, since wild canids exist in all countries
- The issues to be reported could be observed in future cases, and the identified errors would not be made in similar cases
- The strengths and weaknesses of this specific case will be addressed
- Other benefits
    - Exchange of experience among professionals in the fields of agricultural defense, epidemiological surveillance, public health, diagnostic laboratory professionals, among others

Biography

Dr. Francisco Borges Costa graduated in Veterinary Medicine from the State University of Maranhao, Sao Luis, Maranhao - Brazil, and pos-graduated as Master Science in 2009. He then joined the research group of Prof. Marcelo Bahia Labruna at the Department of Preventive Veterinary Medicine and Animal Health of the School of Veterinary Medicine and Animal Science of the University of Sao Paulo, where he obtained his Ph.D degree in 2014. After two years postdoctoral fellowship supervised by Dr. Labruna in the Program in Experimental Epidemiology Applied to Zoonoses, he obtained the position of Professor at the PPGCA/UEMA. He has published more than 80 research articles in various areas.

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A fish farmer's encounter with leptospirosis: A case report

Leptospirosis is a zoonotic bacterial infection primarily caused by Leptospira species. This disease, characterized by a wide range of symptoms, is uncommon in the UK, with an incidence of 0.14 cases per 100,000. This oral presentation is the case of a 56-year-old male fish farmer who arrived at the emergency department with thigh pain, immobility, and symptoms of a flu-like illness, including fever, muscle pain, and dark red urine.

Initial tests revealed renal impairment, metabolic acidosis, hepatitis, thrombocytopenia, and inflammatory markers suggestive of severe sepsis. Early diagnosis of leptospirosis was made through clinical history and blood tests, leading to prompt treatment with intravenous ceftriaxone and rehydration. The patient's condition improved rapidly, and subsequent tests confirmed the diagnosis.

This case highlights the importance of clinical history, particularly occupational exposure, in diagnosing leptospirosis. It underscores the need for low clinical thresholds for this disease, as rapid deterioration can occur without timely intervention.

Audience Take Away Notes

- **Clinical History Importance:** How detailed clinical history, particularly regarding occupational exposure, is crucial for early leptospirosis detection and treatment
- **Diagnostic and Treatment Protocols:** How to interpret preliminary investigations and implement immediate treatment to prevent rapid deterioration
- **Low Clinical Threshold:** The importance of a low clinical threshold for leptospirosis, even in developed nations, to ensure timely medical intervention

Biography

Hamza Rashid is a graduate of Imperial College London and a Doctor completing his foundation years (Intern) in the UK. His interests include general surgery alongside a fascination with tropical diseases and epidemiology, with a particular emphasis on zoonotic infections like leptospirosis. Dr. Rashid has been involved in clinical research and teaching, taking part in several systematic reviews and meta-analyses throughout his university education.

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Gram-negative bacillary arthritis following arthroscopy

Background: The rate of septic arthritis after arthroscopy ranges from 0.15% to 1%. Staphylococci are the leading causative organisms after knee arthroscopy whereas Cutibacterium acnes is often the causative organism after shoulder arthroscopy. Gram-negative bacillary infections are uncommon. Our aim was to describe the clinical, biological, therapeutic characteristics and outcome of gram-negative bacillary arthritis following arthroscopy.

Cases Description: We report 9 cases of gram-negative bacillary arthritis following 8 arthroscopic knee ligament surgery and one arthroscopic shoulder rotator cuff repair. Over this period (18 months), 93 arthroscopies were performed. The sex-ratio was 8 with a mean age of 24 [18-43] years. Risk factors for infection were smoking (n=7), diabetes (n=2), obesity (n=2) and complex surgical procedures (n=2). The mean time to onset of clinical signs was 20 [3-33] days. In all cases, symptoms were not specific including persistent pain (9/9), persistent effusion (5/9) and a low-grade fever (4/9). Laboratory evidence of systematic inflammation was noted in all cases (high C-reactive protein value with a mean value of 49mg/L). Pseudomonas aeruginosa was identified for all patients in joint aspiration collected fluid and deep specimens collected during arthroscopic lavage. All patients underwent emergent abundant arthroscopic lavage with synovectomy in 4 cases. Combination of 2 effective antibiotics, piperacillin- tazobactam or imipenem with ciprofloxacin, was administered intravenously for an average duration of 15.3 [14-21] days. Oral treatment was ciprofloxacin monotherapy. Mean total antibiotic duration was 66 [42-90] days. Eradication of infection was achieved for all patients and functional outcomes were satisfying according to surgeons.

Conclusions: Gram-negative bacillary arthritis following arthroscopy is a healthcare associated infection and a therapeutic emergency. Pseudomonas aeruginosa is an extremely rare causative organism identified in less than 0.2% of cases. Infection is often particularly challenging to diagnose as the clinical symptoms may resemble those often produced by the procedure itself. Consequently, emergent joint aspiration is essential. Outcome depends on an early diagnosis. The treatment must combine emergent abundant arthroscopic lavage with synovectomy as indicated by the stage of infection and administration of effective antibiotics for at least 6 weeks. Early diagnosis and treatment lead to eradication of infection and satisfying functional outcome. Prevention based on asepsis and risk factors control is essential.

Keywords: Healthcare Associated Infections, Septic Arthritis, Bacterial Infections, No Conflicts of Interest.

Audience Take Away Notes

- Septic arthritis after arthroscopy is extremely rare and challenging to diagnose and treat. There are several ways our work could benefit the audience, including
- Providing medical professionals with more accurate and effective methods for diagnosing post-arthroscopy septic arthritis. This could improve patient outcomes and reduce healthcare costs
- Enhancing the understanding of post-arthroscopy septic arthritis among healthcare professionals, medical students, and researchers. This could contribute to the development of new treatments and

prevention strategies for this condition

- Offering a potential source of new research ideas for other faculty members who are interested in studying septic arthritis or related topics
- Providing a practical solution to a problem that could simplify or make a designer's job more efficient by improving the design and implementation of medical devices or equipment used in the diagnosis or treatment of nosocomial septic arthritis
- Improving the accuracy of a diagnosis of nosocomial septic arthritis through the development of more sensitive and specific diagnostic tools, which could reduce the need for unnecessary treatments or procedures and improve patient outcomes
- Overall, our research on septic arthritis could provide numerous benefits to the medical community and potentially have a significant impact on patient outcomes

Biography

Dr. Helmi Ernandes studied at the faculty of medicine of Tunis, Tunisia and graduated as MD in 2020. He obtained the position of Assistant Professor at the same institution. He works in the infectious diseases department of The Mohamed Taieb Kassab Institute of Orthopedics and is specialized in the field of bone and joint infections. He is an ESCMID member, a member of ESCMID Study Group on implants associated infections, ESCMID Study Group on biofils and ESCMID study group on clinical parasitology.

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Ralstonia pickettii periprosthetic joint infection

Background: Periprosthetic Joint Infection (PJI) is the most common and feared arthroplasty complication. Ralstonia pickettii is an opportunistic Gram-negative bacterium, causing nosocomial infections in immunocompromised patients. It is an environmental bacterium that has been also identified in biofilms. However, it remains an extremely rare cause of PJI. We report a case of Ralstonia pickettii PJI following total hip arthroplasty.

Case Description: We present the case of a 62-years-old male patient, that underwent a left cemented total hip replacement surgery. Four weeks later, the patient presented with fever and groin pain. Laboratory findings showed hyperleukocytosis and elevated C-Reactive Protein (CRP). Blood cultures were performed. Radiograph of the pelvis and a horizontal beam lateral hip radiograph of the left hip revealed signs of loosening at the level of both the acetabular and femoral components. An early PJI was diagnosed. An ultrasound guided joint aspiration was performed with a negative microbiological examination. Debridement and change of mobile parts with the retention of fixed prosthetic components were performed. Soft tissues surrounding the implant and periprosthetic interface membrane were taken for microbiological testing. Post-operatively, the patient received empiric intravenous antibiotic therapy based on cefotaxime 150 mg/kg/day and vancomycin 40 mg/kg/day after a loading dose of 15 mg/kg. Evolution was marked by a persistent fever and high CRP. Bacteriological examination of the tissues sampled intraoperatively was negative. The retrieved mobile parts were sonicated. Ralstonia pickettii was isolated from the sonication fluid culture after 8 days of incubation and from blood cultures after 10 days of incubation. The isolated strain was sensitive to imipenem, meropenem, ciprofloxacin and cotrimoxazole. A long-term antibiotic therapy was prescribed based on intravenous imipenem and per os ciprofloxacin (750 mg bid) for 2 weeks followed by 10 weeks of oral ciprofloxacin monotherapy. The clinical and biological evolution was favourable.

Conclusions: R. pickettii remains an extremely rare cause of PJI. Bacteria culture of sonication fluid remains the gold standard in PJI diagnosing. However, when an opportunistic pathogen of low virulence such as Ralstonia is isolated, differentiating contaminant from true pathogen must be based on the clinical context. Optimal management of R. pickettii PJI has not been established.

Keywords: Implant-Associated Infections, Periprosthetic Joint Infection, Bacteria and Bacterial Infections, No Conflicts of Interest.

Audience Take Away Notes

- Ralstonia pickettii periprosthetic joint infections are extremely rare and challenging to diagnose and treat. There are several ways our work could benefit the audience, including:
- Providing medical professionals with more accurate and effective methods for diagnosing and treating periprosthetic joint infections caused by Ralstonia pickettii. This could improve patient outcomes and reduce healthcare costs

- Enhancing the understanding of periprosthetic joint infections caused by Ralstonia pickettii among healthcare professionals, medical students, and researchers. This could contribute to the development of new treatments and prevention strategies for this condition
- Offering a potential source of new research ideas for other faculty members who are interested in studying periprosthetic joint infections caused by Ralstonia pickettii or related topics
- Providing a practical solution to a problem that could simplify or make a designer's job more efficient by improving the design and implementation of medical devices or equipment used in the diagnosis or treatment of periprosthetic joint infections caused by Ralstonia pickettii
- Improving the accuracy of a diagnosis of periprosthetic joint infections caused by Ralstonia pickettii through the development of more sensitive and specific diagnostic tools, which could reduce the need for unnecessary treatments or procedures and improve patient outcomes
- Overall, our research on periprosthetic joint infections caused by Ralstonia pickettii could provide numerous benefits to the medical community and potentially have a significant impact on patient outcomes

Biography

Dr. Helmi Ernandes studied at the faculty of medicine of Tunis, Tunisia and graduated as MD in 2020. He obtained the position of Assistant Professor at the same institution He works int the infectious diseases department of The Mohamed Taieb Kassab Institute of Orthopedics and is specialized in the field of bone and joint infections. He is an ESCMID member, a member of ESCMID Study Group on implants associated infections, ESCMID Study Group on biofils and ESCMID study group on clinical parasitology.

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Baguio General Hospital and Medical Center, Philippines

Foreign fungus: Candida duobushaemulonii bloodstream infection in an immunocompromised host at baguio general hospital & medical center: A case report

Candida duobushaemulonii is a yeast that belongs to the Candida haemulonii species complex. Similar to Candida auris which is an emerging global health threat, C. duobushaemulonii is a major concern in the healthcare system as it is often multidrug resistant. Presenting the 1st reported case of C. duobushaemulonii in the Philippines. This is the case of an 80 year old German national, a long standing immunocompromised patient, who received several cycles of broad spectrum antibiotics due to recurrent bouts of nosocomial infections who eventually presented with fungemia. Initial idenitification of the yeast revealed C. auris but on manual biochemical testing reveled C. duobushaemiulonii which was resistant to all available antifungal therapy in this institution and the Philippines for that matter. As healthcare professionals, we have to be vigilant in suspecting and diagnosing this rare fungal infection in order to give prompt and appropriate treatment. Therefore, it is vital to be vigilant in the proper identification and diagnosis of such opportunistic pathogen and to have the specific antimicrobial agents available.

Introduction: Candidiasis remains as one of the top 5 healthcare-associated bloodstream infections in the world and still causes high mortality rates. It covers a wide range of diseases, from mild clinical infections to invasive and even disseminated forms. In humans, Candida species colonizes the skin, oropharynx and lower respiratory, gastrointestinal, and genitourinary tracts. (Yapar, 2014). Candida duobushaemulonii is a yeast that belongs to the Candida haemulonii species complex. Yeasts in this complex are closely related Candida auris, which is an emerging global health threat because it is often multidrug resistant (MDR) and can cause outbreaks in health care settings (Chawdhary 2014). In the Philippines, there were no reports isolated C. duobushaemulonii bloodstream infections. We report the first documented case of Candida duobushaemulonii fungemia in the Philippines.

Case: The patient is an 80 year old male German national who had been residing in the Philippines for about ten years. His last travel back to Germany was on 2017. He was bedridden since February 2020 from a history of Cerebrovascular disease. He is a known diabetic who had recurrent admissions in our institution due to repeated bouts of pneumonia. His last admission was on June 2020 wherein he was managed as a case of nosocomial pneumonia on top of community acquired pneumonia, complicated UTI, infected sacral decubitus ulcer, UGIB drug induced and dementia and was discharged and improved. Interval history revealed intermittent episodes of productive cough with thick, white to yellowish sputum and noted a progression of the sacral ulcer prompting readmission on October 16, 2021. He was septic and intubated upon admission and went into cardiopulmonary arrest however was revived. He underwent several debridement for his sacral ulcers and underwent tracheostomy.

During the course in the ward, he had several bouts of nosocomial infections such as Catheter Associated UTI (C. albicans), Ventilator Associated Pneumonioa (Carbapenem resistant P. aeruginosa), and infected pressure ulcer (Carbapenem resistant P. aeruginosa). Culture guided therapy was initiated and he was pulled out of septic shock several times. Patient received the following antibiotics: amikacin, amphotericin

B, aztreonam, colistin, vancomycin, meropenem, polymyxin B however, despite culture guided therapy, he succumbed to recurrent hospital infections and into septic shock. On the 120th hospital day, patient still showed no improvement. He had persistent hypotension hence fluconazole was started. Furthermore, blood cultures were collected from revealing Candida auris on two peripheral sites identified via Vitek 2 with no susceptibility testing. Fluconazole was shifted to amphotericin B as empiric therapy. The blood plate containing the fungal colonies was sent for manual biochemical testing and species identification which revealed Candida duobushaemulonii. Despite maximal medical management, his hypotension persisted, his immune response did not recover and overwhelming sepsis led to his demise.

Candida auris is what was initially identified in our microbiology laboratory using the VITEK2. Because this organism is reportable to the national reference laboratory of the country due to the healthcare burden it brings, the isolated species was regrown and was sent to an outside laboratory for confirmation via fungal culture and drug susceptibility testing. C. auris and C. duobushaemulonii are almost alike in microbiological properties. The final isolated candida species turned out to be Candida duobushaemulonii which is also a rare fungal isolate in the Philippines. The identification of Candida duobushaemulonii was done in an outside lab using The Vitek 2 automated identification system (bioMerieux) and was confirmed using biochemical testing.

It is important to note that this paper was written with the consent of the patient’s partner as the patient was encephalopathic.

Discussion: This is the first reported case of C.duobushaemulonii in the Philippines. Despite extensive literature search in medical search engines such as PubMed etc, I have not come across any reports on this organism. However, I have come across similar cases from international journals such as Primary deep cutaneous candidiasis caused by Candida duobushaemulonii in a 68-year-old man: the first case report and literature review by Szu-Yun et al., Deep tissue invasion was confirmed by skin histopathology examination. The pathogen was initially identified as C. haemulonii using the VITEK® 2 system for microbial identification, but was later determined to be C. duobushaemulonii based on sequencing of the internal transcribed spacer region of ribosomal DNA and D1/D2 region of 26S rDNA.

On the issue of drug Multi Drug Resistance and cases on fungemia, a journal published Ramos et al on Emerging Multidrug-Resistant Candida duobushaemulonii Infections in Panama Hospitals: Importance of Laboratory Surveillance and Accurate Identification similiar case was noted in Panama wherein 17 isolates were obtained from 14 patients at six hospitals. Ten patients, including three children, had bloodstream infections, and MICs for fluconazole, voriconazole, and amphotericin B were elevated. Another fungal infection caused by this organism in an immunocompromised patient is written by Frias-De-Leon et al. entitled Superficial candidosis by Candida duobushaemulonii: An emerging microorganism.

Wherein molecular reidentification of two clinical isolates that was recovered from a patient with total dystrophic onychomycosis and isolate from a patient with mucocutaneous candidiasis. patients had diabetes mellitus as baseline disease. These isolates were initially identified as C. haemulonii by the VITEK® 2 system but were later determined to be C. duobushaemulonii based on the amplification and sequencing of a 115-bp fragment of the region of 26S rDNA.

C. duobushaemulonii is an emerging opportunistic fungi which can be an agent for hospital acquired outbreaks especially for immunocompromised patients with prolonged hospital stay. It is a reportable organism to the national health authority and therefore should not be taken for granted. It is typically multi drug resitant and with high level of resistance typically to amphotericin B and azoles. Due to its complex phenotype only molecular-based methods guarantee their accurate identification in most fungal isolates for that matter. Globally C. duobushaemulonii imposes a great threat to the health care community since it can cause ac wide array of invasive infections including blood stream infection such as this encountered to our patient. Furthermore, this pathogen co exists with other pathogenic bacteria which causes a rapid decline in the health status of the patient leading to poor prognosis. This infection is an emerging global health threat and therefore once with high index of suspicion, we must be vigilant to be quick in its identification and immediately report and alarm the national health authority. In our institution, the initial identified organism from the blood isolates was Candida auris, being it a rare isolate, we sent the colonies identified to an outside laboratory for susceptibility testing which later on revealed C. duobushaemulonii using the Vitek 2 which is a compact system uses a fluorogenic methodology for organism identification and a turbidimetric method for susceptibility testing using a 64 well card that is barcoded with information on card type, expiration date, lot number and unique card identification number which identifies some species of different organism for our patient revealed C. duobushaemulonii. Susceptibility testing was done using only antimicrobial available which were Voriconazole, Amphotericin B to which the organism is resistant with and Minimum Inhibition concentration of 8 and 16 ug/ml respectively (Fig. 4). Fluocytosine was included, which had an MIC of 1ug/l interpreted as susceptible. However, the said antifungal is not currently available in the Philippines. The interplay of the unavailability of the specific treatment along with his overwhelming sepsis lead to the demise of the patient.

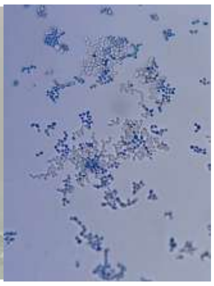

Fig. 1a. C. duobushaemulonii under light microscopy shows oval shaped yeast cells in clusters.

Fig. 1b. C. duobushaemulonii under light microscope shows oval shaped yeast cells in clusters.

Fig. 3. Sabouraud's Dextrose Agar showing white to creamy colonies of Candida duobushaemulonii after 72 hours of incubation.

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Fig. 3. Antimicrobial Sensitivity test result of C. duobushaemulonii.

Conclusion: As health care professionals, we must always consider the possibility of opportunistic pathogens such a C. duobushaemulonii especially for patients with prolonged hospital stay, chronic broad spectrum antibiotic usage and in an immunocompromised state. A high index of suspicion for such infections is vital. We must always practice antimicrobial stewardship to avoid multi drug resistant pathogens which is a consequence of prolonged antibiotic use. C. duobushaemulonii is a reportable organism to the national health authority as it imposes a heavy burden in the health care system.

Acknowledgements: The authors thank the staff of Baguio General Hospital and Medical Center microbiology laboratory department for their cooperation and support.

Conflicts of Interest: The authors have no conflicts of interest to declare.

Ethics Statement: This manuscript has not been published in whole or part elsewhere; Authors have been personally and actively involved abundantly leading to the manuscript and hold themselves jointly and individually responsible for its content.

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Biography

Dr. Hideliz Marie G. Pascua of Baguio General Hospital and Medical Center Philippines. She graduated Doctor of Medicine in 2019 with a Bachelor in Medical Laboratory Science as her pre medical course. She recently finished her residency training in December 2023. She is currently on her Post Residency Deployment Program in Cagayan Valley, Philippines.

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A comparative study on uroculturome antimicrobial susceptibility in apparently healthy and urinary tract infected humans

The uroculturome indicates the profile of culturable microbes inhabiting Urinary Tract Infections (UTIs). UTIs are often caused by opportunistic pathogens and it is necessary to do urine culture to find an effective antimicrobial to treat UTIs. This study targeted to understand the profile of culturable pathogens in the urine of apparently healthy (128) humans and those with clinical UTIs (161). All the urine samples were analyzed for bacteria and fungi to quantify their numbers, their species and antimicrobial susceptibility following standard microbiological methods. In all cases of UTIs microbial counts were never less than 6000 (1.2×104 ± 2.32×103) Colony-Forming Units (cfu)/ mL even from samples where more than one types of bacteria were detected, while in urine samples from apparently healthy humans count ranged from one to 3.33± 1.34×103/ mL. In eight samples (six from UTI cases and two from apparently healthy people) of urine, Candida (C. albicans 3, C. catenulata 1, C. krusei 1, C. tropicalis 1, C. parapsiplosis 1, C. gulliermondii 1) and Rhizopus species (1) were detected. Candida krusei was detected only in a single urine sample from a healthy person and C. albicans was detected both in urine of healthy and clinical UTI samples. In all the samples where fungal strains were detected also had one or more types of bacteria indicating bacterurea. Gram-positive bacteria were more commonly (OR, 1.98; CI99, 1.01-3.87) detected in urine samples of apparently healthy humans (96) than in samples from UTI cases (97). In contrast, Gram-ve bacteria were more common (OR, 2.74; CI99, 1.44-5.23) in urines of UTI cases (117) than in urine of apparently healthy humans. In urine samples, a total of 130 types of microbes were detected. Of the 161 samples from UTI cases, a total of 90 different types of microbes were detected and, 73 had only single type of bacteria while 49, 29, 3, 4, 1 samples had 2, 3, 4, 5, 6 and 7 types of bacteria, respectively. The most common bacteria detected as cause of UTI was Escherichia coli detected in 52 samples, in 20 cases as the sole cause of UTI, other 34 types of bacteria were detected as sole cause of UTI in 53 cases. In 128 urine samples of apparently healthy people, too, 89 different types of microbes were detected either singly or in association with others, from 64 urine samples only a single type of bacteria was detected while 34, 13, 3, 11, 2 and 1 sample yielded 2, 3, 4, 5, 6 and seven types of microbes, respectively. However, similar to urine from UTI cases in the urine of apparently healthy humans E. coli was the most common bacteria detected in pure culture from 10 samples followed by Staphylococcus haemolyticus (9), S. intermedius (5), and S. aureus (5), and similar types of bacteria also dominated in cases of mixed occurrence, E. coli was detected in 26, S. aureus in 22 and S. haemolyticus in 19 urine samples, respectively. A total of 41 species of microbes were exclusively detected in urine of UTI cases, and among them the most prominent was Alcaligenes faecalis (6), Acinetobacter indicus (4) and Streptococcus pyogenes (3), others were detected from one (34) or two (4) samples only. Similarly, 40 types of microbes were detected only from the urine of healthy people, the most common being Mammaliicoccus sciuri and S. cohnii ssp. urealyticus (3 samples each), others were detected from two (7) and one (27) samples respectively. Of the forty microbes detected only in the urine of apparently healthy subjects 28 were Gram+ve bacteria, 11 were Gram-ve bacteria (Aeromonas media, A. trota, Citrobacter amalonaticus, Escherichia vulneris, Hafnia alvei, Leclercia adecarboxylata, Providencia haemabachae, P. stuartii, Pseudomonas testosteronii, Roseomonas rosae and Xanthorhabdus poinarii). The bacteria detected only from the urine of healthy humans, do they have some health benefit or inhabit urinary tract commensally is an area of further investigation. Gram+ve bacteria isolated from urine samples' irrespective of health status were more often (p, <0.01) resistant than Gram-ve bacteria to ajowan oil, holy basil oil, cinnamaldehyde, and cinnamon oil, but more susceptible to sandalwood oil (p, <0.01). However, for antibiotics, Gram+ve were more often susceptible than Gram-ve bacteria to cefalosporins, doxycycline, and nitrofurantoin. On comparing antimicrobial susceptibility of Gram+ve bacteria isolated from urine samples of healthy humans and those suffering from UTI, bacteria from cases of UTI were more often (p, ≤ 0.01) resistant to lemongrass oil, carbapenems, cefalosporins, tetracycline, gentamicin, amikacin, cotrimoxazole, ciprofloxacin, chloramphenicol, and vancomycin but more susceptible to nitrofurantoin (p, <0.01). Gram-ve bacteria from urine of UTI cases was more often (p, ≤ 0.03) resistant than those from healthy humans to cinnamaldehyde, carvacrol, thyme oil, cinnamon oil, more often produced extended-spectrum β-lactamases, carbapenemases, and resisted cefalosporins, tetracycline, amikacin, gentamicin, cotrimoxazole, ciprofloxacin, chloramphenicol, amoxicillin, and colistin but were more often susceptible to lemongrass oil (p, <0.01). The results of the study and their implication in therapeutics of UTIs may be discussed in detail during the presentation.

Biography

Dr. Bhoj R. Singh, after doing BVSc & AH in 1985 (Mathura Veterinary College), He completed his master's degree in Veterinary Public health in 1990 (ICAR-IVRI) and Ph.D. in 1997 (GBPUA&T, Pantnagar). He pursued a year of PDF at IAH Compton, UK and a P.G. Diploma in IPR (IGNOU, Delhi) in 2007. Joined as a scientist in 1991 and progressed as senior scientist (2000), Principal Scientist (2005) and Head of the Division in 2007 in the Indian Council of Agricultural Research and worked at different institutions of the Council. He had published 19 Review articles, 6 books and more than 200 research papers in internationally reputed journals besides contributing 17 book chapters, and 33 technical reports, and drafted the Veterinary vaccines and vaccination policy of India. He has guided 7 PhD and 12 MVSc Students. His important contributions are development of a genetically defined oral vaccine for the control of salmonellosis in equids, a toxoid vaccine for the control of klebsiellosis in fur animals, a toxoid vaccine for control of salmonellosis in poultry birds, a synthetic milk detection kit, a pen-side test for detection of canine parvovirus infection, an ELISA for diagnosis of salmonellosis and germinating seeds model, mouse paw oedema model for toxicity assays and guinea pig model for salmonellosis abortions. His work on the kinetics of zoonotic Salmonella in vegetables and feed and fodder crops, carriage and spread of zoonotic Salmonella by cockroaches, the microbiome of ethnic foods of Nagaland, India (Axone) to identify the probiotic strains, the microbiome of house geckos reproductive tract to understand the vertical transfer of microbes, the microbiome of apparently healthy Mithun and pig reproductive tract to identify potentially pathogenic bacteria carried by them, the microbiome of Azadirachta indica and Ocimum sanctum to establish a relationship with environmental contamination and pathogens residing on plants, genetic regulation of herbal antimicrobial resistance in bacteria and emergence of herbal antimicrobial resistance are the most cited works. He has a long experience as a scientist and administrator while working as scientist, senior scientist and principal scientist in ICAR, director of the National Institute for Animal Health, Baghpat (DAHD) meant for vaccine quality control and quality analysis, in-charge of the National Salmonella Centre, Head Division of Epidemiology, chairman of the Board of Studies of Veterinary Public Health and Epidemiology at ICAR-Indian Veterinary Research Institute, Head of the Department of Animal Sciences at ICAR Port Blair, Act. Joint Director, at ICAR Research Complex Jharnapani Centre, Nagaland, and Chief Bacteriologist NRC on Equine, Hissar. He is a visiting professor of Veterinary Microbiology at GADVASU, Ludhiana, visiting faculty at Times PG Institute, Dehradun, Uttrakhand, and international faculty on Enteric Diseases at the University of Sassari, Italy. His recent work is on the synergy between antibiotics and herbal antimicrobials and the epidemiology of the emergence of antimicrobial drug resistance. He is the most read Veterinary Scientists in India and one of the Topmost e-health Influencers in the world.

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Evaluation of the clinical effectiveness of an early marker system for differentiating between viral or bacterial respiratory infections or febrile infections in a children's hospital during the first post- pandemic season

The aim of the study is the clinical evaluation of an diagnostic marker system that is able to distinguish between bacterial and viral infection, with focus on the influences on therapeutic regimes in primary care and inpatient care.

Material and method: The MeMed- BV® Scores (Diasorin) measures the three non-microbial proteins TRAIL, IP-10 and CRP using CLIA technology on the LiaisonXL. The test result is determined as a score, while a low score indicates a viral and a high score a bacterial infection.

The study included children presenting to emergency departments, as well as inpatients from the children's hospital with suspected acute bacterial or viral infections. The results of the MeMed-BV are compared with the results from cultural and molecular biological routine diagnostics including multiplex PCR systems (MAGPIX-System, Diasorin). A total of 49 patients were included.

For the clinical evaluation, a score was developed that describes whether the various aspects of diagnostics and therapy correlate with the results of the MeMed-BV test and whether options for optimizing the use of antibiotics can be derived from this.

Results: After the patients were discharged, the test results were compared with the case data and the score was applied. All cases were evaluated together with the treating physicians.

The majority of patients showed respiratory symptoms with and without fever. In 30 cases, 34 viral respiratory pathogens were detected and in 8 cases bacterial infectious agents. Gastroenteritis occurred in 12 patients (5 x viral pathogens, 1x bacterial pathogen) Urinary tract infections, appendicitis, otitis and tonsillitis also occurred.

The assignment to bacterial or viral infection was possible in almost all patients; in only 2 cases the result was not clear. The self-developed evaluation score was also able to differentiate well for the majority of patients (Fig. 1) and shows the potential for improvement.

Analyzing the cases we eliminated gastroenteritis, appendicitis and urinary tract infections, due to bad concordance. The new evaluation was additionally stratified according to “bacterial” and “viral” (fig. 2).

We found a good concordance between the MeMed-BV and the clinical picture respectively the diagnostic results. Only the laboratory findings for “bacterial” didn’t matched well, caused by a lack of cultural examinations. Checking the antibiotic therapy, the MeMed BV gave the best results for bacterial infections and viral diseases with high CPR. Viral diseases with low CRP therefore have the highest potential for adaptation to antibiotic therapy.

Conclusions: The MeMed BV assay is a powerful tool in clinical practice when used for respiratory diseases with and without fever. Especially in the case of viral respiratory diseases, despite the use of multiplex PCR systems and the associated improved pathogen detection in clinical management, there is still uncertainty about the assessment of the results and the potential of bacterial superinfections. The MeMed assay has proven to be very helpful and can therefore become an important tool for antibiotic stewardship in pediatrics.

MeMed BV® Score value	number of patients
High Viral	32
Modal Viral	5
Modal Bacterial	6
High Bacterial	4
undetermined	2
Total	49

Table: 1 Results of MeMed-BV

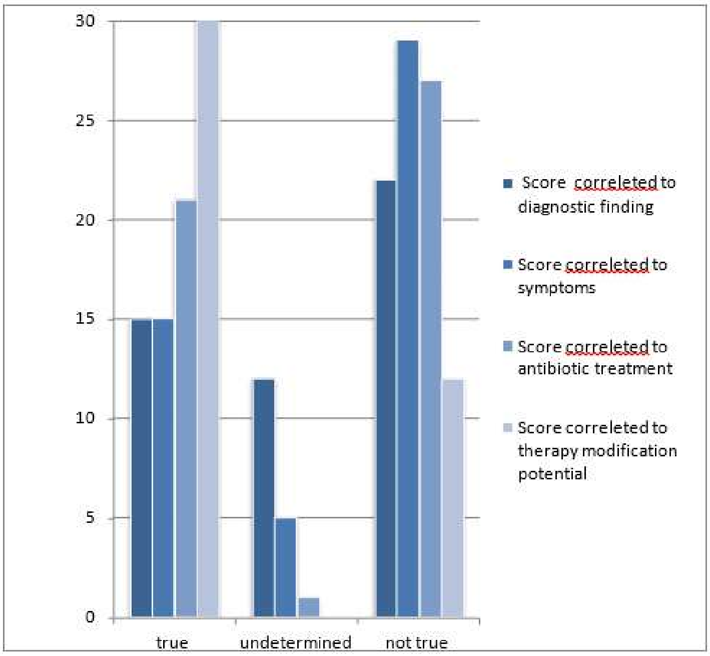

Abb1. Results of clinical Scoring

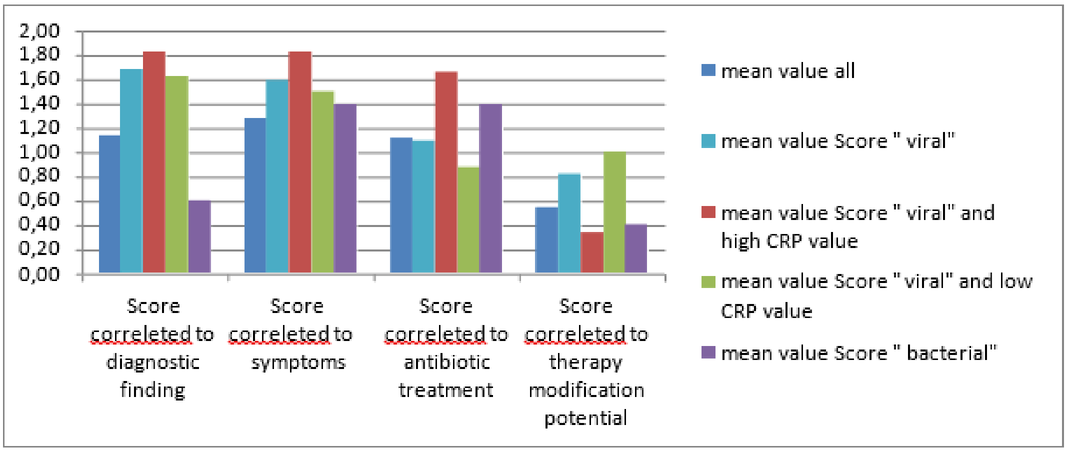

Abb2. Mean value of Scoring after strafication

Jonathan Lambo*, Sirving Keli, Shaheen Khan Kaplan, Temiloluwa Njideaka Kevin

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The descriptive epidemiology of adverse events following two doses of mRNA COVID-19 vaccination in Curacao

Background: Globally, over 13 billion COVID-19 vaccine doses have been administered, which increases the risk of vaccine-related safety concerns. BNT162b2 and mRNA-1273 COVID-19 vaccines have been used for mass vaccinations in Curacao, but information on Adverse Events (AEs) in this population is unavailable. This study describes the characteristics of vaccines that incurred AEs, explores the associations between AEs by vaccine and doses, and estimates the rate of AEs.

Methods: In this retrospective cohort study, data for persons aged 5 years and older who received at least one dose of COVID-19 vaccine at 78 vaccination centres in Curacao between February 21, 2021, and April 5, 2023, were analysed. AE were reported by vaccinees and categorized according to the Brighton's collaboration criteria. Wilson 95% Confidence Intervals (CIs) were calculated for rates of AEs per 100,000 persons vaccinated. Descriptive analysis included frequencies and proportions to describe patterns in rates by age, sex, and number of vaccines.

Results: During the study period, 260,670 doses of COVID-19 mRNA vaccines (59.7% BNT162b2, 40.3% mRNA-1273) were administered to 150,000 individuals (mean age of vaccinees 51 years, 55% females). The vaccines differed significantly in frequency distribution of vaccinees by age, age groups, sex, AEs, and prior COVID-19 infection. Females were more likely to be vaccinated compared to males. Of the 209,720 persons who received two doses of COVID-19 mRNA vaccine, a total of 84 AE reports related to COVID-19 vaccine were received for the study period (overall rate of 40.1 per 100000 persons (95% CI 32.4-49.6)). BNT162b2vaccinees (58.3 per 100000 persons, 95% CI 45.4-74.9)) incurred substantially significant higher AE rate than mRNA-1273 vaccinees (21.9 per 100000 persons, 95% CI 14.6-32.8). There were statistically significant differences in AE rates between males and females. AE rates also varied by the number of doses and by mRNA vaccine group. In addition, overall and by mRNA vaccine group, the rates for AE defined as systemic were higher than those for AE defined as local. By age group, the highest rates were among age group 45-54 years (158 per 100000 persons vaccinated for BNT162b2 vaccine compared with (62 per 100000 persons vaccinated for mRNA-1273 in the same age group (Figure 1). Male BNT162b2 vaccinees has the highest AE rates in the age group 15-24 years (48 per 100000 persons vaccinated) and higher rates than male mRNA-1273 vaccinees in age groups 25-34, 35-44, and 55-64 years. Occurrence of AEs was strongly associated with mRNA vaccine group, sex, number of doses, but not with age, age group, and prior COVID-19 infection. mRNA-1273 was associated with a significantly lower risk of AEs.

Conclusions: AE reporting varied by age, sex, and vaccine used as well as the number of doses. Female predominance of higher rates may be due to biased reporting, although females had higher number of vaccinations administered than males. Future studies should allow for follow up and longer-term reporting of AEs.

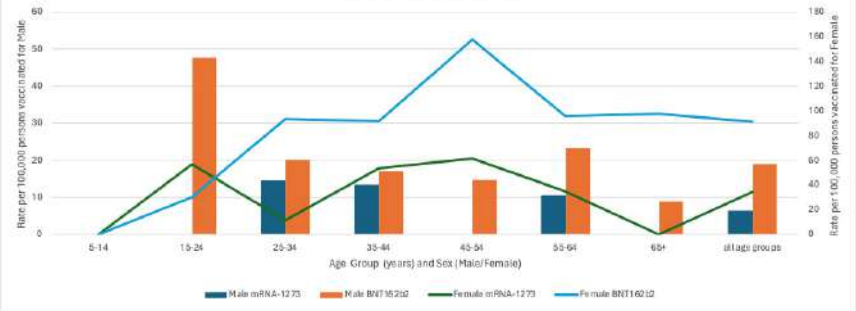


Figure 1 Rates of adverse event (per 100,000 persons vaccinated) among those 5 years and older vaccinated against two doses of COVID-19 in Curacao from February 21, 2021, and April 5, 2023, by mRNA vaccine,sex and age groups

Audience Take Away Notes

- We recommend more real-world studies comparing the effects of different vaccines to reassure the public that the benefits of vaccination outweigh the risks
- Studies should include large sample size, better representation of real-life vaccine populations such as elderly, those with a history of COVID-19, comorbidities, or allergies, all of which are known to increase the risk of AEs, as well as safety profiles, and limited missing information
- This study suggests that there is underreporting and reporting bias for AEs related to COVID-19 vaccination. Future research should be directed at factors that influence reporting and non-reporting of AEs

Biography

Dr. Lambo studied medicine at the University of Vienna and trained as a family physician at General Hospital Linz, Austria. He completed a two-year fellowship in Epidemiology and Public Health at the London School of Hygiene and Tropical Medicine and trained at the Hospital for Tropical Diseases where he obtained his DTM &H RCP (Diploma in Tropical Medicine and Hygiene Royal College of Physician). He served as a Medical Officer at UNICEF and WHO. He is a Professor of Epidemiology and Public Health at the Avalon University School of Medicine. His research group works on surveillance of infectious diseases.

Julissa Soto

Julissa Soto Latino Health Equity Consulting, United States

The power of cultural validation a global innovative strategy when working with vaccines

At the onset of the COVID-19 Pandemic, policymakers and public health officials often cited "vaccine hesitancy" as a key challenge to reaching vulnerable populations, including immigrants, Spanish-speaking communities, Latino communities, and others who have been marginalized. Yet, community-based programs utilizing "Cultural Validation" techniques, such as "Vaccine Sundays," and "One School, One Vaccine at a Time," quickly demonstrated that barriers to access – not hesitancy – were the true culprits.

Cultural Validation is a technique that works to increase access and break down barriers for what many policymakers and public health officials see as "hard to reach populations." The model encourages policymakers and public health officials to research communities, meet communities where they are, and to connect with communities in languages they can not only understand, but also relate to. Demonstrative programs like "Vaccine Sundays" and "One School, One Vaccine at a Time," are also successful because they focus on relationship. Community and public health workers build trust and genuine relationships with principles, school board members, school nurses, or pastors, preachers and other faith leaders. Vaccination events are then held at local schools or churches, with an emphasis on building genuine relationships with community leaders and influencers, as well as culturally relevant marketing strategies, prior to the events. During the event, public health partners and providers focus on providing genuine customer service that demonstrates kindness, caring and cultural validation. As importantly, "Vaccine Sundays," and "One School, One Vaccine at a Time," events are designed around the idea of making vaccinations fun, not scary. Events are often referred to as "vaccine parties" instead of "vaccine clinics". Successful strategies have included providers in superhero costumes, as well as brightly colored mobile vans, among other activities.

This model was proven highly effective during the COVID-19 Pandemic. While Latino and immigrant communities had been described as "vaccine hesitant", events using the Cultural Validation method provided immediate results. The first event saw more than 1297 vaccines administered in what had been described as "vaccine hesitant" communities. In fact, supplies had to be bussed in to keep up with demand, and vaccines were being administered throughout the night. Over the last few years, Cultural Validation techniques have resulted in more than 30,000 vaccinations and the distribution of more than 130,000 testing kits and 100,000 masks.

Biography

Julissa Soto Latino Health Equity Consulting has been a leader in the field of vaccines and immunizations in Colorado and throughout the nation since the onset of the COVID-19 Pandemic. The deployment of her signature community-based intervention strategy, Cultural Validation, has already resulted in more than 30,000 vaccinations and the distribution of more than 130,000 COVID-19 testing kits and 100,000 masks. In fact, her strategies and techniques have earned numerous awards across the country. Governor Jared Polis proclaimed September 20, 2021 as "Julissa Soto Day," for her efforts during the pandemic in Colorado, and in 2023, she received the Immunization Champions Award from the Association of Immunization Managers for the State of Colorado based on the recommendation from the Colorado Department of Health and Public Environment. She was also recognized with the 2023 Distinguished Service Award from the CU Anschutz Medical Campus, an Honorable Mention at the 2023 Immunization Neighborhood Immunization Champion Awards from the National Adult and Influenza Immunization Summit (NAIIS), the 2022 Award for Excellence in the Promotion of Health Equity from the Colorado Public Health Association, the 2022 Equity in Immunization Award from the National Coalition for Immunization Coalitions and Partnerships, the 2022 Big Shot of the Year Award from Immunize Colorado, and the 2022 Heroines of the Pandemic Award from Pikes Peak Women. She received accolades from U.S. Senators Michael Bennet and John Hickenlooper, as well as from many others.

Over the last three years, Julissa Soto Latino Health Equity Consulting has organized and hosted more than 300 community-based vaccine clinics. This success comes from not only from Julissa Soto Latino Health Equity Consulting's specialization in vaccines and immunizations, but also the CEO's own personal and professional connection to communities that face health disparities and barriers to vaccine accessibility. As a Spanish-Speaking, first generation immigrant herself, Julissa is dedicated to forming genuine relationships with the communities she serves as well as the partners she works with; Her background and experience enable her to meet communities where they are and connect with them in culturally relevant languages and methods they can understand and relate to. Her ability to effectively engage diverse and underserved communities has also been widely recognized, earning the 2022 DEI Champions in Advocacy Award from the Colorado Springs Independent, Colorado Springs Business Journal, Southeast Express and Colorado Spring Military Newspaper Group, the 2022 Victor Smith Memorial Award from Colorado Cross-Disability Coalition, the 2017 Centers for Disease Control and Prevention (CDC) Best Practices Award, the 2016 People Who Make a Difference Award from Wells Fargo, and the 2015 William Funk Award for Building Stronger Communities from the Colorado Nonprofit Association.

By combining her lived experience with more than twenty years of community-based health programming experience, Julissa Soto Latino Health Equity Consulting has also become a renowned expert in bridging the gap between providers and communities. Julissa Soto holds key positions as a Vaccine Community Advisory Member at University of Colorado's Children's Hospital and as a Cultural Advisory Board Member at Vaccinate Your Family – a national nonprofit agency that strives to protect people of all ages from vaccine-preventable diseases – and where she shares her extensive health equity expertise to aid in the development of outreach plans to increase pediatric COVID vaccine uptake in marginalized communities. She is also a member of the following organizations and workgroups: the Immunization Workgroup at the National Association of County and City Health Officials, the Health Equity Commission at the Colorado Department of Public Health and Environment, the Denver Catholic Medical Association, the National Hispanic Medical Association, the National Association of Community Health Workers, the Kansas Community Health Worker Coalition, the Conference for Immunization Coalitions and Partnerships National Coalition Conference Planning Committee, the Colorado Department of Health Care Policy and Finance Ambassador Team, the Colorado Suicide Prevention Commission, the Behavioral Health Equity Steering Committee at the United States Substance Abuse and Mental Health Services Administration (SAMHSA).

Karen Ivy Bacsain[1]*, M.D; Jose Manuel Ranola III[2], M.D, FPCP; Charissa Divinagracia[3], M.D, FPCP; Floranie Paredes[4], M.D, FPCP

Universidad de Santa Isabel Health Services, Naga City, Philippines

Pulmonary manifestations of chronic melioidosis in a patient with Type 2 Diabetes Mellitus: A case report

Background: The Philippines, being a tropical country, makes for an interesting reservoir for diverse bacterial flora. One such pathogen is the Burkholderia pseudomallei, a Gram-negative pathogen, found in moist soil and rainwater. Cases increase during the monsoon rains, which occur bi-annually from June to September as well as November to February. Highly susceptible are patients with Type 2 Diabetes Mellitus who are already affected by the presence of chronic inflammation and immune dysfunction.

Objective: To present a case of melioidosis presenting with a two-month history of intermittent episodes of fever associated with generalized body weakness, and chills.

Case: A 55-year-old Filipino female with poorly controlled Type 2 Diabetes Mellitus was admitted in severe cardiorespiratory distress and placed on high flow nasal cannula. Patient was RT-PCR negative and was initially started on Meropenem. Blood Culture and Sensitivity results came out positive for Burkholderia pseudomallei. Meropenem was completed for 7 days. Patient was also started on Ceftazidime, thereafter, the patient gradually improved and was discharged.

Conclusion: Melioidosis is a lesser diagnosed disease entity in the Philippines. Despite advances in antibiotics, it may still be a formidable disease as it is still associated with significant mortality due to sepsis and difficulty of diagnosis.

Keywords: Melioidosis, Type 2 Diabetes Mellitus, Burkholderia Pseudomallei, Sepsis, Community- Acquired Pneumonia.

This presentation will give insights on the treatment and diagnosis of sepsis secondary to Burkholderia pseudomallei in a vulnerable population. In this clinical scenario, rapid recognition and prompt treatment correlates with good outcomes.

Biography

Dr. Karen Ivy Bacsain is a graduate of the University of Santo Tomas Faculty of Medicine and Surgery, Class 2019. She had her post-graduate internship in 2019-2020 in the Manila Doctors Hospital. She is currently in her third year of residency training in the Universidad de Santa Isabel. Health Services, Naga City.

Katarzyna Grudlewksa Buda*, Julia Czuba, Agnieszka Ratajczak, Natalia Wiktorczyk Kapischke, Anna Budzynska, Krzysztof Skowron

Department of Microbiology, L. Rydygier Collegium Medicum in Bydgoszcz, Nicolaus Copernicus University in Torun, Poland

Pheno-and genotypic characterization of Enterococcus spp. isolated from the animal farm environments

Bacteria of the Enterococcus genus are opportunistic microorganisms widely prevalent in the environment. An important source of pathogenic strains of Enterococcus spp. are farm animals and their living environment. Enterococcus faecium and Enterococcus faecalis species are most often responsible for causing infections in humans. Increased antibiotic resistance of strains is often associated with the presence of various virulence factors.

The aim of this study was the assessment of drug susceptibility of Enterococcus spp. isolates from livestock farming environment and the frequency of genes encoding selected Virulence Factors (VFs).

Material for the study consisted of 364 isolates Enterococcus spp. strains from the pig (200, 54.9%), poultry (132; 36.3%) and cattle (32; 8.8%) husbandry environment in the form of swabs and faeces. Species identification of obtained strains was performed using MALDI- TOF MS technique. Antibiotic susceptibility of isolates was assessed by disc diffusion method according to the EUCAST v. 14.0 recommendation. The study evaluated the presence of the selected VFs genes (ebpABC, pil, efaAfs and gelE) was made using PCR method for 40 strains E. faecalis and E. faecium isolated from poultry farm.

The isolated strains belonged to 8 species of Enterococcus spp. with the highest frequency: E. hirae - 144 (39.6%), E. faecium - 120 (33.0%) and E. faecalis - 77 (21.2%). Evaluation of drug susceptibility showed that 279 (76.6%) of the strains were resistant to at least one antibiotic. The highest number of strains showed resistance to streptomycin (n=199, 54.7%). The lowest percentage of resistance was reported for teicoplanin (n=3, 0.8%). Also, high-level aminoglycoside resistance (HLAR) was detected in 6.04% of E. faecalis strains. One vancomycin-resistant E. faecium strain was detected. The study showed the presence of Multidrug - Resistant (MDR) (103; 28.3%) and Extensively Drug Resistant (XDR) (9; 2.5%) strains.

The presence of selected virulence genes was found in 6 isolated strains among 40 tested. Five represented E. faecalis species, and one E. faecium. The study found one strain of E. faecalis carrying all VFs genes included in the study.

The irrational use of antibiotics in agriculture and veterinary practice is considered to be one of the key reasons for the rapid spread of antibiotic resistance among microorganisms. Owing to the fact that farm environments can be a reservoir of antimicrobial resistance and transmission route of antimicrobial resistance genes from commensal zoonotic bacteria to clinical strains, it is of a great importance to public health to monitor trends in this research area.

Audience Take Away Notes

- The presentation highlighted that the livestock environment can be an important reservoir of multi-drug resistant strains and virulence genes
- Characterization of strains present in the livestock environment is extremely important to limit the spread of antibiotic resistance which has public health implications

- The presentation aims to highlight the problem of resistance in commensal strains in the animal husbandry environment

Biography

Dr. Katarzyna Grudlewska-Buda studied biotechnology at L. Rydygier Collegium Medicum in Bydgoszcz, Nicolaus Copernicus University in Torun in Poland and graduated as MS in 2014. She received her PhD degree in 2020 at the same institution. Her research is focused on study of antimicrobial activities, microbial tolerance to stress factors, antibiotic resistance, and assessment of expression levels of virulence genes of clinically important pathogens. Her interests extend to Enterococcus species and characterization of these bacteria from non-clinical sources. Dr. Katarzyna Grudlewska-Buda has published 63 full-text publications and contributed to 5 chapters in monographs.

Keekok Lee
University of Manchester, United Kingdom

Assessing COVID-19 in the context of geopolitics

This contribution is an attempt to clarify some of the issues raised by the COVID-19 pandemic when it hit the globe roughly between 2020 and 2022 from the perspective of geopolitics. It is, therefore, per se, not a discussion from the narrow medical point of view but the political and to argue that Epidemiology, in particular, cannot be adequately understood unless it is explored in a wider context which includes the history, culture, ethics, politics of each nation-state and the relationship between them. This exploration chooses to concentrate on two countries and their respective strategies to cope with the pandemic, namely, the USA on the one hand and the People's Republic of China on the other – the former is paradigmatically a liberal democracy while the latter an autocracy/authoritarian regime. The PRC adopted two strategies (lockdown and mask-wearing) to control the spread of the disease. The USA did not, on the grounds that they were morally and politically abhorrent. American culture, in general, prioritises individual freedom above all other values, including safety and security about health. Chinese culture, in general, prioritises collective freedom above other values and hence endorse restrictions on personal freedoms when these are deemed necessary to ensure health security, such as lockdown, mask-wearing, keeping an appropriate distance from others in public spaces, even avoiding public spaces altogether (even including not going out to shop). Politics apart, how effective are these respective strategies in saving lives? Mortality rates as officially reported by these two countries appear to show that the Chinese approach is more effective.

Biography

Keekok Lee is a graduate in philosophy at the University of Singapore (BA), of Oxford (B.Phil.) as well as of Manchester (PhD). She taught philosophy at the University of Singapore before joining the University of Manchester in 1966, taking early retirement in 1999. Since then, she has continued to research and to publish in numerous domains such as the philosophy of law, politics, genetics, medicine (both Biomedicine and Classical Chinese Medicine) and now geopolitics, using the techniques of analytical philosophy to clarify pressing issues raised in each of these domains. She practises what may be called practical philosophy.

Komal Mushtaq
DHQ Sheikhupura, Pakistan

Measles outbreak – another post- COVID phenomenon: Lessons to be learnt

Introduction: Measles virus is an aerosol borne and one of the most Contagious Pathogens1. Almost every measles virus Infection becomes Clinically manifest, furthermore, it can cause fatal complications and has high morbidity and mortality. Measles virus infection is a vaccine preventable disease. This strategy is also used in developed countries as well because of naturally expected epidemic of measles after few years2. The first symptoms of Measles are fever, cough and coryza followed by maculopapular rash. Mortality in measles is due to complications and under 5 years of age, measles complications are higher.3 Measles cause serious complications among them Pneumonia, otitis media and diarrhea are in acute phase, furthermore, Tuberculosis activation, malnutrition after measles, T-Cell anergy here as well before SSPE (Subacute sclerosing panencephalitis) is a non-treatable and fatal neurological complication which leads to worsening of higher mental functions and eventually cause Death4. In Pakistan, mass immunization against measles in 2018 and Measles-Rubella IMMUNIZATION Campaign was done in 20215. More than 386,000 health professionals, including 76,000 vaccinators and more than 143,000 social mobilizers are mobilised for the two-week campaign supported by Gavi, the Vaccine Alliance, UNICEF, WHO and partners. The children aged between 9 months and 15 years, those aged up to five will also receive the oral polio vaccine, were targeted by the Campaign 6.

In national Study, the number of cases of measles in 2012 was reported to be 14,000 with 210 patients dying of it. Unfortunately, due to a lack of proper surveillance infrastructure, the demographic statistics, including ages of the patients affected by measles in the current epidemic in Pakistan are unknown7. The Covid-19 Pandemic causes disruption in routine EPI services along-with inequality in access to Vaccines. Although WHO emphasize the importance of EPI Vaccinations, however, countries with resource limitation as in Pakistan current Epidemic COVID-19 vaccination was done by EPI Staff which affects routine EPI Vaccination Program 8.

Materials and Method: Study Design: Cross-sectional study. It's a multi-centric study and will be conducted in Mayo Hospital Lahore and Mother Children Complex Sheikhupura.

Sampling Technique: Non- Probability Convenience sampling.

Sample Size: All measles cases in both setup.

Inclusion Criteria: All measles cases which are admitted in Mayo Hospital Lahore and Mother and Children Complex Sheikhupura.

Exclusion Criteria:

- Rash without fever.
- Rash disappear within 72 hours.
- Children admitted with measles in hospital 21 days prior measles infection. Medical record available.

Data Collection Procedure: Measles patients admitted in Mayo Hospital Lahore and mother children complex Sheikhupura were admitted in this study. Patient's gender, age and contact details were taken after their consent. Measles clinical spectrum, vaccination and malnutrition association will be assessed by predesigned Questionnaire performa by researchers.

Data Analysis: All the data will be entered and analysed by SPSS 22.

Objective: To assess the clinical spectrum of measles infection including its complications, association with malnutrition and positive Ig M results.

Operational Definitions:

Suspected Measles Case: A suspected case is one in which a patient with fever and maculopapular (non-vesicular) rash or in whom a healthcare worker suspects a measles.

Confirmed Case: A suspected case of Measles that has been confirmed positive by testing in a WHO accredited Laboratory and vaccine associated Illness has been ruled out.

Pneumonia: pneumonia is an acute respiratory infection that affects the lungs.

Meningo- Encephalitis: Meningo-encephalitis is a serious infection of the meninges (membranes covering the brain and spinal cord) and brain parenchyma.

Diarrhea: Diarrhea is defined as the passage of three or more loose stools or liquid stools per day.

Malnutrition: Malnutrition refers to deficiencies, excess or imbalance in a person's intake of energy or nutrients. In our study, malnutrition refers to deficiency of nutrients which can be classified by using WHO classification. Z score along with anthropometric measures used to classify malnutrition as

Mild -1.0 to 1.9

Moderate -2.0 to 2.9

Severe< -3.0

Questionnaire for the Research entitled as:

Measles Outbreak – Post Covid Phemeneon: Lessons to be Learnt.

A - Demographic Details:

Name -- Age --------------------- Gender ----------------

Address--

Parents Occupation & Monthly Income --

B - Clinical Spectrum of Measles:

Measles case

1. Suspected case
2. Confirmed case (Ig M / PCR)

Complication of Disease

1. Meningo-encephalitis
2. Pneumonia
3. Diarrhea

4. Other

Co-Morbidities

1. Malnutrition

Yes

No

If yes than

- o Mild
- o Moderate
- o Severe

2. If Known case of any other disease --

Vaccination Status:

1. Vaccinated
2. Unvaccinated
3. Catch-up vaccination

- Age ---------------------
- How many months earlier ----------------------
- Routine / SNID -----------------------

Hospital Stay (In Days) --

Zinc Supplementation

a) Yes
b) No

Vitamin A Supplementation

a) Yes
b) No

H/O Measles exposure

a) Family
b) Neighbor/Guest
c) School
d) Hospital
e) None

Biography

Dr. Komal Mushtaq, did Bachelor of Medicine and Bachelor of Surgery from Faisalabad Medical University in 2013. I did my Post-Graduation training from Children Hospital Lahore. I passed my fellowship examination in 2019 with flying colours. I am awarded as Paediatric Ambassador by prestigious Institution, College of Physicians and Surgeons Pakistan. I joined District Headquarter Hospital Sheikhupura as Consultant Paediatrician. Furthermore, I voluntarily support UNICEF Projects for Child diseases management. I have special interest in Preventive Paediatric and Research Projects to improve child care and this very project on Measles reflects ‘From Little acorns mighty oaks do grow.’

Bastos L. F
University Center Assis Gurgacz Foundation, Brazil

Analysis of the influence of the COVID- 19 pandemic on reported malaria cases in Brazilian macroregions between 2018 and 2022

This article aims to identify the impact of the novel coronavirus pandemic on malaria cases in the North, Northeast, Midwest, Southeast, and South regions of Brazil, given the similarity of initial symptoms, the need for reallocation of resources, and the burden on public health systems, factors that may have affected the proper differentiation and timely treatment of both diseases.

Introduction: Malaria is an infectious disease caused by parasites of the genus Plasmodium, which are transmitted to humans through the bite of infected mosquitoes of the genus Anopheles. These parasites multiply in the liver and then infect red blood cells, leading to symptoms such as fever, chills, sweating, headaches, and, in severe cases, potentially fatal complications.

In contrast, Covid-19, officially identified in Wuhan, China, in December 2019, is caused by the SARS-CoV-2 virus. It immediately became a global concern due to its rapid spread, uncertainty surrounding preventive measures, and potential devastating impacts on global healthcare systems. The resulting pandemic has driven intensive research efforts and international collaboration to understand, control, and develop effective vaccines against the disease.

The correlation between the diseases exists since initial symptoms such as fatigue, high fever, difficulty breathing, and myalgia can coexist in both cases. Moreover, malaria prevention and control measures such as distribution of insecticide-treated bed nets and epidemiological surveillance in endemic areas were hindered by the Covid-19 pandemic due to the fact that social isolation was initially the primary measure to reduce the spread of the novel coronavirus.

It is worth noting that hydroxychloroquine was widely considered as a potential therapy, despite the lack of solid scientific evidence initially, for its use in the treatment of Covid-19. This hasty approach led to the indiscriminate administration of the medication, in many cases, raising a series of medical and ethical concerns. One of the less discussed consequences of this practice was the potential underdiagnosis of malaria cases, a disease with similar symptoms, which is effectively treated with this drug. The rampant use of this medication in the context of COVID-19 may have caused confusion in diagnoses, obscuring the distinction between the two diseases and impairing the ability to properly identify and treat malaria.

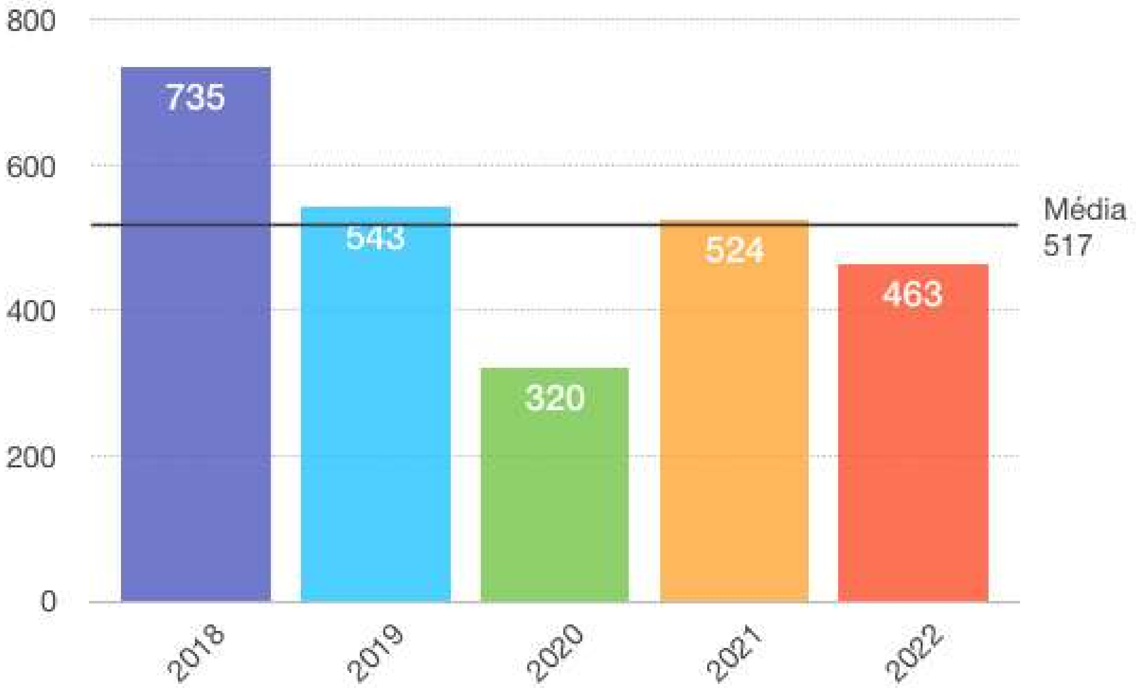
Metodology: For this study, the absolute numbers of reported Malaria cases were analyzed in the Department of Health Informatics of the Unified Health System (DATASUS), from the years 2018 to 2022, across the Northeast, Midwest, Southeast, and South regions of Brazil. Data from the North region were analyzed using the Epidemiological Surveillance System platform (SIVEP). The number of malaria cases was tallied annually in each region covered by the study from 2018 to 2022. It's worth noting that all utilized data were de-identified, lacking patient identification. The obtained data were allocated, tabulated, and processed into spreadsheets and graphs using Microsoft Excel® software.

Keywords: Malaria, COVID-19, Pandemic.

Results: To elucidate the obtained results, the data analysis was subdivided into two distinct categories: the extra-Amazon region, which encompasses the macro-regions Northeast, Midwest, Southeast, and South, and the Amazon region, consisting exclusively of the North macro-region. This approach was adopted due to the significant disparity in the number of malaria cases recorded in the Amazon region compared to the other regions, which could potentially confound the results of this article by obscuring the incidence of malaria in other regions of Brazil.

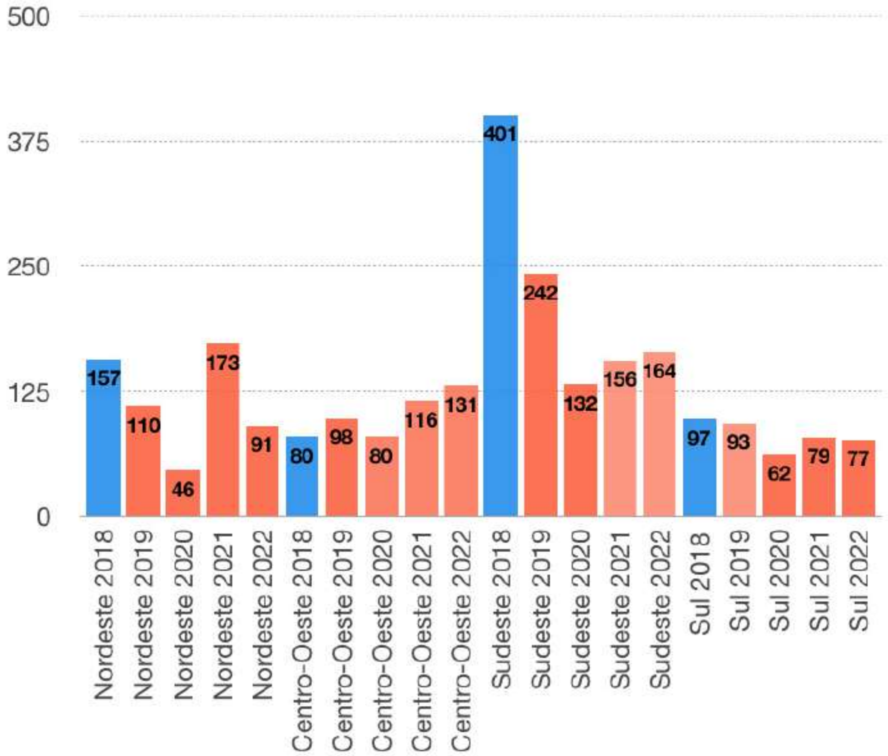
3.1 TOTAL MALARIA CASES REPORTED IN THE EXTRA-AMAZON REGION (NORTHEAST, MIDWEST, SOUTHEAST, AND SOUTH) BETWEEN 2018 AND 2022.

Analyzing the total number of malaria cases reported in Brazil (extra-Amazon region) between 2018 and 2022, a decrease of 41% in the number of reported cases is observed when comparing 2019 to 2020. The 320 cases reported in 2020 represent a reduction of 38.1% compared to the absolute average of all the years analyzed in the study.



Graph 1: Assessment of the absolute number of malaria cases reported to the Unified Health System (SUS) in the extra-Amazon region between 2018 and 2022 and recorded in the DATASUS platform.

3.2 TOTAL MALARIA CASES BY EXTRA-AMAZON MACRO-REGION (NORTHEAST, MIDWEST, SOUTHEAST, AND SOUTH) BETWEEN 2018 AND 2022.



Graph 2: Assessment of the absolute number of malaria cases reported to the Unified Health System (SUS) in the extra-Amazon region annually from 2018 to 2022, recorded in the DATASUS platform.

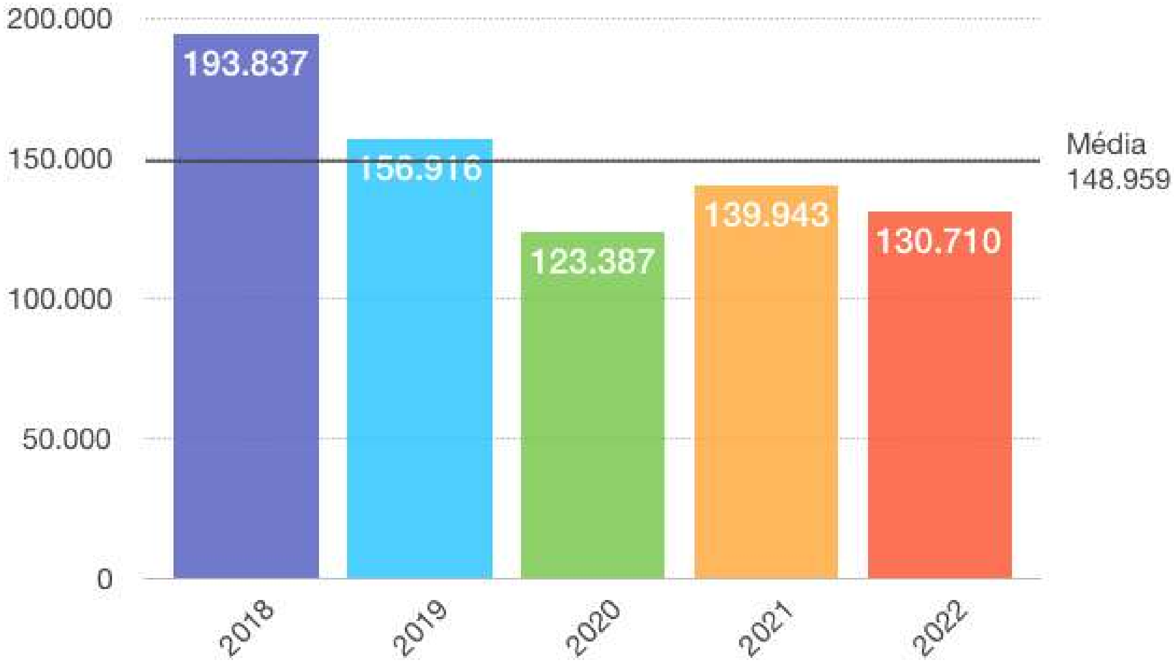
Upon analyzing each extra-Amazon macro-region individually, it was noted that the region with the greatest decrease in the number of reported cases was the Southeast. In Graph 2, we can observe an 85.6% reduction in the number of reported cases between 2019 and 2020 in the Southeast region, with 242 cases reported initially and only 132 the following year.

Conversely, the Midwest region had the smallest decrease in the number of compulsory notifications of the disease, with a reduction of only 18.3% when comparing 2019 to 2020.

In the South region, 93 cases of the disease were reported in 2019, and the following year, 62 notifications were recorded, resulting in a 33.3% decrease in the number of malaria cases.

Lastly, in the Northeast region, between 2019 and 2020, there was a 58.1% decrease in reported malaria cases, and between 2021 and 2022, the reduction was 47.3%, with 173 cases recorded in 2021 and only 91 cases the following year.

3.3 TOTAL MALARIA CASES REPORTED IN THE AMAZON REGION BETWEEN 2018 AND 2022.



Graph 3: Assessment of the absolute number of malaria cases reported to the Unified Health System (SUS) in the Amazon region annually from 2018 to 2022, recorded in the SIVEP (Epidemiological Surveillance System).

Analyzing Graph 3, a reduction of 21.36% in the number of reported malaria cases in the Amazon region is observed when comparing 2019 to 2020. Furthermore, in relation to the average number of cases, a decrease of 17.1% in the number of notifications was noted in 2020.

The results, depicted in Graph 2, analyze the absolute values of malaria cases by macro-region, before the COVID-19 pandemic (years 2018 and 2019) and during the pandemic (years 2020, 2021, and 2022). It confirms a decrease of 85.6% in the Southeast region, 58.1% in the Northeast region, 33.3% in the South region, and 18.3% in the Midwest region, between 2019 and 2020.

Graph 3 examined the absolute values of malaria cases in the Amazon region between pre-pandemic years (2018 and 2019) and pandemic years (2020, 2021, and 2022), confirming a reduction of 21.3% in the number of cases when comparing 2019 to 2020.

Discussion: The COVID-19 pandemic has brought about a profound transformation in the global medical landscape, indirectly impacting infectious diseases such as Malaria. Resource allocation, medical research, and epidemiological surveillance have been redirected to combat COVID-19, affecting the continuity of efforts to control other infectious diseases.

The decrease in the number of reported malaria cases, particularly between 2019 and 2020, involves various factors, including the strain on healthcare systems in Brazil and worldwide caused by the pandemic. It is assumed that this scenario negatively affected the capacity for malaria diagnosis, as the initial symptoms of both COVID-19 and malaria often resemble each other. (3) The high demand for tests, hospital beds, and medical resources for COVID-19 sometimes diverted attention from efforts to diagnose and treat malaria, leading to underreporting of the disease and potentially undiagnosed cases.

This scenario, combined with the indiscriminate use of hydroxychloroquine in the treatment of COVID-19, lacking robust scientific basis, likely resulted in the inappropriate management of cases that actually corresponded to malaria due to the initial similarity in symptomatology between both diseases.

Another factor predisposing to the reduction in reported cases was the period of social isolation, travel restrictions, and limitations on outdoor activities during the COVID-19 pandemic, which may have played a role in the decrease in the number of reported malaria cases. With the limitation of human mobility and the decrease in social interactions, exposure to malaria-transmitting mosquitoes was potentially reduced. These pandemic containment measures may have contributed to the decrease in malaria transmission, resulting in a temporary underreporting of the disease.

An epidemiological study conducted in Mexico, analyzing the indirect impact of COVID-19 on the incidence rates of vector-borne diseases, demonstrated that certain measures such as social distancing and home confinement contributed to temporarily reducing the number of cases of vector-borne diseases, including malaria. The research showed that 609 malaria cases occurred in Mexico in the year 2019, and in 2020, 345 cases of the disease were recorded, corresponding to a 43.4% decrease in the number of cases. During the same period, the extra-Amazonian Brazilian macro-regions also exhibited a similar reduction of 41% between the years 2019 and 2020.

The same article, "Indirect Impact of COVID-19 on Incidence Rates of Vector-Borne Diseases in Mexico" (7), mentions that the Amazon region of Peru also experienced a drastic reduction in malaria cases during the pandemic, which was correlated with the increase in COVID-19 cases that overwhelmed Peru's healthcare systems and public medical institutions. This impact can also be observed in the Brazilian Amazon region, which recorded 159,916 malaria cases in 2019 and 123,387 cases the following year, a decrease of 21.3%.

Another article linking malaria and COVID-19 in native communities of Rio Santiago, Condorcanqui province, in the Amazon region of Peru in 2020, demonstrated that prior malaria infection significantly associates with COVID-19 symptoms such as fever, odynophagia, and respiratory difficulty. During the pandemic, efforts to reduce the transmission of the novel coronavirus led to neglect of other diseases like malaria, a situation similar in Brazil, as evidenced by the reduction in the number of reported cases of the disease in Brazilian macro-regions.

The underreporting of malaria cases was investigated in a study that analyzed the incidence of hospitalizations and mortality related to febrile syndromes and parasitic diseases during the COVID-19 pandemic in Brazil. The results indicated that in 2020, the number of malaria-related hospitalizations in the country represented only 29.31% of the total; however, the mortality rate among hospitalized cases reached 82.55%. This high mortality rate is likely due to underreporting of the disease and late diagnosis, supporting the downward trend in notifications mentioned in this article.

Conclusion: The author successfully achieved the intended goal, which aimed to evaluate the impact of the Covid-19 pandemic on the number of malaria cases in the North, Northeast, Midwest, Southeast, and South macro-regions of Brazil from 2018 to 2022. The results demonstrated that indeed, the pandemic led to a negative variation in the number of reported malaria cases in all macro-regions analyzed in the study, especially when comparing the years 2019 and 2020.

Regarding the total variation in the number of reported malaria cases in the Northeast, Midwest, Southeast, and South regions, a global negative variation of 41% was obtained in the number of compulsory notifications when comparing the pre-pandemic year of 2019 with the pandemic year of 2020. In other words, during the onset of the pandemic (2020), the number of reported malaria cases saw a significant reduction. In the Amazon region, between the pre-pandemic years (2018 and 2019) and the pandemic years (2020, 2021, and 2022), there was a 21.3% reduction in the number of cases when comparing 2019 with 2020.

It is assumed that this decrease may be explained by the overload of the public health system with Covid-19-infected patients, similar symptomatology between the diseases complicating diagnosis, treatments for the new coronavirus lacking scientific evidence leading to underreporting of malaria cases, and social isolation possibly reducing population contamination by the vector.

Biography

Dr. Laura Fermiano Bastos, a physician graduated from the Fundacao Assis Gurgacz in 2024, is recognized for her commitment to academic excellence in cardiovascular surgery. As a speaker, she has presented at significant events such as the 49th Brazilian Congress of Cardiovascular Surgery and the 31st World Congress of Cardiovascular and Thoracic Surgery in 2023. She was awarded for her research on the Impact of Covid-19 on cardiovascular surgery in state of Parana, showcasing her dedication to advancing medicine and addressing challenges in the medical field.

Mark A. Griffiths[1,2], Sandy Francois[1], Melissa N. Cameron[1], Jordan E. Daniel[1], Bridget A. Wynn[1], Sara P. Brown[2], Sarah Thompson[2], Rebeka G. Carter[2], Kelly DeNaples[2], Swaminathan Kandaswamy[1], Evan Orenstein[1,2], Andrés Camacho-González[1,2], Claudia R. Morris[1,2] and Lauren Middlebrooks*[1,2]

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Implementation of opt-out human immunodeficiency virus screening in pediatric emergency departments

The Centers for Disease Control and Prevention recommends HIV screening for all patients ≥13 years. Parts of Metro Atlanta have HIV positive rates at 8-times the national average. Adolescents are the least likely group to know their HIV status and have the lowest rate of linkage to care and viral suppression. Children's Healthcare of Atlanta (Children's) implemented an opt-out HIV testing program in its emergency departments (ED) for patients ≥13 years undergoing venipuncture for any chief complaint at 2 of their 3 sites. The objective is to increase testing in adolescents leading to earlier HIV diagnosis and linkage to care.

Children's electronic medical record EPIC and its population discovery tool were used to compare HIV testing volumes of 13–24-year-olds, 8 months pre-(November 5–July 5, 2023) and 8 months post (July 6–March 6, 2024) clinical implementation. Data for all 3 sites was reviewed and all sites received educational promotion. Results were cross-referenced to determine newly diagnosed adolescents living with HIV (ALHIV) from known positives. The data was compared using descriptive statistics.

A total of 966 patients were tested pre-implementation, 697(72%) girls and 269(28%) boys. Six new ALHIV were identified, 1 male coinfected with syphilis, the average age was 17 and the assignment at birth was (3) male and (3) female. After 8 months of implementation, a total of 1600 patients were tested: 1101(69%) girls and 499(31%) boys. Six new ALHIV were identified; the average age was 16 and the assignment at birth was (5) male, 2 coinfected with syphilis, and (1) female. This demonstrates an overall positivity rate of 0.4% and 1 in 100 boys tested positive (1%). At sites receiving education for 1 week, 5 and 8 months, testing increased by 8%, 72% and 88% respectively. All newly diagnosed cases were linked to care within 1-48 days.

Atlanta remains a hotspot for new HIV cases. Six cases in 8 months highlights the importance of universal HIV testing of adolescents and reflects a public health crisis. The new initiative significantly increased HIV screening among adolescents and will likely identify ALHIV at an earlier stage of infection, facilitating timely access to medical care. This can lead to improved clinical and immunological outcomes and a reduced risk of secondary transmission.

Audience Take Away Notes

- Compare and analyze HIV testing numbers with opt out screening option
- Identify adolescents living with HIV and explore the possibly of coinfected with other sexually transmitted infections
- Assess rate of linkage to care of adolescent newly diagnosed with HIV
- Inform other faculty how to implement something similar in their hospitals and/or clinics
- Provide practical solution to some challenges you may encounter with new clinical implementation in an children's hospital emergency department

Biography

Dr. Lauren Middlebrooks, is an Assistant Professor of Pediatric Emergency Medicine at Emory University and Children's Healthcare of Atlanta. Dr. Middlebrooks received a Bachelor of Arts degree in psychology from Spelman College in Atlanta, Georgia. She then earned a doctorate of medicine from Meharry Medical College in Nashville, Tennessee, where she was inducted into the Alpha Omega Alpha honor medical society. Dr. Middlebrooks remained in Tennessee to complete residency training in Pediatrics at Monroe Carroll, Jr. Children's Hospital at Vanderbilt University, where she served as vice-president of the Minority House-staff for Academic and Medical Achievement and co-chaired the residency's global health interest group. Dr. Middlebrooks then went on to complete fellowship training in Pediatric Emergency Medicine at Emory University, where she cultivated an interest in health equity by working to improve HIV testing in adolescents in the pediatric emergency department. Dr. Middlebrooks, who also serves as chair of her division's faculty recruitment committee, and member of two PECARN sub-committees, was recently awarded a grant from Gilead Sciences, Inc. FOCUS program. She has been working effortlessly and has successfully implemented routine opt-out HIV testing across 3 different pediatric emergency department sites in Atlanta.

Mohammad K. Alshomrani[1]*, Ahmad A. Alharbi[2], Abdullah A. Alshehri[3], Muhammad Arshad[4], Saeed Dolgum[5]

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Isolation of staphylococcus aureus urinary tract infections at a community-based healthcare center in Riyadh

Although S. aureus UTI is known to be associated with other risk factors such as urinary catheterization, long hospital stay, or complicated UTI, our results show the community-acquired presentation of UTI. Trimethoprim-sulfamethoxazole may be used as an effective treatment for UTI caused by S. aureus. S. aureus UTI could be an alarming sign of more invasive infections such as S. aureus bacteremia, though clinical evaluation and finding the source of S. aureus are crucial for effective treatment and prevention of further complications.

The aim of this presentation is to assess the clinical manifestation, risk factors, and comorbidities of the patients with Staphylococcus aureus bacteriuria, and to analyze the antimicrobial susceptibility data of S. aureus isolated from their urine samples. I will discuss the detailed data of 90 isolates of S. aureus were collected from patients with Urinary Tract Infections (UTIs) including their full identification and susceptibility testing, and urinalysis results.

Audience Take Away Notes

- The prevalence of S. aureus as a causative agent of UTI, in comparison to other uropathogens
- Differentiation between community-acquired and hospital-acquired S. aureus UTI, and associated risk factors
- Is S. aureus a true UTI pathogen or a colonizer? Recommendations will be provided to clinicians how to evaluate such cases of S. aureus from urine samples
- Could S. aureus be an alarming sign for a serious infection? Instructions and recommendations will be provided to the treating physicians how detect and manage systemic infections related to S. aureus UTI
- Guidance of antimicrobial therapy based on our antibiogram data

Biography

Mohammad Alshomrani studied at College of Medicine, King Saud University and graduated as medical doctor in 2007. He joined King Saud University Fellowship of Pathology (Microbiology) and received fellowship degree in Pathology (Microbiology) in 2013. He is working now as consultant microbiologist and Head of Microbiology Department in Riyadh Regional Laboratory. He published several studies in different fields of microbiology, including bacteriology, virology, and mycology. He has a special interest in bacterial infections and antimicrobial resistance.

Moussa Al Rufayie
Hillingdon Hospital, London, United Kingdom

An unusual presentation of a case of syphilitic posterior uveitis

Purpose: To highlight different presentations of syphilitic uveitis and macular pathologies.

Setting: Medical retina clinic in Western Eye Hospital, Imperial College Healthcare NHS Trust.

Methods: We studied a case of unusual presentation of syphilitic uveitis. A 51 year old male patient presented to our accident and emergency with a 5 day history of seeing a grey shadow with flashes of light in the left eye, he was diagnosed as haemorrhagic Posterior Vitreous Detachment (PVD). Maculae were flat then with some reticular changes over the Retinal Pigment Epithelial (RPE) layer on Optical Coherent Tomography (OCT) of the left eye only. Two weeks later we saw him in our clinic, he was then complaining of acute drop of the vision in the left eye, he has no medical history, he denies any sexual activity, denies taking any medications or supplements. On examination his vision was 6/6 in the right eye, 6/7.5 in the left eye, normal intraocular pressure, anterior segment exam was unremarkable, fundus of the right eye showed pale macula with haemorrhagic spots and subretinal inflammatory areas and fluid, left eye macula was pale with reticular RPE changes. Fundus Fluorescein Angiography (FFA) showed disc leakage in both eyes with periphelbitis at the macula and on the peripheral retinae in both eyes, there was transillumination of the choroidal fluorescein in the macular areas of both eyes.

Results: We sent him for general blood tests including uveitic work-up, all came back negative except for serology test for syphilis was positive, RPRGU was 1:64. We referred the patient to the genitourinary medical clinic in our trust for further management.

Conclusion: Uveitis can have an atypical presentation of macular haemorrhage and PVD, careful history taking, and a thorough exam could highlight uveitis of any kind. Treatment options are different with different kinds of uveitis.

Financial Disclosure: No Financial Interest.

Syphlitic Pan: Uveitis.

Audience Take Away Notes

- **Recognizing Atypical Uveitis:** Identify unusual signs like macular hemorrhage and PVD
- **Comprehensive History and Examination:** Importance of detailed history and thorough examination in diagnosis
- **Interdisciplinary Referral:** Referral to specialised clinics for comprehensive care
- **Research and Teaching Implications**: Foundation for further research and teaching on atypical uveitis
- **Enhanced Diagnostic Protocols**: Include serology tests for syphilis in the uveitic work-up

Biography

Dr. Moussa Al-Rufayie is a dedicated medical professional from the United Kingdom, having graduated with an MBBS from Imperial College London. He also completed an intercalated BSc in Business Management at Imperial College London. Currently practising in the NHS in London, Dr. Al-Rufayie has gained extensive experience through various jobs in ENT, ophthalmology, paediatrics, geriatric medicine, emergency general surgery, and colorectal surgery. This diverse background has equipped him with a comprehensive understanding of patient care across multiple specialties.

Muhammad Amjad Khan*, Mumtaz Khan, Afreenish Amir, Amna Ali, Tarbia Aamir, Muhammad Waleed, Rabia Tabassum, Kiran Nisa, Aamer Ikram

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Overcoming the challenges of drug resistant fungal infections in developing countries

Over the past few decades fungal infections have emerged as a constantly on the rise global health challenge, resulting in approximately 1.7 million deaths every year. Moreover, the long-term therapeutic application and prophylactic use of antifungal drugs in high-risk patients has promoted the emergence of (multi) drug-resistant fungi, including the extremely virulent strain Candida auris. Therefore, fungal infections have become increasingly severe and an even bigger challenge for developing countries which are more vulnerable to its impacts. High burden of infectious diseases, poverty, weak governance and health systems, and low awareness remain major challenges in the fight against AMR leading to increased prevalence of HAIs including fungal infections, and superbugs like C. auris. Infection-Prevention-Control (IPC) is a key to enhancing healthcare outcomes against such challenges.

National Institutes of Health (NIH)-Pakistan with the support of CDC, initiated a study to improve the early diagnosis and surveillance of C. auris. The study focused on capacity building in laboratory diagnostics, IPC strategies and implementing robust learning data dashboards with provincial stakeholders. After thorough Gap-assessments through site visits and detailed mixed methods at 12 sentinel sites, representing all regions/provinces of Pakistan. Using a phase-wise approach, capacity at each site was enhanced by providing hands-on-trainings and materials to enhance fungal diagnostics, IPC and surveillance of fungal infections at the healthcare facilities.

In two years following the launch of the study, in Microbiology Diagnostics all 12 sites initiated reporting fungal infections to NIH and 5 of the sites have been enabled in confirming their diagnosis independently apart from being the part of the collective reporting system. Data dashboards were developed and implemented ensuring robust data collection and sharing from all sites. A total of 1323 samples have been received at NIH for final identification indicating different fungal pathogens in isolates by March '2024 out of which 21 have been C. auris. Moreover, IPC programs have been initiated at 3 of the sites where they previously did not exist and capacity building activities have been performed to improve the IPC programs at all sentinel sites particularly in terms of outbreak preparedness against fungal pathogens (particularly C. auris).

C. auris is a multidrug-resistant pathogen and is prone to misidentification by available conventional methods, it becomes difficult to detect and manage C. auris infection and also limits the therapeutic options against this deadly pathogen. The emergence of multidrug-resistant C. auris advocates and amplifies the vigilance of early diagnosis and appropriate treatment and management of fungal infections, particularly in developing countries to prevent outbreaks and adverse healthcare outcomes. Through this study a successful and sustainable model for National Fungal Disease Surveillance System (NFDSS) has been devised to enable rapid diagnosis and surveillance of prevalent fungal pathogens throughout Pakistan. Antimicrobial stewardship involving robust IPC methods should be established in hospitals to ensure judicious and appropriate antimicrobial use. Adoption of these strategies will assist developing countries overcome their increased vulnerability to growing AMR.

Audience Take Away Notes

- First of all it highlights the importance of Fungal Pathogens which are generally ignored by healthcare practitioners and prophylactic use of antifungal drugs in high-risk patients leading the emergence of (multi)drug-resistant fungi
- Moreover, it presents a functional and sustainable model for diagnosis, surveillance and management of prevalent fungal pathogens for developing countries which if adopted would not only aid in providing information on burden of fungal infections but also would help combat AMR through targeted treatment and management
- The Model shared also includes robust IPC Measures linked to surveillance to prevent healthcare outbreaks contributing to overall patient and healthcare worker safety

Biography

Dr. Muhammad Amjad Khan, has over 42 years of experience as a Health care professional. He has done fellowship training from University of Kentucky in cardiothoracic Transplantation Pathology and is a Harvard fellow in Infection Control and designing of high containment facilities. He has re-designed and upgraded numerous labs and Tertiary care hospitals all over Pakistan in the Government for management of drug resistant TB cases. Since 1985 he has trained innumerable laboratory staff and healthcare workers in Infection Control and has many publications to his credit. At present he is serving as Coordinator CEOH-NIH Islamabad.

Musa Corr[1]*, PeterAdewuyi[1], Ousman Badjie[2], Lamin Badjie[2], Bah Sadou[2], Mustapha Bittaye[3]

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Have the Gambia met the enrolment target for HIV, the Gambia, 2017-2021?

Background: In 2016, the United Nations General Assembly's Political Declaration on Ending AIDS committed countries to the 90–90–90 targets, which aim to bring HIV testing and treatment to many people living with HIV by the end of 2020. Globally as of 2019, 81% of people living with HIV knew their HIV status, and more than two thirds (67%) were on antiretroviral therapy (ART). This study assessed if HIV/AIDS intervention in The Gambia met the enrolment target between 2017-2021.

Method: We conducted a study among those who sort healthcare at the 45 HIV sentinel sites in The Gambia. The data we extracted from the DHIS 2 included demographic information, HIV test results (positive/negative), and treatment enrollment. We conducted univariate and bivariate analyses.

Results: Of the 177,832 persons tested for HIV, 14,863 (8.4%) were positive. Of the 14,863 persons who were positive for HIV, 56.7% enrolled in HIV treatment. Of the positive, female was 60.9%, Western 1&2 had 66.9% and ages <49 years formed 15.5%. Of those who enrolled, 60.9% are female, 68.1% were from Western 1&2 regions and 70.7% were age 15-24 years. Enrolment was higher among 24 years and below (67.3%) as compared than 25 years and above (53.8 %) [PR=1.7 (95% CI 1.6148-1.9411)]; females (60.6%) enrolled more than males (48.4%) [PR: 1.6 (95% CI 1.5344-1.7517)]; and Western 1&2 regions (68.1%) enrolled for treatment more as compared to other regions (39.9%) [PR: 1.1 (95% CI 1.0272-1.0929)]

Conclusion: The Gambia did not meet the 90% target for enrolment into treatment. Further studies need to be conducted to know why there were low enrolment among males, ages less than 25years and among those living in Western 1&2 Regions. We recommend to National AIDS Secretariat to develop innovative strategies to motivate positive cases to enroll in treatment.

Keywords: HIV/AIDS, Enrollment, positive tests, The Gambia

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Clinical characteristics and outcomes of breakthrough COVID 19 infection among vaccinated patients admitted in a tertiary hospital

Background: Vaccination across countries against COVID-19 have shown to be effective against infection and mortality in different settings. However, recent data describe breakthrough COVID-19 infection among vaccinated individuals. Risk factors and clinical characteristics have been reported in several international settings, but local data are needed to characterize these infections and define correlates of breakthrough and infectivity.

Objectives: To establish the clinical profiles and outcomes of vaccinated patients with breakthrough COVID-19 infection requiring hospitalization in a tertiary hospital.

Methodology: A retrospective cross-sectional study was conducted in a tertiary hospital with 123 patients' record reviewed between December 2021 to December 2023.

Results: Majority of patients were elderly, female sex, married, and with comorbidities. Of the comorbidities, Hypertension, Diabetes Mellitus type II and Chronic Kidney Disease were predominant. Fever was the most prominent symptom but significantly reduced on patients with booster dose. Majority of patients had no infiltrates on chest Xray and no evidence of hypoxemia, with higher probability of these findings among those with booster dose. qSOFA scores of <2 was seen in both study groups. Low to moderate viral load were seen among patients who received booster dose compared to those with primary series alone, regardless of the disease severity. Disease severity on admission were mostly mild to moderate cases. Inflammatory markers such as CRP, ferritin, procalcitonin, ESR, and LDH were shown to be of normal value among vaccinated patients. Low Procalcitonin (PCT) level showed a significant association in patients who received booster dose. Most common complications noted were bacterial pneumonia, acute kidney injury and sepsis but the probability of getting these complications is lesser in patients receiving at least one booster dose compared to those with primary series. Majority of patients had less than 21 days hospitalization with improved disposition upon discharge. Hospital-acquired pneumonia in five patients and myocardial infarction in one patient were the causes of death.

Conclusion: Majority of breakthrough infections were seen among patients withincreasing age, female sex, and presence of comorbidities. Disease severity on admission were mild to moderate, with very few presenting severe or critical disease. Risk factors noted with high disease severity and with poor outcomes were increasing age and presence of comorbidities, elevated inflammatory markers on admission, and high qSOFA scores, regardless of whether booster doses were received or not. There was no significant correlation noted on vaccination status and the clinical profiles of breakthrough COVID-19 infection.

Keywords: COVID-19 Breakthrough Infection, Clinical Presentation and Demographics, Outcomes.

Biography

Dr. Nadine D. Bacalangco Suerte completed her bachelor's degree in Biological Sciences at West Visayas State University-Magna Cum Laude in 2014 and finished her post graduate degree in Doctor of Medicine on the same institution in 2018. She completed her residency training inInternal Medicine in December 2023. During her residency training, she was able to receive awards related to research and was a co-author in a study published in European Society of Cardiology and Interventional Cardiology: reviews, research, resources.

Nawal AlKaabi[1]*, Jehad Saleh Abdalla[1], Suad Hannawi[2], Dima Ibrahim[3], Mustaqeem Siddiqui[4], Hussni Al Hateeti[4], Salah Eldin Hussein[5], Mohammed Bhyat[5], Eva Turgonyi[6], Ahmad Bdair[6], Sana Qamar[6], Sabada Dube[7], Wael El Hallak[8]

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Clinical use of AZD7442 as pre-exposure prophylaxis for COVID-19 in the real-world setting – interim analysis of the evolve study

Background: In response to the COVID-19 pandemic, innovative treatments and preventive measures continue to be pivotal. This interim analysis examines the use of AZD7442, a Long-Acting Antibody (LAAB), as a Pre-Exposure Prophylactic (PrEP) agent against the SARS-CoV-2 virus, aiming to contribute valuable insights into its clinical outcomes in United Arab Emirates and broader applicability.

Methods: This is a multicenter, single-arm, observational prospective study aimed to describe the real-world use of AZD7442 as PrEP against SARS-CoV-2. 408 (87.2%) of the 468 total eligible participants received an initial dose of 600mg, whereas 60 participants (12.8%) received 300mg dose. Participants were followed for up to 12 months to describe COVID-19-related outcomes (medically attended COVID-19, hospitalization, and death), healthcare resource utilization, and quality of life (PROMIS Global-10 for assessing Global Physical Health (GPH), Global Mental Health (GMH) & EQ-5D UK Crosswalk utility). Moreover, data on AEs were collected.

Results: The majority of participants were males (60%) and of Arab ethnicity (73%). Most participants (68.4%) had prior SARS-CoV-2 infection, and the majority (91.5%) were vaccinated with at least one dose of SARS-COV-2 vaccine, 90%, 79%, with two and three doses, respectively, at the study's onset. Following AZD7442 administration, the infection rate of SARS-CoV-2 stood at 3.6%, with 1.7% requiring medical intervention or hospitalization. No COVID-related ICU admissions or COVID-19-related deaths were reported. No adverse events leading to drop-out were reported. Post-enrollment, participants exhibited improvements in both GPH and GMH, as evidenced by T-score elevations at 1, 3, and 6 months. Additionally, EQ-5D UK Crosswalk utility scores displayed marked enhancements in overall health quality following enrollment.

Conclusion: This study underscores the use of AZD7442 as COVID-19 PrEP in a real-world context. The data reveal its utility across a diverse population, including immunocompromised individuals and those with prior vaccination. Notably, it also highlights improvements in physical and mental health post-administration, reinforcing the potential of monoclonal antibodies in COVID-19 prophylaxis.

Funding Statement: This study was funded by AstraZeneca FZ LLC.

Audience Take Away Notes

- The study shows a real-world practice of using mono-clonal antibody AZD7442 as COVID-19 PrEP; the data reveal its utility across a diverse population, including immunocompromised individuals and those with prior vaccination
- This data will help physicians treating immunocompromised patients demonstrate the role of passive immunization in PrEP and provide more confidence in using upcoming generations of long-acting antibodies in COVID-19 PrEP
- Research that other faculty could use to expand their research or teaching
- 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

Biography

Dr. Nawal Al Kaabi is a pediatrician and infectious diseases consultant. She has been the Chair of the Seha Infectious Diseases and Infection Control Council since 2012. She served as the Chief Medical Officer at Sheikh Khalifa Medical City and Chair of the Clinical National COVID-19 Committee. Dr. Al Kaabi graduated from the United Arab Emirates University and completed her Fellowships in Pediatrics and Pediatric Infectious Disease in Canada. She is an American Board-Certified Pediatrician, trained in global research at Harvard University, and American Board-certified in Quality. She obtained a Certified Physician certificate from the American Association for Physician Leadership.

Netty Santoso, PhD

Department of Pathology, Ohio State University College of Medicine, Columbus, OH, United States

Metabolic reprogramming of KSHV infection and tumorigenesis

Kaposi’s Sarcoma-Associated Herpes Virus (KSHV), one of human gamma-herpesviruses, is a large double-stranded DNA virus that establishes long-term persistent infection. Primary infection of KSHV is usually asymptomatic, but its infection causes cancer under immunocompromised states, such as Acquired Immunodeficiency Syndrome (AIDS) and organ transplantation. KSHV highly associates with certain AIDS-defined tumors. KSHV causes Kaposi’s Sarcoma (KS), the most common AIDS-defined soft tissue tumor. KSHV is also the etiologic agent of Primary Effusion Lymphoma (PEL), a rare but aggressive B-cell Non-Hodgkin Lymphoma (NHL) that primarily affects HIV-infected individuals as well. Additionally, KSHV associates with the Multicentric Castleman's Disease (MCD), a distinct lymphoproliferative disorder that most often presents in HIV-infected individuals, which can further lead to the rise of large B-cell lymphoma. There are currently no effective therapies to treat KSHV-associated, AIDS-defined tumors, nor eliminate persistent KSHV infection. Our recent results showed that polyamine biosynthesis and its downstream eIF5A hypusination are required for KSHV viral infection and tumorigenesis, and that in return KSHV regulates the dynamics of these metabolic processes. Furthermore, hyp-eIF5A is required for translation of key KSHV viral proteins, including LANA that is required for KSHV viral episome tethering and its persistent infection. In addition, we demonstrated that certain FDA-approved drugs targeting these metabolic processes are effective to block KSHV persistent infection and growth of KSHV-infected tumor cells. These findings are novel, as it has never been examined that the polyamine-hypusine-eIF5A (hyp-eIF5A) pathway plays a role in regulating KSHV viral infection and tumorigenesis previously.

Audience Take Away Notes

- The audience will learn the polyamine-hyp-eIF5A pathway as a novel host regulatory mechanism of KSHV infection and tumorigenesis
- The audience will be introduced to the therapeutic potential of polyamine-hyp-eIF5A inibition for treating KSHV infection and KSHV+ tumors
- Gives a new insight into mechanisms of KSHV pathogenesis

Biography

Dr. Santoso studied Pharmaceutical Sciences at Purdue University, USA and graduated in 2005. She then pursued research by joining the group of Prof. William Guggino at Johns Hopkins University to study genetic kidney diseases and received her PhD degree in 2011. She joined Dr. Raju Kucherlapati’s group at Brigham and Women’s hospital for a postdoctoral fellowship, where she was involved in TCGA consortium. She obtained the position of an Assistant Professor at the Ohio State University in 2021. Her research has been funded by US Army, NCI, NIDCR. She has published 29 research articles in journals such as Nature, Cell, Science Advances, Nucleic Acid Research, PLos Pathogens.

Nicole Abdullah*, Oona Salomao Erdmann, Sophia Trompczynski Hofmeister, Nicole Kovalhuk Borini, Beatriz Essenfelder Borges, Francisco Beraldi de Magalhaes

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Mechanisms of SARS-CoV-2 neurovirulence in chemosensory dysfunction and prognosis of affected patients: Systematic review

Introduction: Severe acute respiratory syndrome coronavirus-2 virus (SARS-COV-2) was officially identified on January 2020 following investigations of pneumonia cases of unknown origin. Clinical presentation presents variations in symptom duration, severity, and complications. Among the most frequent symptomatic manifestations are chemosensory dysfunctions such as anosmia and ageusia. Also, it may influence an individual's nutrition and culminate in disorientation and social withdrawal. Therefore, the scope of this review is to identify the neurovirulence mechanisms related to chemosensory dysfunction presented by SARS-COV-2 and to evaluate how the remission of olfactory symptoms and their prognosis develop in COVID-19 patients.

Methods: A systematic review of the literature was made, using databases such as PUBMED, VHL, MEDLINE, LILACS, and ScienceDirect. The keywords were consulted on DECS/MESH: (COVID-19 or SARS-COV-2) AND (ANOSMIA OR AGEUSIA) AND (MECHANISM OR DISORDER).

Results: They were elucidated according to the PRISMA methodology. In addition to the flow chart, a table was developed with all the articles included in this review, their respective objectives, study methodology, samples, and results. 13 articles were included.

Discussion: The pathogenesis of SARS-COV-2-related chemosensory dysfunctions includes the destruction of the Olfactory Receptor Neurons (ORNs). The damage results from the action of toxic inflammatory factors, due to an inflammatory storm, such as TNF-α, Interleukin-1B (IL-1B), IL-6 and infiltrating inflammatory cells. Recent histopathological studies showed findings such as leukocyte infiltration in the lamina propria, focal atrophy of the olfactory mucosa, and neuronal fibres in the acute phase of infection. When analysing a patient with persistent anosmia, a massive disruption of the olfactory epithelium and mild chronic inflammatory infiltrate were found. Studies point out that IL-6 acts as an endogenous substance that regulates the olfactory neuronal activity and directly inhibits olfactory function. Both the peripheral and central actions of IL-6 contribute to the pathogenesis of anosmia and ageusia. Peripheral IL-6 acts on the levels of infected cell receptors. Central IL-6 acts at the level of the intermediate taste and smell pathways, especially in the thalamus. The taste (ventral posteromedial nucleus) and smell (dorsomedial nucleus) pathways converge. These nuclei are located close to the hypothalamus, which houses the thermoregulatory centre, an important target of IL-6. In a sample of 67 patients diagnosed with COVID-19, 65.7% reported olfactory dysfunction alone and 8.95% reported an association between olfactory and taste dysfunction. Most patients restore smell perception within 1–2 weeks, likely due to the differentiation of progenitor cells into mature ORNs. However, opposing arguments state that this period is too short to achieve complete neuronal regeneration. A prospective randomised multicentre study demonstrated the effectiveness and speed of olfactory function recovery with corticosteroids therapy in patients with long-term severe olfactory disturbances post-COVID.

Conclusion: Thus, the mechanisms of neurovirulence of SARS-COV-2 involves ACE-2 activity and injury to the olfactory bulb are triggered by the inflammatory cascade with the action of pro-inflammatory cytokines. The prognosis of COVID-19 infection is directly related to the patient's comorbidities but tends to be better in patients who present with anosmia and ageusia early. Female patients were more affected.

Audience Take Away Notes

- The audience will gain a better understanding of the pathophysiological aspects of anosmia and the possibilities of providing more attentive care to patients with the condition. Given the higher prevalence of post-COVID-19 sequelae, where anosmia can last for months or even ad eternum
- Due to the persistence of COVID-19 cases, even after worldwide vaccination campaigns, it is essential for infectious disease doctors to deal with neurosensory sequelae and adequate psychological management for patients suffering from this comorbidity. As well as encouraging a wider range of research in this area
- This area allows us expand studies in the field of prophylaxis, drug treatment and holistic support for COVID-19 patients and those with post-infection sequelae
- With the expansion of studies around pharmacological management of post-COVID-19 sequelae and the increase in reports of patients struggling to overcome the new comorbidity, this study will help professionals to better understand the context of patients in their situation and solidify new pharmacological aspects that can improve the comorbidity

Biography

Miss. Nicole Abdullah is a last year medical student from Faculdades Pequeno Principe, Curitiba, Brazil. Had already published articles correlated with infectious diseases, such as biofilm formation in cardiac devices and nosocomial infections. This research was guided by masters in Infectious Disease and Microbiology: Dr. Francisco Beraldi Magalhaes and Dr. Beatriz Essenfelder Borges.

Nouf Alaboud[1,2]*, Yogini Jani[1,2], Bryony Dean Franklin[1,3]

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Implementing an electronic screening tool to improve antimicrobial prescribing decision-making for paediatric. Patients with suspected sepsis at an academic hospital in England: A before and after study

Background: Sepsis is one of the most common leading causes of death in paediatric patients worldwide. The WHO has defined sepsis as "a life-threatening organ dysfunction caused by a dysregulated host response to infection". Early recognition of the sepsis plays a critical role in reducing mortality rate. Electronic Health Record systems (EHR) are powerful platforms on which screening tools with Clinical Decision Support Systems (CDSS) can be developed and implemented to expedite the sepsis recognition process.

Aim: To examine the impact of using Paediatric Sepsis Screening Tool (PSST) on antimicrobial prescribing decision-making in paediatric patients with suspected sepsis in an academic hospital in England.

Method: Uncontrolled before and after study using data extracted from the EHR system. We included all paediatric patient (≤ 16 years old) who admitted to the Emergency Department (ED) with suspected sepsis from September 2021 to February 2023. Data analysis involved descriptive and comparative statistical analysis were performed by using SPSS version 29.0.

Results: Out of 27,475 ER admissions 820 (3%) patients were recognised as suspected sepsis. In total, 447 (55%) were male, 668 (81%) aged 5 years or less, 301 (37%) admitted in the Autumn, 507 (62%) has fever as chief complaint, 370 (45%) has prescribed antimicrobial medications, penicillins and cephalosporins were the most common used antibiotics (n=194, 52% and n=132, 36%, respectively). The PSST has significantly delayed the screening of sepsis (mean difference=232 minutes, P=<0.001), and prolonged stay at the ED (mean difference=98 minutes, P=<0.001), decreased sepsis documentation rate (Percentage difference= 16%, P=<0.001).=

Conclusion: The utilisation of the PSST has been associated with significant delays in screening patients with suspected sepsis, prolonged stay at the ED, and decreased sepsis documentation rate, highlighting the need for frequent follow-ups with the end users to ensure its potential effectiveness. One major challenge in evaluating screening tools and CDSS within EHRs is the lack of standardised guidelines on how and when to conduct evaluations, leading to inconsistency in evaluation methods and results, making it difficult to compare the effectiveness and impact of different CDSS designs. Therefore, further studies are needed to develop evaluation frameworks and guidelines for EHRs.

Audience Take Away Notes

- Our study shows example of the use of screening tool within EHR system for paediatric patients, its impact, consequences and further recommendations for improvement
- They will clearly notice a major challenge in evaluating screening tools and CDSS within EHRs
- Yes, because most of the hospital nowadays are using integrated EHR systems which has CDSS, that makes our result applicable in most of these hospitals

- It will state the current situation, show the gap in practice and also it will provide suggestions for improvement
- Yes, it will show the needs for evaluation frameworks and guidelines for EHRs

Biography

Nouf Alaboud is a registered clinical pharmacist and academic lecturer from Saudi Arabia. She completed a PharmD and a Master in clinical pharmacy from King Saud University. She is currently pursuing a PhD in health informatics at UCL School of Pharmacy. Her research interest is to study the electronic prescribing system's design features and information content and their impact on prescribing decisions.

Parvin Dehghan*, Raheleh Mostafavi Youssof Abad, Mehrnoush Maherolnaghsh

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Evaluation of the antifungal activity of metabolites produced by soil actinomycetes on the candida species isolated from candidemia

Background: Excessive and inappropriate use of antibiotics can lead to increased antibiotic-resistant strains of microorganisms. Actinomycetes, a versatile microbial group, are well known for producing important metabolites such as antibiotics, enzymes, herbicides, and anticancer substances. This study aimed to identify the bioactive actinomycetes isolated from the soil against Candida species separated from the blood of patients with candidemia.

Materials and Methods: In this study, 12 soil samples were collected from the southwest of Iran. The soil samples were cultured on a special culture medium (Starch Casein Agar) to look for desired actinomycetes. Antifungal activity of seven species of actinomycetes with the best anticandidal activity were chosen by modified overlay agar. Five species of Candida isolated from candidemia patients including Candida albicans, C.glabrata, C.lusitania, C. tropicalis and C. parapsilosis were used for antifungal activity using well diffusion agar. Seven actinomycetes with the best bioactive effects were identified by sequencing of 16SrDNA gene. This gene sequence is then compared by the BLAST program to the gene sequences in the NCBI's databases.

Findings: From the total of 12 soil samples 52 actinomycetes were identified, among them seven showed more bioactive potency against Candida isolates. After doing sequencing, four genera of actinomycetes were identified. Crossiell with four species was the most abundant actinobacteria. Streptomyces, Saccharothrix, and Amycolatopsis were the rest genera of them (one of each).

Two isolates of the genus Crossiella and one isolate of the genus Saccharothrix deserti showed more inhibitory effects on C. parapsilosis. So Crossiella cryophila inhibited this Candida with a halo diameter of 42.5± 13 mm, on the contrary, Streptomyces showed a weak inhibitory effect on all the rest tested yeasts but on the C. parapsilosis with a halo diameter of 35 ±17.3 mm ($P \geq 0/05$). Amycolatopsis alba significantly showed a weaker Antifungal effect on C. lusitana compared to the other species of Candida ($P \geq 0/05$).

Conclusion: The results showed that the soil of southwest Iran is rich in bioactive actinomycetes against pathogenic Candida species that are capable of producing new antifungal metabolites.

It needs more wide investigations to evaluate the metabolites of these new species of actinomycetes. So it is possible to introduce a step towards the acquisition, production, and development of broad-spectrum and effective antimicrobials in the treatment of infectious diseases caused by resistant microorganisms.

Audience Take Away Notes

- They learn more about natural metabolites with anti-fungal effects on different kind of Candida species; the etiologic agents of candidemia
- They will find the interaction of Microorganisms on each other. This lecture will open new ways and new options for search antimicrobial components from the actinomycets around us
- The scientists from biochemistry or pharmacy departments will use to expand their research on this

subject. Excessive and inappropriate use of antibiotics can lead to increased antibiotic-resistant strains of microorganisms

- I believe we are on the first steps of producing new antifungals and we need to cooperate with the other scientists to solve the problem of antifungal drugs against resistant pathogenic microorganisms
- There are insufficient antifungal drugs and also not all the yeasts respond equally to antifungals. Today finding new antifungals is critical
- List all other benefits
    - The soil is rich in bioactive actinomycetes against pathogenic Candida species that are capable of producing new antifungal metabolites
    - It needs more wide investigations to evaluate the metabolites of these new species of actinomycetes. So it is possible to introduce a step towards the acquisition, production, and development of broad-spectrum and effective antimicrobials in the treatment of infectious diseases caused by resistant microorganisms

Biography

Parvin Dehghan studied Medical Mycology at Tehran University of Medical Sciences (TUMS) in Iran. and graduated as MS in 1988. She then joined as instructor to Pathobiology Department in Isfahan University of Medical Sciences (IUMS). She was as lecturer and trained medical Mycology to different medical students. She received her PhD degree of Medical Mycology in 2007 at the TUMS. After raduation, she came back to IUMS and More than 30 post graduate thesis has been supervised by her up to present. She is full Professor at the present and has published more than 60 research articles in scientific journals.

Parvin Dehghan*, Iman Zareie, Hossein Yousofi Darani
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Determining the frequency of trichosporon species and tracking yeast in urine clinical samples using gold nanoparticles

Introduction: Timely identification and treatment of trichosporonosis is important due to the severity of pathogenesis and different treatment from candidiasis and as a result of its high mortality. In this study, in addition to determining the abundance of this fungus in clinical urine samples using past experiences in the function of gold nanoparticles, identification of this yeast based on serological methods for rapid detection of yeast in urine samples has been presented.

Methods: 249 samples of people suspected of urinary fungal infection were analyzed using morphological and molecular PCR-RFLP methods. Antigenic suspension was prepared from different species of Trichosporon. This mixture was injected with complete adjuvant to a healthy rabbit. After injecting 4 booster doses using incomplete adjuvant, blood was drawn from the rabbit. The anti-fungal antibody ability in the rabbit serum was confirmed using the ELISA method. Then the antibody was placed chemically on the surface of gold nanoparticles and the performance of the method was investigated.

Findings: C. glabrata and C. albicans were the most common yeasts isolated from the urine samples. Among isolated yeasts, 4 cases (1.6%) of Trichosporons pp. were reported. The sensitivity and specificity of the gold nanoparticle method in the identification of Trichosporon was determined to be 100%.

Conclusion: Abundance of urinary tract colonization due to Trichosporon was 1.6% during the study period. The results showed that if there is one Trichosporon yeast in five microliters of the urine sample, the mentioned method will be able to identify it within one minute through agglutination.

Audience Take Away Notes

- They learn which yeasts other than candida species can involved urinary tract. How much is the prevalence of Trichosporon in suspected individuals
- Identification and treatment of trichosporonosis is important due to the severity of pathogenesis and different treatment from candidiasis
- The scientist should be pay attention that trichosporon may also isolated from urine and this yeast is resistant to urinary candidiasis antifungals
- We used gold nanoparticle to find this yeast in urine rapidly
- Gold nanoparticles can help to track the trichosporon Yeasts rapidly. It can differentiate trichosporon from the other yeasts
- List all other benefits
    - o This method (agglutination using gold nanoparticles to find antigens) has been used on the blood samples suspected to candidemia in previous research and it was successful to track candida in blood samples

Biography

Parvin Dehghan studied Medical Mycology at Tehran University of Medical Sciences (TUMS) in Iran. and graduated as MS in 1988. She then joined as instructor to Pathobiology Department in Isfahan University of Medical Sciences (IUMS). She was as lecturer and trained medical Mycology to different medical students. She received her PhD degree of Medical Mycology in 2007 at the TUMS. After graduation, she came back to IUMS and More than 30 post graduate thesis has been supervised by her up to present. She is full Professor at the present and has published mor than 60 research articles in scientific journals.

Prof. P. R. Risenga
University of South Africa, South Africa

The lived experiences of HIV-positive young adults regarding adherence to antiretroviral treatment in Tshwane District, Gauteng

Human Immunodeficiency Virus creates disruption in the lives of individuals, families, organisations, and communities at large. The introduction of the antiretroviral treatment brought hope but also brought challenges, especially around the issue of adherence which is important for improved health outcomes. The study intended to gain an understanding of the lived experiences of HIV-positive young adults regarding adherence. The study setting was an antiretroviral clinic situated within a regional hospital in the Tshwane district.

The target population for this study was patients who were receiving antiretroviral treatment at the antiretroviral clinic situated in a regional hospital. The researcher drew a sample of 15 young adults who were on Antiretroviral Treatment (ART) from January 2019 to December 2020 and who defaulted but returned to care. Purposive sampling was used to select participants and the sample was determined by data saturation. A qualitative approach was utilised to conduct the study, using in-depth phenomenological telephonic interviews to collect data. All interviews were digitally recorded and transcribed. Thematic analysis was used to analyse the data.

The findings of the study revealed participants were knowledgeable about the importance of adherence of antiretroviral treatment. There were existing barriers which influenced disclosure, lack of support and difficulties of taking antiretroviral treatment. It was concluded that there is a need to intensify established programmes, encourage people to adhere to their antiretroviral treatment and on-going support and counselling. Understanding adherence patterns of young adults and factors that cause barriers to adherence may help design strategies that can strengthen adherence. Improved adherence results in improved outcomes, decrease opportunistic infections as well as HIV-related mortality.

Key Concepts: ART, HIV, and Adherence.

Biography

Prof. P. R. Risenga passed her Diploma in Nursing Science at the former Gazankulu Nursing College with distinction. Did her basic degree in Nursing, Honours Degree, and Master's degree at UNISA. Did a second master's degree: Masters for International Health Professions and Education: at Maastricht University in the Netherlands and a Doctoral degree at the University of Venda. Published 31 articles in accredited journals including five chapters book. Working at the University of South Africa as a Professor.

Pedro Plans Rubio*, Sofia Godoy, Joan Cayla, Angela Dominguez, Pere Godoy, Diana Toledo, Joan Pau Millet, Ignasi Parron

Public Health Agency of Catalonia, Department of Health of Catalonia, Barcelona, 08005, Spain, Ciber of Epidemiology and Public Health (CIBERESP), Madrid 28028, Madrid, Spain

Factors associated with non-adherence to Tuberculosis (TB) preventive treatment among adult contacts of pulmonary TB cases with latent tb infection in Spain

The aim of this study was to identify factors associated with non-adherence to Tuberculosis (TB) preventive treatment among contacts with latent TB infection for new cases of pulmonary TB cases reported in Catalonia in 2019–2021. All contacts aged 18 years or older with a latent TB infection who received a TB preventive treatment were included in the study. Multiple logistic regression analysis was used to detect the independent factors associated with TB preventive treatment non-adherence; a $p < 0.05$ was considered statistically significant. The percentage of non-adherence to TB preventive treatment found in this study was 23.7%. A multivariable logistic regression analysis determined that the following factors were significantly associated with TB preventive treatment non-adherence among adult contacts: “exposure at school or workplace” (aOR = 3.34), “exposure to an index case without laboratory confirmation of TB” (aOR = 2.07), “immigrant contact” (aOR = 1.81), “male gender” (aOR = 1.75) and “exposure duration < 6 h per week or sporadic” (aOR = 1.60. By contrast, the factor “short-term TB preventive treatment regimen” (aOR = 0.38) was significantly associated with a lower treatment non-adherence. Adherence to TB preventive treatment should be improved among adult contacts of TB pulmonary cases with latent TB infection by recommending short-term treatment regimens and by developing health education activities, with a greater focus on contacts with factors associated with treatment non-adherence.

Audience Take Away Notes

- The audience will know how the factors associated with non-adherence to TB preventive treatment among adult contacts with latent TB infection can be identified
- The audience will know the research strategy necessary to identify and assess the factors associated with TB preventive treatment adherence
- The audience will know the challenges that TB programs must overcome to improve adherence to TB preventive treatment among adult contacts with latent TB infection

Biography

Pedro Plans Rubio is responsible for Health Registries, Public Health Agency of Catalonia, Health Department of Catalonia, Spain. He received his MD from the School of Medicine, University of Barcelona; his PhD from the School of Medicine, University of Barcelona, his MSc in Health Economics from the School of Economics, University of Barcelona, and his MSc in Design of clinical and epidemiological studies from the School of Medicine, University of Barcelona. Specialist in Preventive Medicine and Public Health. Specialist in Labor Medicine. Member of the research group CIBER of Epidemiology and Public Health (CIBERESP), Instituto de Salud Carlos III, Madrid, Spain. Member of the research group “Pertussis transmission in Catalonia and Navarra”. Member of the research group “Global Burden of Metabolic Risk Factors of Chronic Diseases”. He has published more than 100 articles in scientific journals on the epidemiology of infectious diseases, epidemiology of risk factors for chronic diseases and for infectious diseases, seroepidemiology, cost-effectiveness analysis of medicines and health programs, vaccination programs, and health policy. He has published more than 100 articles in scientific journals. He has published the book “Application of the cost-effectiveness of medicines and health programs in the health planning”, Elsevier, 2015. Editor-in Chief of Section “Vaccine Efficacy and Safety” of the journal Vaccines and Editor of several Special Issues of the journal Vaccines. Member of the Editorial Board of the journals Pharmacoeconomics Open.

Pedro Plans Rubio

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Adapted mRNA COVID-19 vaccines have a limited ability to establish herd immunity in the population against Omicron BA.1 and BA4-5 variants of SARS-CoV-2

The emergence of novel SARS-CoV-2 variants has raised concerns about the ability of COVID-19 vaccination programs to establish adequate herd immunity levels in the population. Adapted mRNA COVID-19 vaccines against BA.1 and BA.4-5 Omicron variants can provide a greater immunity against emergent SARS-CoV-2 variants than vaccines against the original variant. This study assessed the effectiveness of adapted vaccines in preventing SARS-CoV-2 infection and the ability of the adapted vaccines to establish herd immunity against emerging Omicron variants. Firstly, a systematic literature review was conducted to estimate the absolute Vaccine Effectiveness (aVE) in preventing SARS-CoV-2 infection using adapted vaccines targeting Omicron variants. Secondly, the ability of the adapted vaccines to establish herd immunity was assessed by taking into account the following factors: aVE, Ro values of SARS-CoV-2, and the use of non-pharmacological interventions (NPIs). The study found a meta-analysis based aVE in preventing severe disease and SARS-CoV-2 infection of 56–60% and 36–39%, respectively.

Nevertheless, the study found that the ability to block SARS-CoV-2 transmission was limited because they could not block the transmission of viruses with greater transmissibility. Firstly, the adapted vaccines could not establish herd immunity against the Omicron BA.1 and BA.4-5 variants without using Non-Pharmacological Interventions (NPIs). Secondly, the adapted vaccines could establish herd immunity only by achieving >80% vaccination coverage, using NPIs with greater effectiveness and when a 20–30% percentage of individuals were already protected against SARS-CoV-2 in the population. New adapted COVID-19 vaccines with greater effectiveness in preventing SARS-CoV-2 infection must be developed to increase herd immunity levels against emerging SARS-CoV-2 variants in the population and reduce the health impact of emerging SARS-CoV-2 variants.

Audience Take Away Notes

- The audience will know how vaccines can prevent and block transmission of infectious agents
- The audience will know what are the critical parameters that must be monitored to assess the ability of vaccines to prevent severe disease and infection
- The audience will know the challenges that COVID-19 vaccination programs must overcome to establish herd immunity against emerging SARS-CoV-2 variants in the population

Biography

Pedro Plans Rubio is Responsible for Health Registries, Public Health Agency of Catalonia, Health Department of Catalonia, Spain. He received his MD from the School of Medicine, University of Barcelona; his PhD from the School of Medicine, University of Barcelona, his MSc in Health Economics from the School of Economics, University of Barcelona, and his MSc in Design of clinical and epidemiological studies from the School of Medicine, University of Barcelona. Specialist in Preventive Medicine and Public Health. Specialist in Labor Medicine. Member of the research group CIBER of Epidemiology and Public Health (CIBERESP), Instituto de Salud Carlos III, Madrid, Spain. Member of the research group "Pertussis transmission in Catalonia and Navarra". Member of the research group "Global Burden of Metabolic Risk Factors of Chronic Diseases". He has published more than 100 articles in scientific journals on the epidemiology of infectious diseases, epidemiology of risk factors for chronic diseases and for infectious diseases, seroepidemiology, cost-effectiveness analysis of medicines and health programs, vaccination programs, and health policy. He has published more than 100 articles in scientific journals. He has published the book "Application of the cost-effectiveness of medicines and health programs in the health planning", Elsevier, 2015. Editor-in Chief of Section "Vaccine Efficacy and Safety" of the journal Vaccines and Editor of several Special Issues of the journal Vaccines. Member of the Editorial Board of the journals Pharmacoeconomics Open.

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A case report of a 22 year old male diagnosed with SLE, with concomitant infections of COVID 19 moderate disease and HIV-AIDS

Background: As the world presently navigates the coronavirus disease 2019 (COVID-19) pandemic, there is a growing need to assess its impact in patients with underlying immunocompromised states, including autoimmune rheumatic diseases, such as Systemic Lupus Erythematosus (SLE), and HIV. Patients with SLE and People living with HIV (PLWH) are unique populations, when considering the risk of contracting COVID-19 and infection outcomes.

Clinical Case: We report a rare case of a 22 year old male, newly diagnosed with COVID 19 moderate disease, SLE in flare, and HIV AIDS, at the same time, in one hospital admission. He initially experienced gradually progressive symptoms of easy bruisability with associated persistent bicytopenia (anemia and thrombocytopenia) and leukocytosis, despite oral corticosteroids, with nonproductive distressing cough, undocumented low grade febrile episodes, and unintended weight loss, thus appropriate referrals to both hematologist and rheumatologist were done. ANA IF titre was significantly elevated, and was managed as Interstitial Lung Disease with Mycophenolate Mofetil, outpatient basis, with relief of symptoms. However, recurrence of previous nonspecific signs and symptoms with accompanying abdominal pain, prompted hospital admission. After a multidisciplinary approach to management of this patient, he was discharged well.

Conclusion: In this report, we highlight the overlapping immunopathogenic mechanisms of COVID, SLE, and HIV AIDS, and how it could provide insight into immune responses occurring between SLE and severe cases of viral infections, as well as it might preempt PLWH about the potential of COVID to affect them in various ways, including the increased risk of COVID-19 acquisition and interruptions of their treatment and care.

Keywords: COVID 19, SLE, HIV AIDS, Immunopathogenic Mechanisms.

Audience Take Away Notes

- This case will show us the impact of COVID 19 in patients with underlying immunocompromised states, including autoimmune rheumatic diseases, such as Systemic Lupus Erythematosus (SLE), and Human Immunodeficiency Virus (HIV)
- This case emphasizes the uniqueness of special population (Patients with SLE and People living with HIV (PLWH)), in terms of the risk of contracting COVID-19 and disease outcomes, hence helping the health care providers in innovating and individualized yet holistic treatment strategies for such patients
- This case will provide an avenue for further researches and studies on the convergence of the immunopathogenesis of COVID 19, or other viral infection, SLE and other autoimmune diseases, and HIV

Biography

Dr. Petersian Alcazaren graduated from West Visayas State University- College of Medicine in 2018, and acquired her license as a physician after passing the Philippine Physician Licensure Examination last September 2019. She then proceeded to a 3-year residency training in Internal Medicine at West Visayas State University-Medical Center, which she completed last December 31, 2022. She then served as the Chief Resident for Clinical Affairs of the department from January 1, 2023 to December 31, 2023. She has several case reports authored and co-authored which were published last 2023 in some international journals, and were also presented in two international research fora on Rheumatology.

Petersian M. Alcazaren*, MD; Tracy Roz P. Mallorca, MD; Lina Amsua, MD; Marie Grace Dawn T. Isidro MD; Aretha Liwag, Helmar Soldevilla, MD

Department of Internal Medicine, West Visayas State University Medical Center, Iloilo City, Philippines

Factors affecting the outcomes of patients with Coronavirus Disease (COVID-19) patients admitted in a tertiary hospital in Iloilo city: A retrospective study

Background: Covid-19 is a viral respiratory illness caused by SARS-CoV-2, confirmed with RTPCR testing. Considering the heterogeneity of clinical picture of COVID-19 disease, and the threats of its variants, the review of current clinical data and outcome of available management strategies will have an impact on future management and recommendations in the local setting.

Objective: This study generally aimed to determine the factors affecting the outcomes of COVID-19 patients admitted in a tertiary hospital in Iloilo City. Specifically, this study aimed to describe the clinicodemographic profile as to severity, outline the baseline diagnostic results, and describe the management strategies of COVID- 19 confirmed cases, determine the distribution of the disease severity as to length of hospital stay, complications, discharge outcomes, and identify significant associations between variables.

Methodology: This retrospective cross-sectional study involved RT-PCR confirmed COVID- 19 cases aged 19 years old and above admitted in a tertiary hospital from January to December 2021. The data were obtained from chart review. Respective statistical tools were used to outline the variables of this study and to determine significant differences between variables, across different groups. A 5% level of significance was used.

Results: There were 229 patients enrolled in this study. Among variables, age, sex, day of illness, and presence of comorbidities, were significantly related to disease severity. Severe and critical cases administered with different management strategies tend to have longer hospital stay, > 10 days, compared with those who did not receive treatment. Mild (28%) and moderate (36%) COVID cases improved or recovered more than more severe cases. Patients with severe disease (50%) at baseline experienced more complications, which are primarily acute respiratory distress syndrome (14.4%), acute kidney injury, (6.1%) and steroid- induced hyperglycemia (3.5%). Patients with lower oxygen saturation (58.2%) and PF ratio (59.7%), higher values of inflammatory markers, and those with infiltrates on their chest X-ray (36.1%) upon admission, were significantly noted to have higher risk of acquiring complications.

Conclusion: Patients who belonged to the higher age group, males, with longer days of illness, and with comorbidities, with lower oxygen level and PF ratio, elevated levels of serum inflammatory markers with findings of infiltrates on chest X-ray, were likely to have a more severe disease, and experienced statistically significant complications. The number of days of illness, and disease severity were also found to be significantly related to the occurrence of complications, as well as administration of various management strategies. Severe and critical patients were significantly identified to have received several management strategies, hence, had higher average hospital stay. Lastly it has been found out that disease severity and occurrence of complications were significantly associated with discharge outcomes. Most patients, regardless of severity at baseline improved, and those with more severe disease on baseline developed complications.

Audience Take Away Notes

- **Healthcare providers:** The results of this study will give a clearer picture of the corresponding outcomes of patients based on their initial characteristics during their admission in the institution. It will improve the health care workers' decision on requesting evidence-based diagnostic tests and providing strategic management for the patients
- **Patients and their families**: The results of this study may help patients and their families understand the reason behind the diagnostics requested and the management administered by the healthcare team. Sufficient knowledge and understanding of these evidence-based practices may increase compliance to the diagnostic requests and prescribed therapeutic regimen
- **Research Community**: The results of this study will provide evidence- based data on the local epidemiological and clinical characteristics, and the management strategies utilized for patients with Covid 19, with their corresponding clinical outcomes. It may aide in formulating future recommendations
- **Policy makers and health officials**: The results of this study will help our policy makers and health officials in making evidence-based health education and scientifically sound regulations and recommendations concerning Covid 19 disease, to be provided to the locality

Biography

Dr. Petersian Alcazaren graduated from West Visayas State University- College of Medicine in 2018, and acquired her license as a physician after passing the Philippine Physician Licensure Examination last September 2019. She then proceeded to a 3-year residency training in Internal Medicine at West Visayas State University-Medical Center, which she completed last December 31, 2022. She then served as the Chief Resident for Clinical Affairs of the department from January 1, 2023 to December 31, 2023. She has several case reports authored and co-authored which were published last 2023 in some international journals, and were also presented in two international research fora on Rheumatology.

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Clinical characteristics and outcomes of pediatric patients with suspected and confirmed coronavirus disease 2019 (COVID-19) infection admitted in a tertiary government hospital in the Philippines

Background: While there is evidence that the burden of COVID-19 infection in hospitalized children is lesser than in their adult counterparts, currently, there are limited reports describing clinical data on COVID-19 patients particularly in pediatric population.

Objective: To describe the clinical characteristics and outcome of Suspected Coronavirus Disease 2019 (COVID-19) infection in pediatric patients admitted at a tertiary government hospital from March 2020-February 2021.

Study Design: Retrospective, descriptive study.

Setting: A Tertiary Government Hospital (Ospital ng Maynila Medical Center) in Manila, Philippines.

Population: Pediatric patients aged 1 day to 18 year old with Suspected/ Confirmed COVID 19 Infection.

Results: The total number of patients included in the study is 213 pediatric patients. There are 7 (3.29%) patients who have tested positive on COVID-19 based on the result of the RT-PCR while 206 (96.71%) have tested negative. The mean age is 5 years old. Majority were male 53.05% while female 46.95%. In COVID-19 positive patients, where 71.43% were male and 28.57% were female. Large portion were from Manila 81.22% and Non-Manilan 18.78%. In terms clinical presentation, most patients had fever 153 (71.83%), cough 109 (51.17%) and dyspnea 86 (40.37%). All COVID-19 positive have varied comorbid conditions while there are 66 (32.03%) COVID-19 negative. Patients were managed with antibiotics 155 (72.77%), inotropes 15 (7.04%), and steroids 51 (23.9%). The median days on the length of stay is around 6 days. In terms of severity of disease, most patients had moderate 179 (84.0%), followed by severe 19 (8.92%) and critical 15 (7.04%). The mean length of stay was 8 days. Majority of patients were discharged improved 91.55%.

Conclusion: The COVID-19 pandemic has had a catastrophic effect on global health which can affect pediatric patients and can cause mortality among them. But most pediatric patients have moderate disease and discharged improved.

Audience Take Away Notes

- The Coronavirus Disease 2019 (COVID-19) pandemic had taken an alarming toll among all age population across the world. While there is evidence that the burden of COVID-19 infection in hospitalized children is lesser than in their adult counterparts, currently, there are only few studies describing COVID-19 in pediatric population. This is a serious public health issue and remains to be a significant cause of morbidity and mortality among Filipino children. Thus, there is a need for further studies for recognition of the disease. This study was designed to review the clinical characteristics and outcomes of Suspected Coronavirus Disease 2019 (COVID-19) in tertiary government hospitals to contribute to the knowledge of COVID-19 in children. The researcher recommend that further studies is required to determine the cause for age-related variations in COVID-19 clinical characteristics, to examine the involvement of children in community transmission, and to develop therapy and vaccinations for the illness

Biography

In 2016, Dr. Ro-Janna Jamahari Jamiri-Sarapuddin received her medical degree from the De La Salle Health Sciences Institute in the Philippines. In 2022, she completed her Pediatric residency training at the Ospital ng Maynila Medical Center in the Philippines. She is currently a visiting lecturer at Western Mindanao State University College of Medicine in the Philippines and a consultant at the Edwin Andrews Airbase Hospital of the Philippine Air Force in Zamboanga City.

S. Gokce Alagoz*, Mustafa Saglam, Tekin Karslıgil
Gaziantep University, Turkey

The role of epstein-barr virus in upper respiratory tract diseases

Objective: Ebstein-Barr virus asymptomatically infects about 95% of adults worldwide. It is the main cause of infectious mononucleosis, which is observed most frequenty in adolescents. Because EBV is an opportunistic virus, it is more difficult to diagnose. It is not the first factor that comes to mind. However, its presence seriously threatens health. It is very important to detect EBV together with other upper tract disease factors.

Material and Method: 184 patients were included in our study. EBV DNA isolation and PCR were performed on throat swab samples in which upper respiratory tract disease agents were detected.

Results: 184 patients (95 women, 89 men) admitted to our hospital with suspected upper respiratory tract disease were included in our study. The average age of female patients was 50, 4 and male patients was 43. The kit we use for upper respiratory tract disease screening includes Adenovirus, Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2), human Metapneumovirus, human Rhinovirus / Enterovirus, Influenza A virus, Influenza B virus, Parainfluenza virus, Respiratory syncytial virus, and Bordetella parapertussis, Bordetella pertussis, Chlamydia pneumoniae, Mycoplasma pneumonia from the bacterial group. EBV positivity was detected in 43 patients with EBV PCR in the throat swab sample of these 184 patients. The EBV PCR lower limit is 157 copy/ml. 9 out of 43 patients are below 157 copy/ml.

Of the 34 EBV (+) patients, 17 were ex. Of the 17 patients, 6 were women (mean age: 57), 11 were men (mean age: 39). Influenza A in 1 of the 17 patients who died; 6 of them were Human Rhinovirus, Enterovirus; 2 had Adenovirus; 1 in Respiratory Synctial Virus; 2 of them were H. influenza, Streptococcus pneumonia was detected in 3 patients and Bocavirus in 1 patient.

Conclusion: Although EBV is an opportunistic and very common virus seen in the community, it does not come to mind in the preliminary diagnosis. These gaps urgently need to be filled, especially regarding the epidemiology and pathogenesis of the virus since more than 90% of the population eventually becomes infected.

Biography

Dr. Gokce Alagoz studied Biology at the Ankara University, Ankara and graduated in 2007. Then I started to MS in hepatology laboratory at the Institute of Biotechnology, Ankara University. I received my PhD degree in 2017 at the Biology, Gaziantep University. I am lecturer at Microbiology department of Medicine Faculty of Gaziantep University. I studied about viruses, molecular microbiology, sequencing and other molecular methods. I have published research articles in SCI(E) journals.

Shweta Chelluboina*, Darshan Kshirsagar, Akhilesh Chandra Mishra, Vidya Arankalle, Shubham Shrivastava

Communicable Diseases Department, Interactive Research School for Health Affairs, Bharati Vidyapeeth (Deemed to be University), Pune, Maharashtra, India

Dynamics of maternal dengue virus antibodies in Indian infants

Dengue is a mosquito-borne viral disease endemic in many countries particularly in the tropical and sub-tropical regions of the world. It is caused by one of the four serotypes of Dengue Virus (DENV). As the four serotypes are co-circulating, multiple encounters with heterologous dengue infection are highly prevalent. The enhanced risk of disease severity associated with secondary infection is mediated by one of the mechanisms known as Antibody-Dependent Enhancement (ADE) in dengue. The pathogenesis of dengue infection is determined by the interplay of neutralizing and infection-enhancing antibodies, particularly relevant in infants and young children. Infants born to dengue-immune mothers acquire maternal antibodies to dengue. Maternally acquired DENV-specific antibodies in infants, though initially protective, decline during the first year of life making them susceptible to primary dengue infections. Because of the introduction of the dengue vaccine in the near future in endemic countries like India, there is an urgent need to generate data on the kinetics of maternal antibodies that may offer a better understanding of the optimal age for dengue vaccination. In this study, we aimed to initially optimize plaque reduction neutralization test and antibody enhancement assay in a 96-well plate for the detection of neutralizing and infection-enhancing antibodies respectively for each of the four dengue virus serotypes. Next, we determined DENV-specific neutralizing and enhancing antibodies in Indian infants at birth, 3, 6 and 9 months of age. All anti-DENV IgG-positive samples showed the presence of neutralizing antibodies against 3 or 4 serotypes at birth. Neutralizing antibody levels decline with the increasing age of infants. Similarly, all anti-DENV IgG-positive samples showed enhancement of infection at a particular dilution against 3 or 4 serotypes at birth. With the increasing age of infants, fold enhancement of infection was highest in 6-month-old infants. In summary, our data suggests that DENV infection–enhancing activity coincided with the decline of neutralizing antibodies. Sub-neutralizing levels of maternally acquired DENV-specific antibodies showed DENV infection–enhancing activity highest at 6 months of age in infants. These maternal antibodies might interfere with the response to dengue vaccines. Therefore, such studies may provide insights into the appropriate age for dengue vaccination in infants born to dengue-immune mothers in endemic countries like India.

Audience Take Away Notes

- This presentation would help the audience to understand the complexities associated with the antibody response to dengue virus infections in infants
- This study emphasizes on the methodologies used to evaluate the antibody response to dengue virus infection
- This study will contribute information about the prevalence of neutralizing and infection enhancing antibody levels in a pediatric population which is most susceptible population to severe dengue infection
- Such a study on a larger scale will provide a practical solution around the age at which the vaccine should be given to children in dengue endemic countries

- It can be used as a starting point to conduct large-scale age-stratified population studies to understand the problems associated with disease severity in dengue infection

Biography

Shweta Chelluboina studied Clinical Virology at Manipal Institute of Virology, India and obtained her Master's degree in 2017. There she worked on the project entitled "Persistence of antibody response in Chikungunya." She then joined the Communicable Diseases department headed by Dr. A.C Mishra and Dr. Vidya Arankalle at the Interactive Research School for Health Affairs, Bharati Vidyapeeth, India. She is in the final year of her Ph.D. working on "Development and comparative assessment of antibody-dependent enhancement assays for dengue viruses" under the guidance of Dr. Shubham Shrivastava. Recently, she was awarded for best poster at VIROCON-2023 and has published two research articles in high impact journals.

Sinisa Skocibusic[1,2]*, Milena Latincic[1], Dario Icanovic[1], Maja Karin[3]

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An effective strategy for eliminating chronic Hepatitis C in individuals with an opioid addiction

Background: The healthcare system in Bosnia and Herzegovina continues to face a significant burden due to the presence of chronic hepatitis C. Individuals who engage in the use of injectable drugs represent a substantial reservoir of the hepatitis C virus, hence presenting an enduring public health concern.

Methods: A novel paradigm encompassing motivation, preparation, treatment, and monitoring of chronic hepatitis C was established with the aim of enhancing patient accessibility and reducing barriers to treatment. The study conducted by the Center for the Prevention and Outpatient Treatment of Addiction in Mostar involved an examination of medical records in order to investigate the sociodemographic and beginning treatment factors for chronic hepatitis C in individuals receiving opioid substitution therapy in the IDU, as well as their family members. These individuals underwent standardized procedures in accordance with the Mostar model.

Results: The research findings indicate a significant success rate (94.7%) in effectively eliminating HCV infection in individuals with addiction through the use of DAA. A cohort of 25 patients underwent diagnostic treatment, with just one patient voluntarily terminating the treatment and one patient succumbing to the condition. Patients who received treatment had an average starting viremia of 795,104 IU/mL. The results of the genotyping analysis indicated a nearly equal distribution of genotypes 1 (52%) and 3 (48%).

Conclusion: This study enhances the comprehension of optimal approaches in the treatment of individuals with opioid addiction and contributes to the investigation of strategies for efficiently managing infectious diseases in susceptible demographics. The model exemplifies a relevant instance of a successful public health initiative, and its implementation can serve as a source of inspiration and direction for other communities in Bosnia and Herzegovina grappling with the task of eliminating HCV among this vulnerable population.

Audience Take Away Notes

- This presentation will add to fresh viewpoints and ideas for the effective treatment of blood-borne infections, particularly chronic hepatitis C among hard-to-reach population, in nations where access to contemporary hepatitis C treatment is restricted. A treatment that works well can serve as a helpful example for listeners when it comes to potential improvements to the health system or local working circumstances

Biography

Sinisa Skocibusic is a healthcare practitioner by profession. The individual embarked on a postgraduate program in "Medical Care and Public Health" with a particular focus on infectious diseases. He performed a crucial role during the COVID-19 epidemic as a subspecialist in intensive care medicine. Aside from his clinical practice, he imparts knowledge to aspiring physicians at the Medical School in Mostar. The individual in question has held the position of director at the Center for Addiction Prevention and Outpatient Treatment in Mostar since 2015 and subsequently assumed the role of director at the Institute of Public Health of the Federation of Bosnia and Herzegovina since 2021. He has authored or co-authored an additional 11 scientific papers that have been published in journals that are indexed in relevant databases. Furthermore, he has contributed to the publication of five scientific publications in other journals and has made contributions to two edited volumes.

Sira S. Owibingire[1]*, Elison N. M. Simon[1], Iren Kida Minja[1], Siren Fromreide[3], Innocent J. Mosha[2], Edda A. Vuhahula[1], Daniela E. Costea[3]

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Need of monitoring human papillomavirus infection among oral and oropharyngeal squamous cell carcinoma patients from setting with high incidence of cervical cancer

Background: There has been a global upsurge of Oropharyngeal Cancer (OPC) cases associated with increased Human Papillomavirus (HPV) infection. In Tanzania and Sub-Saharan African countries data on the same is lacking and HPV among OPC patients is not investigated routinely. The recommended practice, however not practiced in most LMICs, is to determine HPV infection status to oral and Oropharyngeal Squamous Cell Carcinoma (OPSCC) before treatment since the positive cases are treated with de-escalated regime because they respond better to treatment.

While the burden of HPV in cervical cancer is well established the role of HPV is not well documented in countries where cervical cancer is endemic. Without baseline data it may be difficult to later quantify the effect of HPV vaccination in reduction of OPC. It is better to start now establishing means of monitoring the prevalence of HPV in both OPC patients and where possible the health individuals in settings where HPV related cervical cancer is more prevalent.

Aim: This study aimed at determining the occurrence of HPV status to OPSCC through p16 Immunohistochemistry (IHC) and In Situ Hybridization (ISH).

Materials and Methods: The study was done at Muhimbili National Hospital (MNH) and MUHAS Dental Clinic from August 2020 and Dec 2022. The biopsies were taken from the cases clinically suspected to have OPSCC. Following confirmation of OPSCC histologically, the blocks of 218 patients were obtained and screened for possibility of obtaining quality tissue materials for Tumour Microarray (TMAs) for IHC and ISH whereby blocks for 172 patients qualified. Tissues were transferred to Haukeland University Hospital (Norway) where TMAs were prepared, and then IHC and ISH were done. In addition, IHC for p53 was performed to search for association of occurrence of these biomarkers.

Results: Out of 172 cases of OPSCC the p16 overexpression was found in 15 cases (8.72%) which had over 70% of cells in the specimen stained. In-situ hybridization was done in all cases and only 2 (1.16%) were positive. The majority of p16 positive cases showed only weak stains on ISH. The majority of the 15 cases which showed p16 overexpression were located on the tongue followed by mandibular gingiva and buccal. Two thirds were males and 40% were aged below 60 years with almost all at clinical stage IV.

Conclusion: Findings concur with research done elsewhere in sub-Saharan Africa showing that HPV infection among OPSCC is low. Among these few cases males dominated. Given the current situation of genital HPV infections, there is a need for constant surveillance of the same for oral and pharyngeal area.

Recommendation: There is a necessity to routinely determine HPV status using p16 IHC and RNA ISH among OPSCC cases in Tanzania before initiation of treatment for the sake of estimating prognosis and for constant surveillance of HPV burden.

Audience Take Away Notes

- HPV infection is not determined routinely in OPC patients in most of the LMICs
- Up-to-date the complete staging of OPC as the 8th AJCC edition is not possible in settings where HPV infection is not determined
- The role of HPV infection among OPC patients is low but should not be ignored
- While the burden of HPV in cervical cancer is well established the role of HPV is not documented in countries where cervical cancer is endemic
- Without baseline data it may be difficult to later quantify the effect of HPV vaccination in reduction of OPC
- It is better to start now establishing means of monitoring the prevalence of HPV in both OPC patients and where possible the health individuals in settings where HPV related cervical cancer is more prevalent

Biography

Dr. Sira Owibingire graduated with Doctor of Dental Surgery (DDS) degree from the University of Dar es Salaam, Tanzania and later MDent in Oral and Maxillofacial Surgery from the Muhimbili University of Health and Allied Sciences (MUHAS) in 2017. He received Fellowship in Head and Neck Oncology at Tata Memorial Centre in India in 2019. He is a Senior Lecturer and Oral and Maxillofacial Surgeon at MUHAS School of Dentistry. He is conducting studies in oral and pharyngeal cancer (OPC), among other objectives he examined the role of HPV. He has published over 45 research articles in SCI(E) journals.

Sukki Ho

School of Nursing, The Hong Kong Polytechnic University, Hong Kong

Effect of a multimodal infection control programme in the reduction of bacterial contamination in the nasogastric feeding tube hubs in residential care homes for elders

Nasogastric Tube (NG tube) feeding in Residential Care Homes for the Elderly (RCHEs) carries the risk of contamination at the NG tube hub, a crucial connection point in the enteral feeding process. This contamination can lead to the spread of harmful microorganisms, potentially resulting in serious complications such as mortality. However, there is limited research on the effectiveness of Infection Control Programs (ICPs) in reducing NG tube hub contamination.

This study aimed to assess the impact of a comprehensive ICP on reducing bacterial contamination in NG tube hubs, enteral milk, and the hands of RCHE staff, while also evaluating its effectiveness in enhancing the staff's knowledge and skills in NG tube feeding. The research utilized a single-blinded cluster-randomized controlled trial involving eight RCHEs. The intervention group received a 12-week multimodal ICP, including educational sessions on infection control measures related to NG tube feeding, while the control group did not receive this intervention.

The ICP sessions, which involved various teaching methods such as PowerPoint presentations, videos, group discussions, and practical workshops, were tailored to accommodate the staff's shift schedules. Bacterial samples were collected from residents' NG tube hubs, enteral milk, and staff's fingertips for analysis. Pre- and post-intervention data on NG tube feeding knowledge and skills were also gathered and compared between the two groups.

Eight RCHEs with 140 residents and 250 RCHE staff participated in the study. Results showed a significant reduction in the total bacterial counts of the NG tube hubs within the intervention group before and after the intervention (p=0.04), as well as between groups (p=0.001). Both groups had 19 contaminated NG tube hubs at baseline. After intervention, the number of contaminated NG tube hubs was reduced to 13 in the intervention group but no changes were found in the control group. In addition, the total bacterial counts of the enteral milk was significantly reduced between groups (p=0.001) while there was no enteral milk contamination in either group before and after intervention.

The knowledge and skills in NG tube feeding was increased significantly in the intervention group (p=0.001) and was significantly improved compared with the control group after intervention (p=0.001). There were significant reductions in the total bacterial counts in right and left fingertips of the RCHE staff of the intervention group within group (p=0.001) and between groups (p=0.001) after intervention. Also, the number of fingertips contaminated was significantly reduced within the intervention group (p=0.001) and between groups (p=0.001). These findings underscore the effectiveness of the multimodal ICP in minimizing bacterial contamination and enhancing infection control practices in NG tube feeding.

In conclusion, the study highlights the positive impact of the ICP on reducing bacterial contamination in NG tube hubs and promoting proper hand hygiene among RCHE staff. Continuous implementation of such programs in RCHEs is recommended to sustain and further improve infection control practices in NG tube feeding.

Audience Take Away Notes

- This study on infection control programs (ICPs) in NG tube feeding at residential care homes for the elderly (RCHEs) demonstrates significant reductions in bacterial contamination at NG tube hubs, enteral milk, and staff's hands. The findings highlight the effectiveness of comprehensive ICPs in enhancing staff knowledge and skills, reducing contamination risks, and promoting proper hand hygiene. Healthcare professionals in RCHEs can benefit from implementing similar multimodal ICPs tailored to their schedules to improve infection control practices, minimize bacterial contamination, and ultimately enhance patient safety in NG tube feeding. his research that other faculty could use to expand their research or teaching?
- The research on the impact of the comprehensive infection control program (ICP) in reducing bacterial contamination in NG tube feeding in residential care homes for the elderly provides valuable insights that can improve the accuracy of future research designs and assist in addressing design problems in similar studies. The study's findings offer new information on the effectiveness of ICPs in minimizing contamination, enhancing infection control practices, and improving staff knowledge and skills in NG tube feeding. This information can guide the development of more targeted and effective interventions in future research, helping researchers design studies that aim to reduce risks associated with NG tube feeding and improve overall care quality in residential care settings. The study's results can inform the design of interventions and protocols aimed at reducing bacterial contamination and promoting proper infection control measures in similar healthcare settings, ultimately contributing to better patient outcomes and quality of care

Biography

Dr. Sukki Ho is an Associate Professor of Practice of the School of Nursing, The Hong Kong Polytechnic University (The PolyU). Her expertise is infection control nursing, teaching and research. She has contribution in nursing research with publications in the areas of N95 respirator fit test. Her doctoral research topic is related to infection control nursing care for chronically ill patients in the residential care homes for elders. Besides, she obtained the outstanding academic awards during her doctoral study in infection control specialty. Dr. HO has reinforced and brought new information of the hospital infection control practice specific to the prevention of COVID-19 infection to the staff and students of The PolyU during COVID-19 pandemic. She obtained Faculty Award/ Prizes for outstanding achievement in services (Team member) from the Faculty of Health and Social Sciences, The PolyU. She also serves as clinical coordinator of the Master of Nursing Programme.

Susannah Colt[1,2]*, Hannah W. Wu[1,2], Mario A. Jiz[3], Blanca R. Jarilla[3], Jonathan D. Kurtis[1,4], Jennifer F. Friedman[1,2]

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Inflammation-adjusted vitamin A deficiency is associated with higher schistosoma japonicum infection intensity among children and adolescents in the Philippines

Background: Children with intestinal schistosomiasis are at risk for undernutrition, anemia, linear growth stunting, and impaired cognitive development. Vitamin A deficiency impairs immune function against parasitic pathogens. In rodents, dietary-induced vitamin A deficiency causes higher schistosome worm and egg burden, higher mortality, and a reduced immune response compared to replete vitamin A status. In humans, applying an inflammation-adjustment strategy to vitamin A blood biomarker measures is necessary to estimate vitamin A status during periods of infection or inflammation. To our knowledge, this is the first study to examine relationships between inflammation-adjusted vitamin A status and human schistosomiasis burden.

Methods: This is a secondary analysis using stored sera collected from a cohort of children and adolescents with Schistosoma japonicum infection from Leyte, The Philippines who were followed for 18 months. The original study, conducted from 2002-2003, measured S. japonicum infection intensity by Eggs Per Gram of stool (EPG) using the Kato-Katz method, measured C-Reactive Protein (CRP) in blood sera, and collected demographic information of age, sex, and Socio-Economic Status (SES). The current analysis added ELISA measures of vitamin A Retinol-Binding Protein (RBP) and alpha-1-Acid Glycoprotein (AGP) from stored sera collected at baseline. The Thurnham Correction Factor (TCF) inflammation-adjustment method was applied to measures of RBP using co-circulating measures of CRP and AGP to estimate vitamin A status. A sample of N=40 participants was randomly selected based on S. japonicum EPG distribution. Statistical analyses, including multivariate linear regression, was conducted using SAS Studio 3.8 (SAS Institute Inc., Cary, NC).

Results: There were 39 participants with S. japonicum infection included for analysis. The median age was 13.4 years (9.9-16.3 IQR) and 61.5% were male. The median infection intensity at the baseline visit was 83.3 EPG (23.3-206.7 IQR), and the proportions of infection intensity categories were 53.8% light (1-99 EPG), 35.9% moderate (100-399 EPG), and 10.3% heavy (≥400 EPG). After applying the TCF correction to RBP values, 14 participants (35.9%) were categorized as vitamin A deficient (RBP < 0.7 μmol/L). Using a multivariate regression model adjusting for age, sex, and SES, vitamin A deficiency was associated with higher S. japonicum infection intensity (EPG) compared to those with replete vitamin A at the baseline visit ($p=0.0172$). Baseline vitamin A status was not found to be associated with S. japonicum infection intensity (EPG) at subsequent visits (1, 3, 6, 9, 12, 15, or 18 months after baseline).

Conclusions: After adjusting for inflammation, more than one third (35.9%) of the sample was vitamin A deficient. We report an association between vitamin A deficiency and increased schistosomiasis egg burden at the baseline visit. These results agree with findings reported from animal studies and represent an important discovery for our understanding of nutritional modulation of infection, specific

to schistosomiasis. There is often an overlapping geographical burden of micronutrient deficiencies and neglected tropical diseases. In combination with preventive chemotherapy for schistosomiasis, nutritional interventions improving vitamin A status may lead to reduced morbidity for children and adolescents living in endemic areas.

Audience Take Away Notes

- This study demonstrates how to estimate vitamin A status in the context of infection. Inflammation-adjustment is an important technique because hepatic secretion of vitamin A into the bloodstream is reduced by inflammatory cytokines during the acute phase response, which can invalidate assessment during infection. Inflammation-adjustment should also be applied to ferritin measures for the assessment of iron status
- Improved estimation of vitamin A status using inflammation-adjustment allows for widespread investigation of vitamin A deficiency and the immunologic response to all types of human infections–previously hampered by the inability to estimate status during an acute phase response
- Better understanding for how undernutrition and micronutrient deficiencies impact immunopathology from infections can offer opportunities for improved interventions and reduced long-term morbidities

Biography

Dr. Colt holds bachelor’s degrees in biology and anthropology from the University of Rhode Island (2006) and a postgraduate diploma in public health from the University of Auckland (2009). She earned her doctoral degree in the concentrations of nutrition, epidemiology, and infectious disease immunology in 2019 from Cornell University. In 2020, Dr. Colt joined the Center for International Health Research (CIHR) at the Warren Alpert Medical School of Brown University where she studies schistosomiasis-related morbidities among pregnant women and children. In recent years, she received awards from the Thrasher Foundation (2022) and the National Institutes of Health (2023) to investigate relationships between vitamin A deficiency and schistosomiasis immunopathology.

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Insights into West Nile Virus seroprevalence in wild birds and equines: A focus on Madrid province, Spain

West Nile Virus (WNV), classified under the Orthoflavivirus genus and Flaviviridae family, is a re-emerging flavivirus perpetuated in an enzootic cycle between avian hosts and mosquito vectors. Periodic outbreaks of WNV in humans and horses can result in neuroinvasive disease and fatalities. Spain, particularly Andalusia, Extremadura, and Catalonia, has experienced numerous WNV outbreaks. In 2020, an outbreak in Andalusia and Extremadura reported seventy-seven human cases, including eight fatalities. WNV seropositivity has been identified in horses in the Community of Madrid, but, to the best of our knowledge, wild bird transmission remains unreported in this region. To assess WNV seroprevalence, wild birds from a wildlife rescue center and privately owned equines were sampled. Results showed thirteen birds (8.2%) and one equine (4.0%) positive using a WNV competitive Enzyme-Linked Immunosorbent Assay (cELISA). Four avian samples (2.5%) and one equine (4.0%) were confirmed positive for specific WNV antibodies through microneutralization testing (VNT). Positive birds comprised both migratory and resident species, including juveniles and adults. The presence of seropositive resident and juvenile birds, particularly a nestling and a fledgling, suggests local flavivirus transmission within Madrid. The potential circulation of flaviviruses, including WNV, within Madrid Community raises concerns, necessitating further surveillance in mosquitos, wild birds, and horses.

Audience Take Away Notes

- The audience can increase their knowledge on WNV situation in Spain in both wildlife and horses
- This research aids professionals in public health, wildlife management, and veterinary medicine by providing insights into WNV transmission dynamics and seroprevalence in Madrid
- Other faculty members can utilize this research to expand their knowledge on WNV epidemiology, wildlife disease dynamics, and the effectiveness of surveillance strategies
- It offers a practical solution by identifying potential WNV circulation in an urban environment and underscores the importance of targeted surveillance in mosquitos and wild birds to mitigate transmission risks
- It enhances design accuracy by offering new data on WNV seroprevalence in various avian species, contributing to better-informed decision-making in disease management
- Other benefits include raising awareness about WNV transmission risks and promoting collaboration between different researchers in this area

Biography

Dr. Ayllon completed her degree (2005) and PhD in Veterinary Medicine (2009) at the Complutense University of Madrid, Spain and is currently Lecturer at Complutense (UCM) and Alfonso X el Sabio (UAX) Universities in Spain and collaborating researcher at Fiocruz, Brazil. Her research experience includes the study of infectious diseases that impact both veterinary and human health and antimicrobial drug- resistant microorganisms. She has held two postdoctoral positions at Free University of Berlin, Germany (2012-2013) and Oswaldo Cruz Institution, Brazil (2015-2019), focused on the entomo-virological surveillance of different pathogens. She has published 23 research papers in SCI Journals and is member of different research groups: Health Surveillance (UCM); Diagnosis and Control of Zoonoses in Carnivores (UAX); Antimicrobial Resistance (UAX); Spanish Society of Microbiology (SEM); AVEPA and ESCMID.

Dr. Anupama Bappal, Dr. Atul Kamath, Dr. Vidya Hegde, Dr. Rashmi Jain, Dr. Rashmi S, Dr. Rosshini Kummararaj*

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Story of the wandering worm

Introduction: A parasite may look docile and harmless but it can create havoc in human eyes. Early detection and timely treatment can prevent blindness. We report three cases of parasites in the eye with varying presentations.

Case 1: A 76-year-old gentleman, a pet lover and a gardening enthusiast reported with complaints of foreign body sensation in his left eye. Examination showed subconjunctival mobile worm in the inferior bulbar conjunctiva which was removed under topical anesthesia.

Case 2: A 10-year-old boy reported with complaints of gradual painless diminution of vision in his left eye for 6 months. Posterior segment examination showed a motile subretinal nematode with multimodal grey-white lesions in the outer retina suggestive of Diffuse Unilateral Subacute Neuroretinitis (DUSN). The worm was photocoagulated and the child was given a course of antihelminthic treatment.

Case 3: 40 year old gentleman a trekker, came with complaints of difficulty while reading. Visual acuity was 6/6 in each eye. The posterior segment of the left eye showed Retinal pigment epithelial track in a criss-cross fashion throughout the retina-sparing fovea(path taken by the nematode). An immobile coiled worm was seen in the pars plana region suggestive of a dead nematode.

Conclusion: It is important to suspect nematodes in tropical countries and refer patients to ophthalmologists for early detection and prevention of blindness.

Audience Take Away Notes

- As a clinician, it is important to rule out and consider parasites as a differential diagnosis for unilateral vision loss
- As seen in case one it is important for clinicians to consider parasites as a differential diagnosis when patients presents with non specific foreign body sensations
- These reports show how parasites can affect human eyes

Biography

Dr. Anupama Bappal graduated from Kasturba Medical College,Mangalore in1999. She has done Comprehensive Ophthalmology fellowship from Sankara Eye Hospital, Coimbatore. She is a fellow of Medical Retina from Sankara Nethralya Chennai. She has a special interest in Retinopathy of prematurity and innovations in ophthalmology education. She has conducted instruction courses in state conferences and has publications in National and International Journal.

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Investigation of molecular epidemiology of carbapenem-resistant acinetobacter baumannii group in Taiwan

The Acinetobacter baumannii group (AB-group), encompassing A. baumannii, A. pittii, A. nosocomialis, along with recent additions A. seifertii and A. dijkshoorniae, have emerged as prominent nosocomial pathogens with a global presence. Infections with antibiotic-resistant Acinetobacter spp., especially carbapenem-resistant A. Baumannii (CRAB) or multidrug-resistant A. baumannii, are associated with an elevated risk of mortality compared to susceptible strains, and their prevalence in nosocomial infections has been steadily rising. CRAB strains were categorized as a critical priority pathogen by the World Health Organization toward combatting increasing antibiotic resistance and developing advanced therapy. Molecular characterization techniques, such as blaOXA-51-like PCR and rpoB sequencing, exhibit superior discriminatory capability compared to conventional approaches for the AB group. A total of 492 Acinetobacter spp. strains were collected from two hospitals in Taiwan and were classified using MALDI-TOF MS, blaOXA51-like PCR and rpoB sequencing: 94.5% (n=465) of A. baumannii and 5.5% (n=27) of Non-A. Baumanniii (NAB). Out of 492 isolates, 49.3% (n = 240) were defined as Carbapenem-Resistant (CR) strains with the MIC value of Imipenem (IMP) and Meropenem (MEM) ≥ 4 mg/L, including CRAB (n = 237) and Carbapenem-Resistant NAB (CR-NAB) (n = 3). All CRAB and CR-NAB were screened carbapenemase genes by multiplex PCR assay. All CR isolates were negative for blaOXA-143-like, blaKPC, blaGES, blaVIM, blaSPM, blaGIM, and blaSIM. Out of 237 CRAB strains, 72.6% carried blaOXA-23-like, 22.8% carried blaOXA-24-like, 3.3% were co-carriage of blaOXA-23-like-blaOXA-24-like and 1.3% harbored blaOXA51-like only. Among CR-NAB strains, 2 strains were co-carriage of blaOXA58-like and blaIMP, and one strain carried blaNDM-1. The rates of the predominant carbapenemase genes from 2015 to 2021 were further compared and showed slight changes during these years. Interestingly, we found a strain with harbored blaNDM-1, featuring the rpoB allele (rpoB-85) closely aligned with A. seifertii, and exhibiting remarkably high MIC levels of 128 mg/L for both IMP and MEM. Whole-genome Sequencing indicated that the strain harbored a plasmid-borne blaNDM-1, designated pAS39-2 (approximately 47 kb). pAS39-2 also carried genes conferring resistance to aminoglycosides and bleomycin and featured a Ti-type conjugative operon. This plasmid was transferred effectively from A. seifertii to A. baumannii strains by in vitro conjugation. Moreover, pAS39-2 closely resembled plasmidsfound in A. soli and A. pittii in Taiwan, harboring the potential for transmissible multidrug resistance and contributing to the escalating spread of antimicrobial resistance. The current study reports on the molecular epidemiology of AB group isolates collected over a span of 6 years, revealing the carriage rate and types of carbapenemases present in A. baumannii and NAB strains in Taiwan. These findings offer valuable insights for monitoring the epidemiology and dissemination of this pathogen.

Biography

Dr. Quyen studied Biotechnology at HCM City University of Technology, Vietnam, and graduated with a Bachelor of Engineering in 2014. She then joined the research group of Associate Professor Pan in the International Biomedical Science (IBS) Master's program at China Medical University, Taiwan, from which she received her master's degree in 2020. Following six months of research assistance supervised by Dr. Pan at the Microbiology and Immunology Laboratory, she began her Ph.D. program at the same university in the Biological Science and Technology department in 2021, where she continues to study. She has published 5 research articles in SCI(E) journals.

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Efficacy of oral 20-hydroxyecdysone (BIO101) in adults with severe COVID-19 (COVA) : A randomized, placebo-controlled, phase 2/3 trial

Background: SARS-CoV-2 infects human cells through interaction between its spike protein, and ACE2, a key element of the RAS. Thus SARS-CoV-2 may induce an imbalance of the RAS leading, among other symptoms, to severe pneumonia associated with COVID-19. We hypothesized that MAS-receptor activation by 20-hydroxyecdysone (20E) could modulate the protective arm of the RAS, leading to a reduced rate of respiratory failure and early death among hospitalized patients with COVID-19.

Methods: Double-blind, randomized, placebo-controlled phase 2/3 trial. Randomization: 1:1 oral 20E (350 mg BID) or placebo, up to 28 days or until an endpoint was reached. Primary endpoint: mortality or respiratory failure requiring high-flow oxygen, mechanical ventilation, or extra-corporeal membrane oxygenation. Key secondary endpoint: hospital discharge following recovery.

Results: 238 patients were randomized between August 26, 2020, and March 8, 2022. At day 28, a reduction in the risk of early death or respiratory failure was observed: 43.8% (p=0.0426) (HR 0.44) in the ITT population; and HR 0.41 (p=0.037) in the PP population. On day 28, proportions of patients discharged after recovery were 80.1%, and 70.9% in the 20E and placebo groups respectively, (adjusted difference 11.0%, 95% CI [-0.4%, 22.4%], p=0.0586). Treatment emergent adverse events of respiratory failure were more frequent in the placebo group (22.7% vs. 31.7%) respectively.

Interpretation: 20E significantly reduced the risk of death or respiratory failure. This finding suggests that 20E is an important drug candidate to treat adults hospitalized with severe respiratory symptoms due to COVID-19.

Biography

Professor Valerie Pourcher is Head of the Department of Infectious Diseases at the Pitie-Salpetriere Hospital, Paris. Her areas of research concern immunocompromised patients: patients infected with HIV, patients who have undergone a transplant and those with infectious complications from chemotherapy or biotherapies. Her top areas of expertise are AIDS, COVID-19, Kaposi sarcoma, HPV, HBV, JC virus.

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Profiling, prescribing patterns, and infection rates among inpatients at orthopedics wards: Prospective interventional implementation study (AMSP-PIIS)

Background: Trauma represents a significant public health issue in India, with substantial morbidity and mortality. Rapid access to appropriate care is essential for favorable post-injury outcomes. However, resource allocation strategies ensuring equitable access in developing nations are not well defined. Orthopedic surgeries are significant contributors to Surgical Site Infections (SSIs) globally. The inappropriate use of antibiotics contributes to Antimicrobial Resistance (AMR), a critical global health concern. Antimicrobial stewardship is advocated as a key strategy to address AMR, yet practical examples of stewardship in trauma centers are limited. This study aims to assess profiling, prescribing patterns, and infection rates among inpatients in orthopedics wards at a level 1-trauma center in India.

Methods: This prospective interventional study focused on patients admitted to orthopedic wards following traumatic injuries.

Results: Over a 6-month period, 408 patients with traumatic injuries were included in the study. The demographic profile revealed a mean age 38.7+13.7, with 80% male and 20% female patients. Lower limb fractures were the most common injury, followed by spinal injuries. The majority of patients were prescribed antibiotics prophylactically. The mean length of stay was 10.96 days. Patients who developed confirmed surgical site infections were 4.4%, with Klebsiella pneumoniae and Escherichia coli being the most commonly isolated organisms. Most patients were discharged from the hospital.

Conclusion: This study highlights the necessity of implementing antimicrobial stewardship programs tailored to orthopedic patients. Such programs are critical for optimizing antibiotic use, combating AMR, and reducing the incidence of Hospital-Acquired Infections (HAIs). Addressing implementation challenges and enhancing prescribing practices are vital steps toward mitigating antimicrobial resistance and advancing patient care within orthopedic settings.

Audience Take Away Notes

- Our study focuses on Profiling, prescribing patterns, and infection rates among inpatients admitted to the Orthopedic Ward of our trauma center
- Antibiotic stewardship activities play a crucial role in infection control, emphasizing appropriate prescribing practices
- Evaluate current prescribing patterns for inpatients in the Orthopedic Ward

- Assess infection rates and their correlation with prescribing practices
- Implement an antibiotic stewardship intervention focused on appropriate prescribing and transitioning from intravenous to oral therapy when feasible
- This study serves as an implementation-focused intervention aimed at improving prescribing practices and infection control across our trauma center. We aim to optimize patient outcomes and reduce healthcare-associated infections in the Orthopedic Wards

Biography

Dr. Vineeta Arora completed her studies in Clinical Pharmacology at KLE University, India, graduating in 2012. She later earned her PhD from JLN Medical College -KLE University in 2021 and later completed a Master in Public Health. Dr. Vineeta Arora is currently a Research Scientist III at the JPNA Trauma Center, All India Institute of Medical Sciences, New Delhi, India. She has published more than 10 research articles in SCI (E) journals in different areas of research.

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To identify and distinguish cytokine storms based on manifestations, and to protect human from infectious disease by targeting cytokines

The recent global outbreaks of infectious diseases such as SARS and COVID-19 have inflicted damage on both individuals and societies worldwide. To develop scientific strategies for prevention and precise treatment measures to counteract such outbreaks is imperative. After 28 years of research, we have formulated a novel medical theory and precision treatment model aimed at infectious disease outbreaks. This groundbreaking theory has undergone rigorous scrutiny of the underlying concepts governing the progression and dynamic evolution of infectious diseases. Moreover, it has successfully addressed the longstanding scientific enigma of cytokine storms, which has eluded resolution in modern medicine for the past half-century. By establishing a framework for the precise diagnosis and treatment of cytokine storms, our research represents a significant advancement in the field of medicine with profound implications for the diagnosis and treatment of various human diseases. The elucidation of the scientific complexities surrounding cytokine storms signifies a monumental milestone in medical progress and holds immense potential to revolutionize global healthcare practices. Our theory stands poised to rapidly discern critical features of cytokine storms associated with any outbreak, present or future, thereby equipping the medical community, the World Health Organization (WHO), and governmental bodies with the necessary tools to devise strategic interventions and implement precise diagnosis and treatment protocols. Given the recurrent emergence of new epidemics worldwide, the expeditious dissemination of this groundbreaking theory is paramount.

Cytokines are unique polypeptides that serve as primary messengers, exerting significant influence in the development, progression, and evolution of diseases, particularly infectious ones. Comprising various cytokines, receptors, and associated molecules, the cytokine network plays a pivotal role in regulating physiological responses. Despite decades of study, cytokine storms have remained a perplexing challenge in the medical community for over 50 years. Our research introduces novel concepts regarding cytokine storms: they manifest through diverse abnormal patterns and intensities, representing a comprehensive dysfunctionality within the cytokine network, rather than mere irregularities in individual cytokine levels. The ultimate dysfunctionality within the cytokine network and the disease manifestations hinge on the predominant cytokines within the imbalanced network, or the cytokine storm itself. Identifying the features of a cytokine storm relies on recognizing the disease manifestations it induces.

According to our new theory, the cytokine profile of COVID-19 reflects an imbalance and dysfunctionality stemming from heightened activity of TGF-β and platelet-derived growth factor (PDGF), with a notable emphasis on the excessively elevated activity of TGF-β. A defining symptom of this profile is fatigue. The pathogenesis of these symptoms follows a specific mechanism: TGF-β binds to its receptors, triggering a series of pathological processes and resultant manifestations. Fatigue arises from mitochondrial dysfunction and decreased Na+-K+-ATPase activity induced by TGF-β. Additionally, TGF-β promotes the secretion of bronchial mucus, leading to the production of thick mucus and pulmonary sputum embolism, impairing normal respiratory function and potentially precipitating severe complications such as life-threatening infections and shock. Furthermore, TGF-β acts as a potent immunosuppressive agent, significantly dampening immune function and impeding recovery. Its inhibitory effects on lymphocyte proliferation and differentiation contribute to reduced peripheral blood lymphocyte counts. These findings were disseminated by Chinese media and supported by various publications, including an article published in Frontiers in Public Health in 2021.

In summary, we propose that the characteristics of a cytokine storm can be discerned through the manifestations of diseases. We have unravelled the abnormal regulations and dynamic patterns of cytokine storms in human illnesses. This breakthrough enables us to identify the cytokine storm feature and administer precise treatment for any future infectious diseases worldwide. For instance, we can now identify the cytokine storm feature of the current dengue fever outbreaks occurring in numerous countries. This discovery serves to protect human from the severe consequences of infectious disease outbreaks, facilitating precise diagnosis and treatment for viral infectious diseases and making personalized, precise pathophysiological treatments.

Biography

Dr. Shen graduated from Peking University as MS in 1989 and from Peking Union Medical College, Chinese Academy of Medical Sciences with MD in 1999. He is president of Shenzhen Anti-cancer Association, Shenzhen Chairman of Tumor Prevention and Treatment Union, Council Member of Tumor Committee of World Chinese Medicine Union. Over 100 papers have been published in national and international journals. His specialization focuse on medical oncology and comparative research on TCM and western medicine. He is director of Hongkong Tianyou Medical Research Institute and Shenzhen Tianyou Medical Institute, professor of Shenzhen Hospital, Southern Medical University.

Dr. Feng has been engaged in clinical research on malignant tumors since 2009. Her major achievements include a randomized prospective cohort study on the prophylactic use of antiviral drugs in HBV carriers during chemotherapy, as well as a study on the high-risk factors of local recurrence after breast-conserving surgery in HER-2 positive breast cancer. Dr. Feng received her Ph.D. degree in 2018 with a focus on tumor biology and drug development. In 2019, Dr. Feng was appointed as the Vice-Chairman of the Clinical Oncology Nutrition and Metabolism Branch of the Shenzhen Anti-Cancer Association.

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The mechanism of the suppression of experimental fungal keratitis by histone deacetylases inhibitors

Fungal keratitis is one of the leading causes of blindness of infected corneal diseases, but the pathogenesis of fungal keratitis is not fully understood and therefore the treatment of the disease by medication is still under investigation. In the current study, we sought to study the effect of HDAC inhibitor Suberoylanilide Hydroxamic Acid (SAHA) on experimental fungal keratitis in mice. SAHA (25 mg/kg) (n = 30) or vehicle (DMSO) (n = 30) was delivered through Intraperitoneal injection (IP) 24 hours after the fungal inoculation, and the same amount of SAHA injection or DMSO was followed at day 2. The expression of histone H_3 (H_3), Acetylated Histone H_3 (AC-H_3), Histone Deacetylase 1 (HDAC)1, Tumor Necrosis Factor-α (TNFα), and Toll-Like Receptor 4 (TLR4) in surgically excised specimens from the patients and mice with fungal keratitis were detected by immunohistochemistry. The expression of mRNAs for Interleukin-1β (IL-1β), TNFα, and TLR4 were evaluated in the corneas of the mice with fungal infection and the control corneas by real-time PCR. The quantification of IL-1β and TNFα in the corneas of the mice with fungal infection was determined by ELISA. The inhibitory effect of SAHA on mice fungal keratitis was revealed by GMS and H&E staining. We found that the downregulation of histone acetylation and upregulation of HDAC1 expression were associated with the increased inflammation response in fungal keratitis not only in humans but also in experimental animals. SAHA was able to inhibit experimental fungal keratitis in mouse by suppressing TLR4 and inflammatory cytokines such as TNFα and IL-1β; the inhibition of HDAC may be a potential therapeutic approach for the treatment of fungal keratitis.

Audience Take Away Notes

- Anti-fungal therapy is the common approach to control fungal induced inflammation. Unfortunately, medications for anti-fungal infection have limited efficacy and drug-resistance rapidly develops, suggesting that fungal keratitis is a complex disease and other mechanisms may participate in the pathogenesis of the disease. Recent studies have demonstrated that epigenetic mechanisms can affect numerous pathologic conditions, including infectious diseases, we also observed the inhibitory effect of SAHA on mice fungal keratitis. Our study, to the best of our knowledge, is the first to investigate the effects of HDACi in a mouse model of fungal keratitis. The usage of HDACi in fungal keratitis may be a promising venue and alternative treatment to traditional antifungal therapy. So other faculty could use this research to expand there research
- Through this research, we found that the usage of HDACi in fungal keratitis may be a promising venue and alternative treatment to traditional antifungal therapy
- It will improve the accuracy of a design, or provide new information to assist in fungal keratitis research

Biography

Dr. Xiaohua Li studied Ophthalmology at Zhongshan University, China and graduated as M.D and Ph.D in 2005. She then worked in Ophthalmology department of Henan Provincial People's Hospital. After one year fellowship supervised by Dr. Narsing Rao at the Pathology Laboratory of Doheny Eye Institute, USC, USA, and one year fellowship supervised by Dr. Deming Sun at the Immunology Laboratory of Doheny Eye Institute, UCLA, USA, she obtained the position of an chief physician at the Henan Provincial People's Hospital. She has published more than 20 research articles in SCI(E) journals.

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Estimating the effectiveness of non-pharmaceutical interventions during COVID-19

During the initial outbreak of COVID-19, governments worldwide implemented various Non-Pharmaceutical Interventions (NPIs) to help control the spread of the virus. Our study focused on assessing the impact of these interventions in the United States during the first wave of the pandemic. We conducted three separate analyses. First, a prototypical Bayesian hierarchical model was employed to gauge the effectiveness of five NPIs - gathering restriction, restaurant capacity restriction, business closure, school closure, and stay-at-home order, in the 42 states that experienced over 100 deaths by the end of the wave. The effectiveness of a sixth NPI, the mandate to wear facemasks, was assessed using counterfactual modeling which is a variant of the prototypical Bayesian hierarchical model that allows us to answer the question what if the state had imposed the mandate or not. The third analysis used an advanced Bayesian hierarchical model to evaluate the effectiveness of all six NPIs in all 50 states and the District of Columbia, and thus provide a full-scale estimation of the effectiveness of NPIs and the relative effectiveness of each NPI in the entire USA. Our results reinforce earlier results on the general effectiveness of NPIs in arresting the spread of the disease.

Audience Take Away Notes

- The audience will be equipped with evidence-based knowledge about the effectiveness of various NPIs
- The use of Bayesian hierarchical models provides a framework that can be adapted and applied to other diseases or in different contexts
- Educators can use the evidence from this work to communicate the importance of NPIs to the public, which can lead to better compliance with public health guidelines and a more informed citizenry that understands the rationale behind such measures

Biography

Dr. Yuhang Liu studied Applied Mathematics and Statistics at Stony Brook University and received her M.S. in 2017. She then joined the research group of Dr. Wei Zhu at the Center of Excellence Wireless and Information Technology (CEWIT) at Stony Brook University. She received her Ph.D. degree in 2022 at the same institution. Dr. Liu's research interests cover a broad spectrum of public health issues related to infectious diseases. Utilizing advanced statistical and machine learning methodologies, Dr. Liu aims to provide data-driven insights that can enhance strategies for managing and mitigating infectious disease outbreaks. Following her doctoral graduation, Dr. Liu obtained a role as a Biostatistician with Moderna Services, Inc.

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POSTERS

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An imitation game: Syphilis infection and increased odds of neurologic morbidity

Background: The World Health Organization (WHO) estimated the global incidence of syphilis among adults to be approximately 7.1 million in 2020. The following year, the American Centers for Disease Control and Prevention (CDC) reported a 32% increase in the incidence of primary/secondary (early) syphilis in the United States between 2020-2021. Treponemal Central Nervous System (CNS) invasion is estimated to occur in approximately 25-60% of cases, however, the current WHO/CDC standard of care for early syphilis does not achieve CNS clearance. This raises concern for a preventable burden of neurologic morbidity secondary to treponemal CNS persistence and subsequent neurosyphilis. Our central hypothesis is that individuals with history of syphilis infection will experience greater odds of neurologic morbidity relative to their uninfected counterparts.

Methods: An FQHC-based, preliminary 10-year retrospective analysis (01/2013-12/31/2022) of deidentified Electronic Medical Records (EMR) was undertaken in summer of 2023. The exposure of interest consisted of grouped ICD-10 codes representative of early syphilis infection with neurologic outcomes defined as ICD-10 diagnoses reflective of the principle clinical manifestations of neurosyphilis. Unadjusted, bivariate analysis was performed for preliminary assessment of exposure-outcome association.

Results: 3,711,053 EMR from an academic health system were included in final analysis. 5,981 patients were found to have a diagnosis of syphilis. Patients with syphilis exposure had significantly higher odds for stroke (OR = 5.14; 95%CI = 4.71-5.61), dementia (OR = 20.68 ; 95%CI = 19.27–22.19), sensorineural hearing loss (OR= 5.75; 95% CI= 5.07-6.2), and blindness (OR= 15.74 ; 95%CI = 14.31-16.54) relative to unexposed patients.

Conclusion: Syphilis infection was associated with significantly increased odds of neurologic morbidity across all representative outcome measures queried. These data are concerning as they suggest a clinically significant limitation to the current WHO/CDC standard of care for early syphilis. We plan to more rigorously evaluate our hypothesis in a follow-up study that will utilize regression analysis to determine the independent effect of syphilis exposure adjusting for multiple confounders.

Biography

Dr. Aaron Briggs studied Biology at Dartmouth College, USA. During his course of study he was accepted early to Geisel School of Medicine (SOM) at Dartmouth through the Early Assurance Program. Dr. Briggs graduated from Dartmouth College with a BA in biology in 2015 and began medical school at Geisel shortly afterward. In 2019 Dr. Briggs graduated Geisel SOM with honors as the elected president of Dartmouth Alpha Omega Alpha and went forward to pursue general pediatrics residency at the Children's Hospital of Philadelphia. Learning that a public health approach would be required to address disease and health disparity at the population level, Dr. Briggs adjusted his training to Preventive Medicine in 2022 and is now a PGY3 senior resident physician with the University of California San Diego General Preventive Medicine Residency Program.

Dr. Ahsan Ehtesham[1]*, Dr. Ahmed Abdelghafar Masaad Alsayed[2], Dr. Samah Farouk Abdullah Mohamed[3], Dr. Zubair Shahid[4], Dr. Tamer M. M. Abdalghafoor[1]

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A rare case of aortic aspergillosis in an immunocompetent patient with no pre-existing cardiac pathology – A case report

Background: Cardiac aspergillosis is a rare form of Invasive Aspergillus infection that carries high mortality despite aggressive treatment. It usually occurs in patients with underlying cardiac abnormalities such as cardiac lesions, prosthetic valves, cardiac devices, and heart transplants.

Case Summary: A 30-year-old male with right-sided body numbness had a CT Head revealing a suspected neurocysticercosis lesion. Initial labs showed mildly elevated CRP and normal procalcitonin. Echocardiogram found a mass on the aortic valve and a thick left atrial wall. PET CT revealed a hypermetabolic mass around the heart and aortic root. IgG4 levels were high and tissue biopsy was needed for confirmation. However, the patient developed bilateral lower limb ischemia and weakness, requiring emergency surgeries. The biopsy showed invasive aspergillosis, treated with Amphotericin B. Unfortunately, the patient deteriorated into septic shock despite treatment.

Discussion: This clinical case accentuates several challenges encountered in the management of aortic aspergillosis in a patient with a low suspicion of invasive aspergillosis. Firstly, it emphasizes the importance of considering the rare possibility of invasive aspergillosis in immunocompetent patients, even with no known risk factors. Secondly, it brings out the recognition of the rapid progression of Aspergillosis endocarditis with poor outcomes. Finally, it emphasizes that early surgical treatment and early histological diagnosis with early initiation of antifungals can save lives.

Keywords: Aspergilloma, Aspergillosis, Endocarditis, Disseminated, Heart, Infection, Mortality, Limb Ischemia, Embolectomy, Case Report.

Acknowledgments: Department of Pathology, Hamad Medical Corporation for providing the histopathology images.

Funding Information: Nothing to declare.

Conflict Of Interest: Nothing to declare.

Biography

Dr. Ahsan Ehtesham graduated from Dow University of Health Sciences in 2016. He is currently a resident in training in cardiothoracic surgery since 2020 at the prestigious Hamad Medical Corporation. He is an active researcher with a growing portfolio of articles, researches, and case reports. Currently he has 4 published articles, with 5 more projects underway.

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Acute HIV infection presenting as eczema herpeticum and herpes simplex keratitis: A case report

Introduction: Eczema Herpeticum (EH), also known as Kaposi's varicelliform eruption, is an unusual, severe manifestation of herpes simplex infection. It usually presents in pediatric patients with history of atopic dermatitis. It can be a life-threatening disease with mortality risk due to complications of systemic infection. Herpes simplex keratitis is a potentially blinding disease due to infection and inflammation of the cornea. Persons with immune deficiencies and Human Immunodeficiency Virus (HIV) infection are at increased risk for herpes keratitis. We present a case of eczema herpeticum and herpes keratitis in a Colombian patient with acute HIV infection.

Case Presentation: A 30 year-old Colombian male with past medical history of atopic dermatitis presented to the emergency room with complaints of three days of a facial rash and eye pain. He initially had pruritus, edema and palpebral erythema of the right eye. On the third day of symptoms, he presented fever and noted a painful erythematous rash on his right frontal region, right periorbital region and dorsum of the nose, with multiple umbilicated papules and vesicles, and some superficial ulcers. Additionally, he experienced severe pain in the right eye, with blurry vision and epiphora.

On physical examination, erythema, multiple vesicles, papules and "punched-out" erosions were noted on the nose, right upper eyelid, right frontal and cigomatic region, and the scalp. Cervical lymphadenopaties were noted. Conjunctival injection, chemosis, and decreased corneal sensation were noted on eye examination. Oral examination was unremarkable

Polymerase Chain Reaction (PCR) for Herpes Simplex Virus-1 (HSV-1) was positive. Intravenous and ophthalmic acyclovir were started. Laboratory studies revealed White Blood Cells (WBC) count of 4970/uL, neutrophils were 3830/uL, lymphocytes were 480/uL; platelet count was 127000/uL. Human Immunodeficiency Virus (HIV) testing was positive. Viral load was 26712 copies/mL. CD4 count was 228 cells/mm^3. Highly Active Antiretroviral Therapy (HAART) was started.

Discussion: Eczema herpeticum is an unusual superinfection caused by herpes simplex virus. It usually affects patients with atopic dermatitis, but it has also been described to affect patients with Hailey-Hailey disease, pemphigus, mycosis fungoides, and Sezary syndrome. The most commonly compromised regions include the face, neck, and thorax. EH is characterized by painful, vesicles, pustules, ulcers and umbilicated papules. Risk factors include younger age, nonwhite ethnicity and psoriasis. Disruption of the epithelial barrier and immunosuppression allow a widespread infection. Around 10% of EH patients have eye involvement. Herpes keratitis is the leading infectious causes of corneal ulcers and blindness in the world. Primary infection occurs after inoculation of mucosal or skin surface. Clinical manifestations include conjunctivitis, chemosis, blurry vision, reduced corneal sensation and corneal ulcers. Herpes keratitis can be clinically diagnosed, although PCR and viral culture may be performed for diagnostic confirmation. Treatment with antivirals reduces viral replication, severity of the lesions and prevents complications.

Conclusion: Eczema herpeticum is a severe infection of the skin that affects persons with underlying skin disorders. It may be life-threatening, particularly in immunocompromised patients. Herpetic keratitis is a potentially blinding disease caused by HSV. Both conditions should be considered in HIV patients. Early antiviral treatment is of paramount importance to prevent associated morbidity and mortality.

Audience Take Away Notes

- To identify an unusual dermatologic finding in HIV patients
- To recognize a life-threatening complication of atopic dermatitis
- To be aware of the association between eczema herpeticum and herpes simplex keratitis

Photo of the patient

Biography

Dr. Vivas studied Medicine at Icesi University, Cali and graduated as MD in 2020. He joined the research group of Dr. Tobon MD, PhD at Centro de Investigación en Reumatología, Autoinmunidad y Medicina Traslacional (CIRAT). He has published 9 research articles in SCI(E) with over 55 citations. He currently works as a physician in the emergency department in Armenia, Colombia.

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Multi-omics workflow for the identification of discriminant markers associated with trypanosoma cruzi populations

Introduction: Trypanosoma cruzi (T. cruzi) is a protozoan parasite that causes Chagas disease. This zoonotic disease is transmitted to human by blood-sucking triatomine bugs. According to WHO, Chagas disease is affecting 30 000 new cases and is causing 13 000 deaths per year mainly in Mexico, Central and South America. The life cycle of T. cruzi implies a differentiation of non-infective to infective forms within the triatomine gastrointestinal tract and an intracellular progression of T. cruzi infection in human. After surviving the acute stage, patients progress in a large part to an asymptomatic chronic infection. In around 30-40% of the cases, they can progress towards further complications such as cardiomyopathy and gastrointestinal tract mega syndrome. Currently, knowledge limitations of the mechanistic processes associated with the persistence of T. cruzi compromise the development of improved treatments for Chagas disease.

To improve the understanding of Chagas disease, two populations (replicating epimastigotes and replicating amastigotes) have been isolated. An integrated proteome and transcriptome profiling method has been performed to identify discriminant markers/pathways associated with the stage of infection.

Material & Methods: Intracellular amastigotes can be isolated by repeated passage of infected host cells through a syringe needle. This is a rapid procedure but with safety issues. Fluorescently tagged amastigotes can be further sorted using an Aria BD cell sorter. This technique achieves a higher purity with a lower yield and can be time-consuming. Cells were inactivated with a nonionic detergent (Cell Disruption Buffer, PARIS kit - Thermo) and frozen until preparation. Samples were then divided in two for parallel proteomic and transcriptomic analysis.

Results: A clear separation of amastigote and epimastigote populations was observed for both the transcriptome and the proteome profiles. An additional separation of the amastigote populations was observed for both techniques. This separation could be explained by the difference of infection stages between the replicates (optimization of the isolation procedure). A higher number of down regulated genes and proteins was observed in amastigotes compared to epimastigotes. An off/on pattern of protein expression was observed mainly in amastigotes (590 proteins were absent in amastigotes and present in epimastigotes).

Conclusion: A robust method was developed to explore the transcriptomic and proteomic profiles of diverse parasite populations from a single sample. The observed distinction in transcriptomic and proteomic profiles of amastigotes and epimastigotes might be explained by their intracellular or extracellular states, respectively. Identification of differentially expressed genes and proteins between populations will further allow to select discriminant markers/pathways. The ability to sort different amastigote sub-populations, will be of interest to isolate “dormant/quiescent” parasites that may have a role in treatment failure. Low input and/or single-cell approaches are needed to deeply investigate these relevant populations.

Audience Take Away Notes

- We propose a full workflow to isolate and analyze different populations of Trypanosoma cruzi
- The initial steps of the workflow are common to the proteomic and transcriptomic analysis limiting the number of samples and cells required for this multi-OMICS analysis
- This integrated proteome and transcriptome profiling method will bring insight in the mechanisms involved in T. cruzi differentiation and treatment resistance

Biography

Dr. Amy Hesketh studied Biology with a special focus on Genetics at the Clermont Auvergne University, France and graduated as MS in 2017. She then joined the research group of Dr. Olivier Mathieu at the Institute of Genetic, Reproduction and Development (iGReD). She received her PhD degree in 2021 at the same institution. She obtained the position of Research Fellow at the BIOASTER institute and is now Team Leader of the Genomics and Transcriptomics team.

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The comparative effectiveness of antipyretics between oral paracetamol and intravenous metamizole in fever patient

Background: Fever is the most commonly encountered issue in hospitalized patients. The most frequently used antipyretics to address fever are paracetamol and metamizole. The choice of drug administration route is considered to potentially reduce the treatment period, and also affects the number of payments based on the Indonesian Case-Based Groups (INA-CBGs) by the Indonesian Health Insurance (BPJS Kesehatan).

Aims: This study aims to analyse the comparative effectiveness of antipyretics between oral paracetamol and intravenous metamizole in fever patients at the Inpatient Installation of RS Bala Keselamatan Bokor in September-October 2019.

Methods: An observational analytical design with Independent T-Test was used with inclusion and exclusion criteria. Inclusion criteria: fever patients (axillary temperature ≥ 37.5°C, aged > 18 years, willing to be a respondent, capable of active communication, and receiving therapy with oral paracetamol or intravenous metamizole. Exclusion criteria: aged < 18 years, hypersensitivity reactions to paracetamol or metamizole, patients with brain involvement diseases resulting in hypothalamic set-point disturbance.

Results: The study was conducted on 20 fever patients with the characteristics of 13 males (65.4%) and 7 females (34.6%). The mean initial temperature in the oral paracetamol group was 38.73°C and after 1 hour it became 36.53°C. In the intravenous metamizole group, the mean initial temperature was 38.66°C and after 1 hour it became 36.56°C. The temperature decrease after 15 minutes in the oral paracetamol group (1.45) was higher than the mean value in the intravenous metamizole group (0.42). However, after 30 minutes (Sig. $0.563 < 0.05$) and 1 hour (Sig. $0.744 < 0.05$), the temperature did not significantly decrease.

Conclusions: There was a significant difference ($p < 0.05$) in the temperature decrease in the oral paracetamol group compared to the intravenous metamizole group at the 15th minute.

Keywords: Paracetamol, Metamizole, Antipyretic.

Biography

Dr. Diva Farica Sholihah studied Medical Doctor at the Islamic University of Malang and graduated as MD in 2018. Dr. Andi Purwanto is an Internist at Salvation Army Hospital graduated as GP from Brawijaya University Malang Indonesia in 2002, as Internist from Airlangga University Surabaya in 2015. He then joined the Indonesian Medical Association and member of Indonesian association of Internal Medicine.

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A case of late onset prosthetic valve endocarditis with cerebral thromboembolic episodes and aseptic meningitis

This case report describes a 57-year-old man with a history of Coronary Artery Bypass Grafting (CABG) and mitral valve replacement who presented with fever, rigors, and focal neurological symptoms. The patient was diagnosed with late-onset Prosthetic Valve Endocarditis (PVE) complicated by cerebral thromboembolic episodes and aseptic meningitis. In this presentation, attendees will be guided through a detailed exploration of late-onset Prosthetic Valve Endocarditis (PVE) utilizing a captivating case study as the focal point. The discussion will unravel the intricate nuances of this challenging clinical entity, encompassing diagnostic dilemmas, therapeutic approaches, and clinical ramifications. By dissecting the complexities of late-onset PVE, participants will gain invaluable insights into its pathophysiology, clinical manifestations, and management strategies, equipping them with essential knowledge to navigate this intricate terrain effectively.

The presentation commences by elucidating the clinical presentation of late-onset PVE, emphasizing its protean nature and the diagnostic challenges it poses. Through the analysis of the presented case, attendees will develop a comprehensive understanding of the varied clinical manifestations of late-onset PVE, ranging from fever and rigors to focal neurological deficits. This exploration serves to underscore the importance of maintaining a high index of suspicion for infective endocarditis in patients with prosthetic valves, particularly in the context of atypical presentations.

Subsequently, the discussion delves into the diagnostic workup of late-onset PVE, elucidating the role of various investigative modalities in establishing a definitive diagnosis. Attendees will gain insight into the limitations of conventional diagnostic techniques, such as transthoracic echocardiography, and the pivotal role of transesophageal echocardiography in confirming the presence of vegetations on prosthetic valves.

Moreover, the presentation navigates through the therapeutic landscape of late-onset PVE, addressing the complexities of antibiotic therapy and the potential role of surgical intervention. Attendees will be guided through the rationale behind antibiotic selection, including considerations for antimicrobial coverage and duration of therapy. Furthermore, the discussion will explore the indications and timing of surgical intervention in late-onset PVE, highlighting the importance of a multidisciplinary approach in optimizing patient outcomes.

Audience Take Away Notes

- Enhanced understanding of the clinical manifestations and diagnostic considerations of late-onset PVE
- Insight into the optimal management strategies, including antibiotic selection and the role of surgical intervention
- Appreciation of the importance of timely recognition and treatment of embolic complications to improve patient outcomes

- Recognition of the diagnostic limitations of transthoracic echocardiography and the utility of transesophageal echocardiography in confirming the diagnosis
- Application to Audience
  - Attendees will be equipped with the knowledge and skills necessary to recognize and manage late-onset PVE effectively in their clinical practice
  - This presentation serves as a valuable resource for faculty seeking to expand their research or teaching in the field of infectious diseases and cardiology
  - The insights provided offer practical solutions for clinicians and designers, streamlining diagnostic and therapeutic decision-making processes
  - Improved accuracy in diagnosis and treatment planning will lead to better patient care and outcomes, ultimately enhancing the efficiency and effectiveness of healthcare delivery

Biography

Dr. Christodoulou studied in Aristotle University Medical School in Thessaloniki and graduated in 2019. He then worked as a rural service doctor in Naxos General Hospital for one year. Then he worked in Larnaca General Hospital, in the Internal Medicine Clinic, as a junior doctor for 4 months. He is currently working as a resident doctor of Internal Medicine in Serres General Hospital in the 3rd year of his residency. He has participated in the ECIM 2024 with one poster presentation and in the 15th Panhellenic Infectious Diseases Conference with three poster presentations.

Andrew Kimera[1]*, Joan Mutyoba[2], Lynn Atuyambe[2], Nelson Mukiiza[3], Andrew Basenero[3]

[1]College of Health Sciences, Makerere University College of Health Sciences, Kampala, Uganda
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Hepatitis B vaccination uptake and associated factors among communities targeted for mass vaccination in Gulu, Uganda

Background: Hepatitis B Virus (HBV) is associated with several acute and long-term complications and vaccination is the cornerstone of prevention. A recent outbreak in Gulu, Uganda, one of the districts covered by a mass vaccination campaign, suggests low uptake of HBV vaccination.

Objective: To determine uptake and completion of HBV vaccination and associated factors among residents of Gulu, Uganda.

Methods: This was a cross-sectional study among residents of Gulu in Northern Uganda; Gulu city representing urban Gulu and Gulu District representing rural Gulu. A total of 434 adults (>18 years) that had been residents of this area for at least 5 years at the time of study were recruited. A pretested study questionnaire was used to obtain data for socio-demographics, perceptions, and knowledge on HBV vaccination as well as measure uptake and completion. Additionally, 10 key informant interviews were conducted. The uptake, completion and factors associated to HBV vaccination were determined. Thematic analysis was used for qualitative data.

Results: The median age of participants was 33 (IQR: 26-44) years; 246/434 (56.7%) were females. Out of 434 respondents, 182 (41.9%), 141 (32.5%), 87 (20%) had ever received at least one dose, at least 2 doses and all the 3 doses of the vaccine. 47.8% of those vaccinated completed. Factors related to: Non-uptake were not being aware of the vaccination campaign, myths about the vaccine, inaccessibility of the vaccine and fear; Incompletion: lack of awareness of need to complete, poor access to vaccination points or sites and myths; and for uptake of hepatitis B vaccine were being female, Adj. PR: 1.33 (1.09 – 1.61), urban residence, Adj. PR: 1.49 (1.19-1.88), low perceived risk Adj. PR: 1.58 (1.31-1.91), perceived lack of safety of Vaccine-Adj. PR: 2.83 (1.27-6.32) and awareness about the mass vaccination campaign, Adj. PR: 2.36 (1.52-3.67). Factors associated with completion of the hepatitis B vaccination schedule were urban residence, Adj. PR: 2.67 (1.58-4.49) and low perceived risk PR: 2.94 (1.98-4.37). Health facility factors that influenced uptake and completion were: inadequate mobilization and low sensitization; stock outs; inadequate facilitation for health workers; VHTs Distance from facility; health worker knowledge gaps; poor attitude towards none routine vaccination by some health workers; mistrust of the government; myths and fear of side effects.

Conclusion: The uptake and completion of Hepatitis B vaccine were low in Gulu (41.9%, 20%). Sex, residence, perceived risk to Hepatitis B, perceived safety of the vaccine and awareness of the mass vaccination campaign independently influenced the uptake of the vaccination. Whereas, residence and perceived risk to Hepatitis B with completion. The government therefore should invest in creating awareness to the health workers and masses and also bring vaccination services closer to the community by empowering the community health workers.

Audience Take Away Notes

- The uptake rates of the Hepatitis B vaccine in highly endemic communities of Sub-Saharan Africa
- The unique factors that affect the Uptake and completion of the vaccination series during Mass vaccination campaigns to inform on key strategies for intervention
- Possible further research areas in for vaccine uptake to improve on the level of protection
- Success pointers of vaccination in the highly endemic Sub-Saharan Africa as a step in reducing the Global burden of Hepatitis B infecetion

Biography

Dr. Kimera Andrew is currently a finalist Paediatrics resident at the College of Health Science, Makerere University; Uganda with special interest in Infectious disease prevention through vaccination. He holds a Masters of Public health from Makerere and studied Hepatitis B vaccine uptake following mass vaccination in highly endemic regions of Uganda. He also has experience in Hospital Management and underwent a short training in management studies at the Uganda Management Institute, Uganda. His passionate about child health, disease prevention and policy analysis. He is also a dedicated Husband and father of 2 back working with C-Care IMC now 8 years.

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[2]Department of Pediatrics, School of Medicine, Makerere University College of Health Sciences, Kampala, Uganda and Research Department, Joint Clinical Research Centre, Kampala, Uganda.
[3]Rinecynth Advisory, Kampala, Uganda

Immune response to Hepatitis B vaccination among children under 5 in a highly endemic country in Sub-Saharan Africa: Uganda

Background: Hepatitis B virus vaccination plays a crucial role in preventing Hepatitis B infection, particularly in high-risk groups such as children under-five, who have a 60-90% higher chance of seroconversion. As per the World Health Organization (WHO), about 5–10% of infants may not respond effectively to the vaccination, leaving them vulnerable to Hepatitis B virus and its complications. The paucity of data on the Immune response to hepatitis B Virus vaccination among children raises the question of how protected our children in Uganda are against Hepatitis B.

Objective: To determine the immune response to Hepatitis B vaccination and associated factors among children under five attending the outpatient care at Mulago Assessment Centre Pediatrics clinic.

Methods: This was a cross-sectional study among children (1 to < 5) years attending MAC Paediatrics clinic at Mulago National Referral Hospital who met the eligibility criteria in the month of February, 2023. All children 1-5 whose caregivers gave consent were enrolled and a pretested study questionnaire was administered by trained research assistants. Blood samples taken for analysis; Hepatitis B core antibody screening and anti HBs Ag titres by Electrochemiluminescence using the Cobas 6000. Descriptive analysis using proportions was used to determine the immune response as good or Poor response. Logistic regression analysis was done to determine factors that were independently associated with the different categories of immune response.

Results: Total of 301 children under 5 years, majority aged 2 years (29.6%). All were negative for the Hepatitis B core antibody. The immune response from 2 IU/ml to 1000 IU/ml with median titres of 86.2 IU/ml (IQR: 14.5, 239.4). 77.4% (233/301) (95% CI: 72.3% - 81.8%) had a good response and 58.4% (136/233) (95% CI: 51.9% - 64.6%) very good responders. Younger age and caregiver HIV status being negative were found to be independently associated with a good immune response.

Conclusion: Children at MAC Paediatrics clinic had a protective level of antibodies to HBV vaccine at 77% which is still less than the expected 95% by WHO. Younger age and negative parental HIV status were independently associated with good response. Emphasis should be made on birth dose, booster to at risk groups and periodic studies to monitor the response in children.

Audience Take Away Notes

- Information on the immune response to the vaccines being used against the Hepatitis B virus especially in Sub Saharan Africa that is highly endemic
- The possible key issues that affect the response to vaccination against Hepatitis B that could be used for targeted interventions
- Possible further research areas in the Immunological response to Hepatitis B vaccination among children

- Global strategies in place to eliminate Hepatitis B and how they are being implemented especially in Africa
- Success pointers of vaccination in the highly endemic Sub-Saharan Africa as a step in reducing the Global burden

Biography

Dr. Kimera Andrew is currently a finalist Paediatrics resident at the College of Health Science, Makerere University; Uganda with special interest in Infectious disease prevention through vaccination. He holds a Masters of Public health from Makerere and studied Hepatitis B vaccine uptake following mass vaccination in highly endemic regions of Uganda. He also has experience in Hospital Management and underwent a short training in management studies at the Uganda Management Institute, Uganda. His passionate about child health, disease prevention and policy analysis. He is also a dedicated Husband and father of 2 back working with C-Care IMC now 8 years.

Ashin Mehta*, BS; Timothy Yung, MD; Whitt Davis, DO; Jennifer Choi, DO; Sanjay Singh, MD

Department of Internal Medicine, Medical College of Wisconsin, Milwaukee, WI, United States

PD-associated peritonitis: A case first for aquamicrobium

A 56-year-old male with end-stage renal disease undergoing home peritoneal dialysis presented with abdominal pain, nausea, and altered mental status. White blood cell count was 12.3 10e3/uL, urinalysis was positive for 2+ blood, and peritoneal fluid contained a total nucleated cell count of 1840 with 98% neutrophils. The patient was empirically treated with intravenous piperacillin-tazobactam and vancomycin, and a 2% mupirocin ointment was applied around his peritoneal catheter site. Following this treatment, he showed significant symptomatic improvement. On hospital day three, the patient's fungal culture and Methicillin-resistant Staphylococcus aureus came back negative, but his aerobic/anaerobic culture was positive for Aquamicrobium lusatiense. Aquamicrobium is an aerobic gram-negative rod which until recently had only been isolated from wastewater and contaminated soil. In 2021, two cases of Aquamicrobium infection in humans were reported. Both resulted in endophthalmitis following cataract surgery. To our knowledge, this was the third case of Aquamicrobium infection in a human and the first example of this agent causing peritonitis. Following identification of the infectious agent, the patient was transitioned to intraperitoneal vancomycin and cefepime. Two days into the new treatment course, the patient's peritoneal fluid demonstrated a total nucleated cell count of 5 with a 40% neutrophil composition. The patient was discharged home after a seven-day inpatient stay with instructions to continue cefepime 1g via intraperitoneal injection for three weeks. On the day of discharge, his white blood cell count was 4.4 10e3/uL.

Audience Take Away Notes

- This presentation provides insight on the treatment of a bacterial infection which currently has only three known cases in humans
- Due to its rarity, no guidelines on medically managing Aquamicrobium exists. The two previously reported cases with this infection failed conservative treatment and had to be surgically managed. This presentation serves as a guide for clinicians if they encounter a patient with an Aquamicrobium infection
- This presentation will provide clinicians with awareness to consider Aquamicrobium in a patient who has a culture positive for gram negative rods but negative for common infectious agents

Biography

Ashin Mehta studied Human Biology at the University of Southern California, United States and graduated as BS in 2015. He then joined the research group of Dr. Thomas Anderson at Stanford University where he investigated the efficacy of focused ultrasound to inhibit nerve conduction and reduce post-operative pain. Following this, he began medical school at the Medical College of Wisconsin and will receive his MD in 2025.

Aiki Raji C. O*, Ahmed S. O Olojede, O. A. Fagbohun
Department of Veterinary Microbiology, University of Ibadan, Nigeria

Molecular detection and charcterization of protoparvoviruses in bats and lion in Ibadan, Nigeria

Protoparvoviruses are a diverse genus of small, non-enveloped, single stranded DNA viruses in the Parvovirinae subfamily of the virus family Parvoviridae. Three of the fifteen member species of this genus have been associated with human infections, while some others infect domesticated animals. Parvoviruses are ubiquitous in nature and they possess a diverse host range. Mammalian parvoviruses are potential zoonotic agents, especially if they make incursions with the right mutations into the human ecosystem. As such, there is the need to constantly monitor the parvoviruses circulating in mammals in order to further elucidate the viral diversity, evolution and host-virus interactions. Bats are known to harbor a diverse array of viruses, including several that are highly pathogenic in humans.

Fecal samples were collected from eleven Fruit Bats (Eidolon helvum) and one lion at the Zoological Garden, University of Ibadan, Nigeria. DNA were extracted from the samples using the QiagenTM DNA extraction Kit. A 350 bp portion of the VP2 gene was amplified in order to detect the presence and determine the species of protoparvovirus present. The amplicons were purified and sequenced. The sequences obtained were analysed.

Five of the twelve samples were positive, with the expected band size of 350 bp, four of these were from bats while the only sample from a lion was also positive, the nucleotide sequence analysis confirmed the presence of canine parvovirus in all the samples, with some nucleotide mutations noted. Multiple sequence alignment revealed mutations at positions G4A, A18T, G36A and G 207A in the bat samples while the lion sample showed mutations at positions G4A, A18T and G207A.

David Mejia, Ph.D
Universidad Peruana Cayetano Heredia, Peru

Current situation of Cystic Echinococcosis in Peru

The Cystic Echinococcosis in Peru, is an important problem in public health and in the economy, causing great economic losses both in livestock production and in the recovery of the health of the affected human population (Naquira C., 2010). Human Cystic Echinococcosis has a worldwide distribution, occurring in many parts of South America, including Peru, Argentina, Bolivia, Uruguay, Chile and the southern part of Brazil (Cucher et al., 2016; Pavletic et al., 2017). In Peru, E. granulosus sensu stricto (G1 genotype) was mainly identified in all animal hosts, while, the E. canadensis (G7 genotype) was only identified in cysts from pigs and alpacas. This is the first report of E. granulosus sensu stricto and E. canadensis in llamas and alpacas, respectively (Sanchez et al., 2022).

In my country, the accumulative incidence rates fluctuate between 39 and 79 cases per 100,000 inhabitants. However, since 1980, hydatidosis has not been treated by the state and is one of the neglected diseases (Moro et al., 1997; Perez et al., 2007; Rafael et al., 2008; Irabedra & Salvatella, 2010). In studies carried out on animals in the department of Junín, an 87% prevalence is reported in sheep and between 32 and 79% in dogs, these being the highest reported prevalences in South America (Cardona, 2013; Carmena, 2013). A study in the andean region of Peru with echographic examination and X ray test, the overall prevalence of human cystic echinococcosis was 5.5% (52/949) and the 95% confidence interval varied from 4.1 to 7.1% (Chumbe et al., 2007).

The prevalence of human echinococcosis in this endemic area of Peru is one of the highest in Latin America, due to the close interaction with dogs, as they shepherd the flocks, plus poor sanitation and hygiene conditions in the area (Chumbe et al., 2007). A study in the Tacna Region of Peru found a 4.96% prevalence of echinococcosis in bovine species for the period 2001-2010, the prevalence for sheep was 91% for the period 2001-2010; and the human prevalence rate in the Tacna Region is 10 x 100 000 habitants for the period 2001-2010 (Velasco et al., 2010). High prevalence in Peru and even more so in the central Andean region: Cerro de Pasco, Junín, Huancavelica (Guerra et al., 2015). Currently progress is very slow to deal with this zoonosis, personally I'm in charge of educating or giving talks to the inhabitants of the endemic areas or towns of Peru. Also, I'm working (my doctoral thesis) on the generation of Alpaca antibodies for the serological diagnosis of this disease.

Appendix: 1

Lachaqui, Canta – Peru, 4000 msnm. December 31, 2020.

Huancavelica, Peru 4500 msnm July 2022.

Biography

David Mejia PhD (c) Veterinarian PhD candidate, Student of the Doctoral Program in Sciences (Biochemistry and Molecular Biology) at the “Cayetano Heredia” Peruvian University. He then joined the research group of Molecular Biotechnology (at the same university). He received his Master degree in 2020 at the San Marcos University (Peru) working in the Genetics and Molecular Biology Laboratory (2016-2018). He has published 1 article and participated in National and International Conferences.

David Kent Stiles*, PhD; Ashish Bhandari, MS; Harish Shankaran, PhD; Helen Wei, PhD; Shane Rowley, PhD; Gaurang Patel, MD; Brian Lu, MD

Recursion Pharmaceuticals, Inc., Salt Lake City, UT, United States

REC-3964, a first-in-class molecule for the prevention of recurrent clostridioides difficile infection

REC-3964 is an oral, novel, diazepinedione-class chemical entity identified from Recursion's high-content phenotypic imaging platform. REC-3964 inhibits toxins associated with Clostridioides Difficile Infection (CDI).

In a disease-relevant hamster model of acute CDI, REC-3964 extended survival in a dose-dependent manner. In this same model, REC-3964 significantly extended survival compared to bezlotoxumab. Monotherapy was safe and well tolerated when administered as single doses up to 1200 mg and multiple doses up to 900 mg in a healthy volunteer, single- and multiple-ascending dose study (n=90). Exposures (AUC) increased approximately dose-proportionally across dose ranges tested, and half-life ranged from approximately 7–10 hours. All Treatment-Emergent Adverse Events (TEAEs) were mild in severity with no serious adverse events, deaths, or TEAEs leading to discontinuation. No clinically relevant effects on vital signs, ECG parameters (including QTcF), or other laboratory parameters were observed in the study.

Planned study REC-3964-201 will evaluate recurrent CDI (rCDI) reduction with REC-3964 after initial clinical resolution. Based on preclinical data indicating a dose-dependent treatment effect, two doses of REC-3964 are being explored.

Overall, these data demonstrate that REC-3964 is a safe and well-tolerated, orally bioavailable, small molecule Clostridioides difficile toxin inhibitor with potential to prevent rCDI in high-risk patients.

Audience Takeaway Notes

- Clostridioides Difficile Infection (CDI) is a leading cause of diarrhea in people treated with antibiotics, and those with extended stays in healthcare settings are at especially high risk. CDI is recurrent in >20% of patients and can lead to severe colitis, sepsis, organ failure, and death
- C. difficile toxins inactivate Rho GTPase inside cells of the gut lumen, which induces apoptosis and barrier dysfunction, driving CDI pathophysiology
- Current standard of care for CDI is vancomycin or fidaxomicin with added intravenous bezlotoxumab for high-risk patients
- Recursion's approach to drug development identified REC-3964, a small molecule that blocks C. difficile toxin enzymatic activity without affecting the host enzyme, preventing toxin-mediated damage. REC-3964 rescued barrier activity and extended survival in CDI animal models
- This first-in-human study showed that REC-3964 administered orally had favorable pharmacokinetic and safety profiles across doses in healthy volunteers and is suitable for evaluation in the planned phase 2 study in patients with CDI

Biography

David Stiles has been working as a clinical pharmacologist and pharmacometrician in the pharmaceutical and drug delivery industry for 18 years. Previous employers include Medtronic, Pfizer, Vertex, and Vigil Neuroscience working in clinical areas such as neurology, pain management, cystic fibrosis, and rare disease. He is currently a clinical pharmacologist employed at Recursion, supporting clinical and nonclinical drug development. He has a PhD in Systems Engineering with a focus on biomedical applications from Oakland University.

Dr. Dorarca Lynch*, Dr. Rhea O' Regan, Prof. Catherine Fleming

Infectious Diseases Department, Galway University Hospital, Galway, Ireland

HAV-ing a Moment

Clinical case: We present a case of a 32-year-old Indian gentleman admitted to a tertiary hospital in the West of Ireland Hospital with a weeklong history of fevers and right upper quadrant pain complicated by the development of clinical jaundice. His past medical history was significant for previously treated Malaria. 3 weeks prior to presentation to our hospital, he travelled from Southern India, spending time in Mumbai before relocating to Ireland. In Mumbai he noted being bitten by numerous mosquitos as well as consuming street food including fresh watermelon.

Initial work up demonstrated thrombocytopenia of 124 x109L (150-400x109L), haemoglobin of 15g/dL (13.0-17.0g/dL) and Bilirubin of 95g/dL (1-21g/dL). Liver function tests were grossly deranged with ALT of 2000 u/L (0-40u/L) and INR of 1.3.

Patient was investigated extensively for Fever in Returning traveller work up. Multiple malaria blood films returned negative and blood cultures remained sterile. HIV, Hepatitis B, C and E were not detected. Leptospirosis, Chikungunya and Dengue serology returned negative. Hepatitis A IgM subsequently returned positive with HAV IgG negative.

Ultrasonography of his abdomen showed a thickened oedematous appearing gallbladder wall consistent with acute acalculous cholecystitis.

The patient clinically and biochemically improved with supportive therapy.

Background: Hepatitis A is the leading cause of hepatitis worldwide. It is an RNA virus which is spread by direct contact with persons who have been infected or by ingesting contaminated water or food, with an incubation period of 14 to 28 days. It occurs sporadically and in epidemics worldwide with a tendency for cyclic recurrence. The virus is endemic in low-income countries where sanitary conditions are poor. Interestingly improved living conditions in certain countries has reduced the incidence of Hepatitis A infection, however, this can lead to more severe disease in susceptible adults who have not acquired immunity in childhood. The changing epidemiology of Hepatitis A sees a higher proportion of symptomatic cases as the average age of infection increases. Mandatory vaccination for high-risk groups is being called for in certain parts of India following outbreaks of Hepatitis A earlier this year.

Acute acalculous cholecystitis is inflammation of the gallbladder without evidence of gallstones. This is a very rare complication of Hepatitis A. The pathophysiology of acalculous cholecystitis during acute viral hepatitis remains unclear.

Audience Take Away Notes

- Highlighting the importance of globalization and the changing epidemiology of Hepatitis A as well as the changing spectrum of imported illnesses seen in tourists and migrants presenting to hospitals and community-based practices throughout Ireland
- The role of vaccination in high-risk areas as a preventative measure

- The importance of a thorough travel history and epidemiological risk factors when presented with a patient with a fever returning from travel
- Acalculous cholecystitis is a very rare complication of acute viral Hepatitis A

Biography

Dr. Dorarca Lynch graduated with a first-class honours' degree in medicine from University of Galway, Ireland in 2019. She has been working in general medicine since graduation in Ireland and Australia, with a specific interest in Infectious Diseases. She is a member of the Royal College of Physicians of Ireland since completing her examinations in 2023. She is currently completing the Basic Medical Specialty training in the West of Ireland. She plans to pursue a career in Infectious Diseases in Ireland commencing higher specialist training in the coming years.

Edeline Anne L. Dondonilla, RND, MD[1]*; Grace Malayan, MD, FPPS, FPAPP[2]; Ma. Lucila M. Perez, MD, MSc, FPPS[3]

[1]Ospital ng Makati, Metro Manila, Philippines
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Five year profile and outcomes of pediatric patients diagnosed with tuberculosis at a Tertiary Hospital in Makati, Philippines (2016-2020)

Background: The Philippines ranks fourth worldwide in tuberculosis incidence and is considered as a high-burden country of tuberculosis in the world. Differences in the pathophysiology and clinical presentation of TB in children make diagnosis more challenging than in adults.

Objectives: This study aims to provide a socio-demographic profile and treatment outcomes of admitted patients and managed as cases of Pulmonary and Extra-Pulmonary Tuberculosis at Ospital ng Makati Department of Pediatrics from January 2016 to December 2020.

Design: Descriptive.

Methodology: 127 children aged 18 years old and below who were diagnosed with tuberculosis (Pulmonary and Extrapulmonary Tuberculosis) and admitted at Ospital ng Makati Department of Pediatrics from January 2016 to December 2020 were included in the study.

Results: From the 127 patients included in this study, 91 (71.65%) have Pulmonary TB (PTB) while the remaining 36 (28.35%) have Extrapulmonary TB (EPTB). In general, there are more male patients who contacted Tuberculosis. In most of the age groups, male PTB patients shows more symptoms than female PTB patients. Symptoms are more prominent in ages 1 – 3 years. Aged 14-18 years old presented with the most cases. And TB Meningitis was the most common EPTB.

Conclusion/Recommendations: This study highlights the importance the synergistic use of thorough history taking, physical examination, clinical presentation and laboratory findings in diagnosing tuberculosis, and the importance of timely identification of TB cases which may consequently be used in further improving outcomes to achieve the eventual eradication of Tuberculosis.

Keywords: Tuberculosis, Pulmonary Tuberculosis, Extra-Pulmonary Tuberculosis, Clinical Profile, Descriptive.

Audience Take Away Notes

- Tuberculosis, being an endemic disease in the Philippines still heavily burdens the population, particularly the pediatric population. In this new era of technology and globalization, the progression, disease burden and societal impact of tuberculosis will not only effect 3rd world countries, but can also impact other regions, and even globally. The study aimed to present the profile and outcomes from a five-year period (2016-2020). During which, in 2020, the COVID-19 Pandemic has started, which heavily influenced the health-seeking behaviors of patients, and thus, also impacting the results of this study. It can also give the audiences an overview of the disease burden, and how this affects the pediatric population who are very vulnerable in contracting tuberculosis. Tuberculosis in the young is not just a specific age group problem, but is also reflective of the disease containment in all ages which can give light to future projects and researches for better implementation in early recognition of the disease and improvement on compliance with treatments. Knowledge on the profile and outcomes will also aid in further investigation of the impact of COVID-19 and other emerging infectious diseases in the management and outcomes of Tuberculosis. This in turn can help not just the medical community but also policy makers in future projects on the road to eradication of tuberculosis not just in the Philippines but the whole world

Biography

Dr. Edeline Dondonilla studied BS Nutrition and Dietetics as her undergraduate degree at University of the Philippines – Los Banos and completed her degree of Doctor of Medicine in University of the Perpetual Help DALTA-Jonelta in 2016. She underwent her Medical Internship training at Victoriano Luna Medical Center in 2017. She underwent and completed her training specializing in Pediatrics in 2021 in Ospital ng Makati – a tertiary local government hospital in the Philippines.

Eduardo Ferracioli Oda[1]*, Tatiana Tanaka[1], Michele Soares Gomes Gouvea[2], Joao Renato Pinho[2], Veronica Coelho[3], Carlos Eduardo Hirata[1], Joyce Hisae Yamamoto[1]

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Low-volume direct multiplex PCR for etiological diagnosis of infectious uveitis

Purpose: To describe the pathogens detected in intraocular fluid of individuals with active uveitis using a low-volume direct multiplex PCR.

Methods: Eighty-six individuals with active uveitis were included in this study between July, 21 and November, 23. All participants had at least (2+) cells in Anterior Chamber (AC) or vitreous haze. Samples were obtained by AC paracentesis (81 samples) or pars plana vitrectomy (5 samples). We also included 23 control samples, being aqueous humor from cataract surgery (21 samples) and vitreous humor from epiretinal membrane surgery (2 samples). Twenty µl of the sample was analysed through a qualitative direct multiplex real-time Polymerase Chain Reaction (PCR) assay, developed by Japanese researchers for uveitis diagnosis purpose. It detects Herpes Simplex Virus (HSV) 1 and 2; Varicella-Zoster Virus (VZV), Cytomegalovirus (CMV), Epstein-Barr Virus (EBV), Human Herpes Virus 6 (HHV6), Human T-Lymphotropic Virus (HTLV), Treponema pallidum and Toxoplasma gondii. This multiplex PCR was validated mainly in Japan. This study was approved by Institution Ethics Committee (CAAE 91413918.5.0000.0068) and all participants signed the informed consent form.

Results: The clinical characteristics of the uveitis were as follows. Anatomic classification were mainly anterior (39 patients; 45.3%) and posterior (37 patients; 43%). The onset/course of the uveitis: first acute episode in 32 patients (37.2%), recurrent in 28 patients (32.5%) or chronic in 29 patients (33.7%). Overall positivity was 23.5% (20/86 samples); among acute uveitis, it was 28.8% (17/59 samples) and, among infectious uveitis (diagnosis before intraocular fluid analysis), it was 35.1% (20/57 samples). Herpes virus was detected in 10 samples (50%). The agent detected and final diagnosis based on clinical and PCR results were: EBV in three samples (VZV PCR+ acute retinal necrosis and coinfection with EBV; PCR- toxoplasmosis but EBV+ in two cases); CMV (CMV associated anterior uveitis in two cases) and HHV6 (HHV6 associated anterior uveitis in two cases) in two samples, each; VZV (VZV associated acute retinal necrosis), HSV2 (HSV2 associated acute retinal necrosis) and HSV1 (HSV1 associated acute retinal necrosis) in one sample each. Toxoplasma gondii was detected in 9 samples (45%) and all cases had retinochoroiditis. HTLV and T. pallidum were detected in one sample each and both cases had diffuse uveitis. The strip PCR changed the etiological diagnosis in five cases (5.8%; 3 cases of herpetic uveitis to toxoplasmosis, one case of syphilis to toxoplasmosis and one case of toxoplasmosis to herpetic uveitis). Detailed results are shown in Tables 1 and 2.

Conclusion: For uveitis etiological diagnosis, direct strip PCR was able to demonstrate the infectious agent in almost one fourth of our sample, using just a small sample volume, remaining material for further analysis of this valuable low-volume sample. The multiple pathogens selected encompass the most important infectious uveitis etiologies. Further, even though most patients were under use of topical and/or systemic therapy, we could not observe interference of treatment in PCR positivity.

Table 1. Clinical data of participants with uveitis (n=86)

	NIU (n=29)	Infectious Uveitis (IU)			
		Overall (n=57)	Herpetic (n=24)	Toxoplasmosis (n=25)	Other (n=8)
Age, median (range), years	50 (19 - 82)	53 (20 - 77)	54.5 (22 - 74)	47 (20 - 74)	44.5 (26 - 77)
Gender, F/M (%)	22/7 (75.8/24.2)	22/35 (38.6/61.4)	11/13 (45.8/54.2)	7/18 (28/72)	4/4 (50/50)
Strip PCR positivity, n (%)	0 (0)	20 (35.1)	7* (29.2)	11 * (44)	2 (25)

One sample were positive for VZV and EBV, two cases with final diagnosis of toxoplasmosis were positive for EBV.

Table 2. Clinical characteristics of participants with herpetic or toxoplasmosis uveitis according to Direct Strip multiplex PCR result

	Herpetic uveitis						Toxoplasmosis uveitis		
	Anterior uveitis			Posterior uveitis					
	PCR + (n=5)	PCR – (n=15)	P	PCR + (n=2)	PCR – (n=2)	P	PCR + (n=9)	PCR – (n=16)	P
Anterior chamber / vitreous cells	2 (2 - 3)	2 (2 - 3)	>0.999§	3 (3 - 3)	3 (2 - 4)	>0.999§	2 (2 - 3)	3 (2 - 4)	0.297§
Duration of active uveitis in days	63 (9 - 115)	43.5 (2 - 204)	0.767§	31.5 (27 - 36)	75.5 (67 - 84)	0.333§	39 (9 - 258)	22.5 (3 - 339)	0.054§
No treatment*, n (%)	2 (40)	8 (53.3)	>0.999†	0 (0)	0 (0)	-	1 (11.1)	8 (50)	0.087†
Antiviral or antibiotic systemic treatment, n (%)	2 (40)	2 (13.3)	0.072†	1 (50)	2 (100)	-	3 (33.3)	9 (56.2)	0.411†

Results are represented as median and range, * no topical or systemic treatment, ** EBV positive cases were not included in this table, §Mann-Whitney test, †Fisher's exact test.

Audience Take Away Notes

- The importance to analyse intraocular fluid in the diagnosis of uveitis
- Methods that propose to test to multiple pathogens, in low-volume sample and is rapid should be pursued
- In our study, this direct Strip PCR demonstrated to be a useful tool for diagnosing the etiology of infectious uveitis

- The use of only a small volume (20μl) and with no extraction step make this method easy to perform and allow the ophthalmologist to use the remaining sample for other analysis (as microbiological culture or flow cytometry)
- Overall positivity was 23.5%; considering only infectious uveitis it was 35.1%; anterior chamber or vitreous cell count (SUN) and treatment did not interfere in PCR positivity

Biography

Dr. Eduardo Ferracioli Oda studied in the University of Sao Paulo Medical School and there received his medical degree in 2015. He completed his Ophthalmology residency in the same institution in 2019 after focusing his studies in Uveitis. During his fellowship in Uveitis, Dr. Ferracioli-Oda started his PhD protocol about ocular fluids analysis through multiple tests (as PCR, cytokines profile and metagenomics).

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Assessment of tick diversity and potential pathogen transmission in two ecological niches: Implications for zoonotic disease surveillance

Ticks play a significant role in disease transmission, rivaling mosquitoes in importance, yet knowledge gaps persist regarding ticks of public health importance. Their remarkable diversity stems from complex life cycles and interactions with hosts, leading to their ubiquity across diverse animal species. This study aimed to assess tick diversity in the Ghanaian Shai Hills Resource Reserve and surrounding communities. Tick specimens were collected from various hosts, including wild animals like Struthio camelus, Python regius, and Equus quagga, and domestic animals like Bos taurus, Canis lupus familiaris, Felis catus, and Ovis aries. Amblyomma variegatum emerged as the predominant tick species on domestic hosts outside the reserve, while Rhipicephalus evertsi prevailed among ticks from captive wild animals within the reserve. Amblyomma variegatum, particularly prevalent on Bos taurus, which freely moves and forages in the reserve's buffer zones, was observed across both study sites. Given its association with zoonotic diseases like Crimean-Congo hemorrhagic fever and African tick-bite fever, the presence of Amblyomma variegatum underscores the risk of pathogen transmission. Molecular analysis targeting the cox-1 gene confirmed tick species identification. The findings emphasize the importance of surveillance and management strategies to mitigate the public health risks posed by ticks and the pathogens they carry, urging further investigation into the specific pathogens transmitted by these vectors.

Keywords: Ticks, Amblyomma Variegatum, Resource Reserve, Rhipicepahlus Evertsi, Bos Taurus.

Audience Take Away Notes

- **Identification of High-Risk Tick Species:** By identifying Amblyomma variegatum as the predominant tick species, particularly prevalent on domestic hosts such as Bos taurus, the audience will recognize the importance of this species in disease transmission. This information can guide targeted surveillance efforts and help prioritize control measures to mitigate disease spread
- **Recognition of Zoonotic Disease Risks:** The study highlights the association of Amblyomma variegatum with various zoonotic pathogens, including Crimean-Congo hemorrhagic fever and African tick-bite fever. This awareness can alert public health professionals and veterinarians to the potential risks of tick-borne diseases and inform preventive measures to protect both human and animal populations
- **Potential for Further Research and Education:** The findings provide a foundation for future studies on tick ecology, disease epidemiology, and wildlife management strategies. Other faculty members could use this research to expand their teaching and research agendas, contributing to a broader understanding of tick-borne diseases and ecosystem health
- **Solutions for Disease Control:** By identifying high-risk tick species and associated pathogens, the study offers practical solutions for disease control and management. Findings from the study can inform the development of targeted interventions, such as vector control measures and vaccination strategies, to reduce the burden of tick-borne diseases on human and animal populations

- **Public Health Awareness:** Improved knowledge of tick diversity and disease risks enhances public health preparedness and response capabilities. Health professionals can use this information to educate communities about tick-borne diseases, implement early detection and surveillance systems, and develop effective disease prevention and control strategies

Biography

Miss Elinam Adzo Agbobli, a researcher in Biological Sciences, completed her post-baccalaureate studies at the University of Ghana. Joining the Noguchi Memorial Institute for Medical Research, she contributes to the Gyan laboratory's work on 'Blood-Brain Barrier, Cerebral Malaria, and Exosome Study'. Passionate about scientific inquiry, she focuses on biomedical research, particularly infectious diseases. Miss Agbobli has presented her findings through multiple oral and poster presentations, showcasing her dedication to advancing scientific knowledge. Her commitment to addressing health challenges highlights her potential as a future leader in the scientific community.

Laelson Rochelle Milanes Sousa[1], Renata Karina Reis[1], Milton Jorge De Carvalho Filho[2], Hemilio Fernandes Campos Coelho[3], Ana Cristina De Oliveira E. Silva[3], Elucir Gir[1]*

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Prevalence of physical and/or mental health symptoms for four weeks or more due to COVID-19 among Brazilian nurses

Introduction: Long COVID comprises a complex, multidimensional, progressive and impactful syndrome characterized by the persistence of residual symptoms after the initial COVID-19 infection, without an alternative diagnosis or associated condition.

Objective: To identify the prevalence of physical and/or mental health symptoms for four weeks or more due to COVID-19 and associated variables among Brazilian nurses.

Method: A cross-sectional study was carried out using an online survey with 3,697 nurses from all regions of Brazil, which included capitals and the interior of the country. Data were collected through an adaptation of the respondent-driven sampling method to the virtual environment. The prevalence of physical and/or mental health symptoms for four weeks or more due to COVID-19 among Brazilian nurses was identified through the variable: "Have you had any physical and/or mental health symptoms persist for 4 weeks or more due to COVID-19?" (YES NO)". The statistical association was verified using Pearson Chi-Square.

Results: 3,697 nurses participated in the study, 3,081 (83.3%) female, 1,791 (48.4%) white, 1,946 (52.6%) had been diagnosed with COVID-19 only once and 381 (10.3%) had been diagnosed confirmed with COVID-19 three times. The main symptoms were: respiratory 785 (21.2%); circulatory 743 (20.1%); fatigue 2,018 (54.6%) and cognition 1,836 (49.7%). The prevalence of physical and/or mental health symptoms for four weeks or more due to COVID-19 among Brazilian nurses was 61.6% (2,279). The following variables had a statistically significant association with the persistence of physical and/or mental health symptoms for four weeks or more due to COVID-19 among Brazilian nurses: number of times of confirmed diagnoses ($p<0.001$); incomplete vaccination schedule ($p<0.001$); presence of chronic disease ($p<0.001$) and sex ($p<0.001$).

Conclusion: It is concluded that conditions prior to diagnosis and incomplete vaccination schedule were related to the persistence of physical and/or mental health symptoms for four weeks or more due to COVID-19 among Brazilian nurses.

Descritores: Nurses, COVID-19, SARS-CoV-2, Post-Acute COVID-19 Syndrome.

Audience Take Away Notes

- Identification of the prevalence of physical and/or mental health symptoms for four weeks or more due to COVID-19 and associated variables among Brazilian nurses
- Variables associated with the prevalence of physical and/or mental health symptoms for four weeks or more due to COVID-19 among Brazilian nurses

Biography

Dr. Elucir Gir studied nursing in at the University of Sao Paulo, Ribeirao Preto College of Nursing. Full professor since 2004 (PhD, MNSc.RN) with the General and Specialized Nursing Department, Graduate Program in Fundamental Nursing. Vice Dean of University of Sao Paulo, Ribeirao Preto College of Nursing, Coordinator of NAIDST and RENAIDST. She has published more than 280 research articles in journals.

Laelson Rochelle Milanes Sousa[1], Andressa Silva Torres dos Santos[1], Milton Jorge De Carvalho Filho[2], Hemilio Fernandes Campos Coelho[3], Ana Cristina De Oliveira E Silva[3], Elucir Gir[1]*

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Prevalence of COVID-19 diagnosis among Brazilian nurses after complete vaccination schedule

Introduction: Facing the COVID-19 pandemic caused damage to the physical health of nurses, especially those who worked on the so-called front line, as they were exposed to constant risks of contamination, exhaustive workload and difficulties in the availability of inputs, such as equipment Personal Protection (PPE).

Objective: To identify the prevalence of COVID-19 diagnosis among Brazilian nurses after a complete vaccination schedule.

Method: A cross-sectional study was carried out using an online survey with 4,780 nurses from all regions of Brazil, which included capitals and the interior of the country. Data were collected through an adaptation of the respondent-driven sampling method to the virtual environment. The prevalence of COVID-19 diagnosis among Brazilian nurses after a complete vaccination schedule was identified using the variable: “Have you had a confirmed diagnosis of COVID-19 after a complete vaccination schedule? (YES/NO)". The statistical association was verified using Pearson Chi-Square.

Results: 4,780 nurses participated in the study, 3,968 (83.0%) were female, 275 (5.8%) provided assistance to indigenous populations, 290 (6.1%) provided assistance to riverside populations, 289 (6.0%) provided assistance to quilombola populations, 1,065 (22.3%) did not receive quality PPE, 632 (13.2%) did not receive sufficient PPE for use. The prevalence of COVID-19 diagnosis after a complete vaccination schedule was 39.5% (1,887 nurses). The following variables had a statistically significant association with the diagnosis of COVID-19 after a complete vaccination schedule: provided assistance to riverside populations ($p=0.041$); provided assistance to quilombola populations ($p=0.046$) and sex ($p<0.001$).

Conclusion: It is concluded that, despite the availability of vaccines and nurses' adherence to vaccination, complementary actions for prevention are necessary, such as standard precautionary measures and considering the type of assistance provided.

Audience Take Away Notes

- Identification of the prevalence of COVID-19 diagnosis after a complete vaccination schedule
- Variables associated with the diagnosis
- Prevention recommendations to improve the physical health of nurses

Biography

Dr. Elucir Gir studied nursing in at the University of Sao Paulo, Ribeirao Preto College of Nursing. Full professor since 2004 (PhD, MNSc.RN) with the General and Specialized Nursing Department, Graduate Program in Fundamental Nursing. Vice Dean of University of Sao Paulo, Ribeirao Preto College of Nursing, Coordinator of NAIDST and RENAIDST. She has published more than 280 research articles in journals.

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Treatment of Iron-deficiency anemia reduces pneumonia- and bacteremia-associated hospitalizations

Introduction: The safety profile of oral iron supplementation is well established and generally benign, but many practitioners limit iron supplementation in patients hospitalized for infectious causes, even in the presence of Iron-Deficiency Anemia (IDA). Nearly all human pathogens require iron, and must obtain it from the host, so administering iron during an infection is feared to exacerbate the infection. However, IDA itself is associated with worse outcomes in many infections, so iron stores must be balanced for optimal outcomes.

Objective: In this study, we examine the relationship between IDA, iron supplementation, and infection in hospitalized patients.

Methods: Inpatient admission data for pediatric patients from multiple institutions, from 2020 to 2023 were retrospectively analyzed for infectious diagnoses on or during admission, IDA (defined by the intersection of abnormal HgB, abnormal MCV, and abnormal RDW) and prescribed iron supplements. Of 91,029 total hospital admissions, 7344 patients had IDA, of whom 1994 were prescribed iron. 3249 patients were prescribed iron with no IDA by these criteria. Chi-squared analysis was performed on infection category: bacteremia, urinary tract infection (UTI), pneumonia, and meningitis, to find a correlation between IDA and infection, or iron supplementation and proportion of hospitalized patients with each infection.

Results: IDA correlated significantly with all infections analyzed. Iron supplementation in patients with no IDA correlated with increased likelihood of bacteremia and meningitis, but not UTI, and correlated inversely with pneumonia. In patients with IDA, iron supplementation correlated with decreased likelihood of pneumonia and bacteremia, but had no effect on meningitis or UTI.

Discussion/Conclusion: Our data describe the effects of anemia and iron in various infections. IDA correlates with an increased likelihood of all infections analyzed, on or during hospitalization, and iron supplementation increases proportions of certain infections only in patients without IDA. For patients with IDA, iron supplementation appears to be, at worst, benign in terms of risk of infection. However, iron supplementation actually decreases pneumonia at or during admission, regardless of IDA status. The lung is a unique immune organ, in which alveolar macrophages play a key role in homeostasis and infection control, and these macrophages require iron for multiple antimicrobial pathways. Thus, based on these data, and supported by an understanding of lung immunity, providing iron to iron-deficient patients is critical to support immune function, particularly to combat pneumonia.

Audience Take Away Notes

- Pediatric hospitalists and Infectious Disease specialists may refine their recommendations for treatment of iron deficiency anemia in the setting of serious bacterial infections
- Academic faculty may improve their teaching regarding risks and benefits of iron supplementation with regard to risk of infection

- Research clinicians may use this information as a basis for future studies to examine the relationship between iron and specific pathogens

Biography

Dr. Brownhill studied Molecular and Cellular Biology at the Johns Hopkins University and graduated with MS in 2011. He then attended Boston University School of Medicine, where he completed his combined MD and PhD degrees in 2022, working in the laboratory of Dr. Igor Kramnik at the National Emerging Infectious Disease Laboratories (NEIDL) in Boston, MA, USA. He is currently completing his residency training in Pediatrics at Jacobi Medical Center in New York, USA, after which he intends to pursue a fellowship in Pediatric Infectious Diseases.

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Effective reduction of SARS-COV-2 RNA levels in transfected lung cells using a tailor-made therapeutic oligonucleotide

More than four years after the outbreak of the COVID-19 pandemic, the SARS-CoV-2 virus is still causing lasting damage around the world, impacting the health and lives of many. Preventive measures, such as widespread administration of vaccines, is playing a role in reducing the severity of cases. For those who require treatment, clinicians can try to treat the disease and its symptoms with existing drugs. However, an effective therapy specifically targeted against SARS-CoV-2 is still lacking.

Here, we report the antiviral potential of a tailor-made oligonucleotide-based inhibitor targeting SARS-CoV-2, called ASC1R, which showed spontaneous cellular uptake and a remarkable >94% efficacy in reducing RdRp RNA levels in transfected lung cell lines following a single application.

The therapeutic potential of the structurally unique ASC1R could translate into substantial clinical benefits for patients with COVID-19, while the versatility of the platform could be exploited in the development of analogue antivirals for other viral diseases. The findings could help meet the global challenge of developing new and safe treatment modalities.

This work was supported by the Slovak Research and Development Agency under Contracts No. PP-COVID-20-0007 and APVV-21-0220.

Audience Take Away Notes

- Therapeutic oligonucleotides represent a promising pharmaceutical perspective for the treatment of many pathological conditions, including those of viral origin
- ASC1R showed spontaneous cellular uptake reaching 30 million molecules per cell without cytotoxicity
- ASC1R reduced RdRp RNA levels in transfected human lung cells with a remarkable efficiency of >94% after a single application

Biography

Dr. Razga has more than 20 years of professional experience in oncology with a focus on biotechnology within the last decade. He is trained in Physical and Biomolecular chemistry and has a primary research interest in RNA structure and function. He is currently leveraging his expertise in the development of new therapeutic modalities using the antisense platform to develop quality healthcare products that have the potential to redefine treatment outcomes. He is the author of more than 60 scientific papers and developed several proprietary technologies aiming at precise diagnosis and personalized therapeutic approaches.

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Incremental value of an ultra rapid phenotypic antimicrobial susceptibility testing in patients with bloodstream infection: a modeling approach

Background and Goal: When Bloodstream Infection (BSI) is suspected, empirical broad-spectrum Antimicrobial Treatment (AMT) is immediately initiated after sampling for blood cultures. In the context of an increasing rate of multidrug-resistant organisms, rapid microbiological investigations—identification of the causative agent and Antimicrobial Susceptibility Testing (AST) – are key to minimize time on inappropriate therapy, to limit the selection of resistant strains and to limit AMT-associated toxicity. This study aimed to quantify the health and economic gains achievable by replacing the current Standard of Care (SoC) with an ultra-rapid AST directly performed from blood cultures.

Methods: A decision-tree model was developed to compare between SoC (isolation in culture medium + MALDI-TOF-MS + VITEK 2 AST), which has a Time to Results (TTR) of 51 hours(h), rapid ASTs (5h<TTR<8h), and FASTinov Ultra-Rapid (UR) AST (TTR=2h), in hospitalized patients with BSI. Outcomes of interest were mortality, hospital Length of Stay (LoS) and costs. Outcomes were linked to TTR through the duration of inappropriate therapy. Inputs were based on the literature. Conservatively, due to lack of evidence, AST TTR was assumed not to impact outcomes in patients initiating appropriate empirical therapy. A time-horizon of 30 days was considered, and the payer perspective was adopted.

Results: The 2h TTR UR-AST test allows for decision-making in the same medical shift, while rapiASTs likely yield next day intervention, and SoC requires at least 3 days to achieve AST based optimized regimen. In that context, in the overall BSI patient population, replacing current SoC with FASTinov UR-AST allows reductions of 8.0% in mortality (12.4% vs 13.5%), 30.1% in LoS (6.7 vs 9.6 days) and 28.0% in costs (6,148€ vs 8,542€)When comparing the 2h TTR UR-AST to rapid ASTs, the benefit is estimated to result in a reduction of 8.0% in mortality, 15.7% in LoS (6.7 vs 7.9 days) and 14.3% in costs (6,148€ vs 7,177€).

Conclusion: Availability of AST results on the same medical shift reduces mortality, LoS and costs of hospitalized patients with BSI.

Audience Take Away Notes

- The audience will be able to assess the benefits of the ultra-rapid AST in their own health care setting (by easily adapting the model inputs with their own specific data)
- The audience will be informed about the available evidence linking time to AST results and outcomes (mortality, length of stay and costs), thereby highlighting the critical relevance of an efficient process to patient outcomes

- The audience will be provided with a tool supporting the economic argument for an ultra-rapid AST which can be used at the health facility board level to facilitate its acquisition and implementation

Biography

Filipa is a researcher at Nova University Public Health Research Centre and a founding partner at Incremental Action Consulting, Lda (INCA), with strong experience health economics and outcomes research (HEOR) data generation, acquired through a solid academic background followed by 25+ years working in Health Economics. He is highly proficient in model design and optimization for maximum product differentiation across markets. Before setting up her company, He was the HEOR lead for the European Region at Gilead Sciences Inc. He had a PhD in Public Health and Health Economics, a post-graduation in Epidemiology and Medical Statistics from the London School of Hygiene and Tropical Medicine. She is a FullBright scholar and a Fundacao para a Ciencia e a Tecnologia scholar, among others.

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Rare fungal infection in chronic lymphocytic leukemia: Scopulariopsis as a clinical challenge

A 59-year-old male with a history of relapsed refractory Chronic Lymphocytic Leukemia and associated hypogammaglobulinemia presented to our medical service with neutropenic fever, a skin lesion, and progressive pulmonary infiltrates.

He had been evaluated for cough and neutropenic fever 7 weeks prior and was treated for Aspergillus and had interval improvement. He was receiving chemotherapy with Rituximab, Etoposide Phosphate, Vincristine Sulfate, Cyclophosphamide, and doxorubicin (R-EPOCH), in addition to ibrutinib. Antimicrobial prophylaxis regimen included voriconazole, trimethoprim-sulfamethoxazole, and acyclovir. Computed Tomography (CT) of the chest demonstrated bilateral multifocal areas of consolidation and nodularity (Figure 1).

Pertinent work-up included negative bacterial and fungal cultures from blood and a Bronchoalveolar Lavage (BAL) specimen, negative serum and BAL Aspergillus antigen, negative pneumocystis polymerase chain reaction and cryptococcal antigen from BAL, negative serological testing for endemic fungi, and a serum (1,3)-β-D-glucan of 124 pg/mL (reference range < 60 pg/mL). After five days of broad-spectrum antimicrobial therapy there was no clinical or radiographic improvement. The patient was started on liposomal amphotericin B and transitioned to posaconazole after initial improvement. CT chest two weeks into treatment demonstrated improving infiltrates. Treatment was switched to caspofungin given concern for possible a possible interaction between chemotherapy and posaconazole. He remained profoundly neutropenic during this time-period.

On arrival to our institution, examination was notable for fever (temperature 38.2C), crackles in the right-lung base, and a new papular lesion on the right parietal scalp (Figure 2). CT Chest demonstrated new bilateral nodules and ground glass opacities. A diagnosis of disseminated Scopulariopsis sp. infection was confirmed via matrix-assisted light desorption ionization-time of flight mass spectrometry. The patient was escalated to combination therapy with liposomal amphotericin B and caspofungin. Terbinafine was subsequently added. In managing Scopulariopsis infections, clinicians face numerous challenges due to the rarity of the condition and its propensity for affecting immunocompromised individuals. Effective management requires a multi-faceted approach, beginning with a high index of suspicion for fungal infections, especially in patients with hematologic malignancies, solid organ transplants, or those receiving.

Repeat bacterial and fungal blood and sputum cultures were negative. Serum (1,3)-β-D-glucan was 71 pg/mL, and serum aspergillus antigen remained undetectable. Bronchoalveolar lavage (BAL) was performed, and after three days of incubation there was growth of a filamentous fungus on fungal cultures (Figure 3). Subsequent fungal cultures obtained from a biopsy of the papular lesion grew the same organism.

In managing Scopulariopsis infections, clinicians face numerous challenges due to the rarity of the condition and its propensity for affecting immunocompromised individuals. Effective management requires a multi-faceted approach, beginning with a high index of suspicion for fungal infections, especially in patients with hematologic malignancies, solid organ transplants, or those receiving immunosuppressive therapies. Early diagnosis is crucial, relying on a combination of clinical suspicion, imaging studies, and microbiological testing, including fungal cultures and microscopy to identify characteristic features such as dark brown colonies and septate hyphae.

Figure 1: Computed tomography of the chest with bilateral consolidation

Figure 2: Red papule, right parietal scalp

Figure 3a: Fungal culture

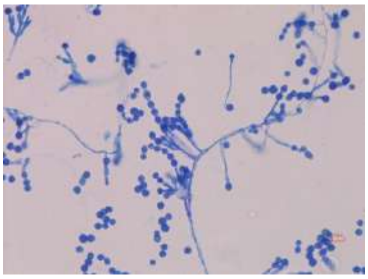

Figure 3b: Microscopy of fungal cultures with lactophenol blue staining

Audience Take Away Notes

- This case challenges the reader to identity the etiology of an invasive mold infection involving the lungs and skin. While rare, infections with Scopulariopsis sp. are increasing
- When considering the differential diagnosis for an IMI in an immunocompromised host, an understanding of the prevalence of various fungal species is paramount

- Characteristic features of Scopulariopsis sp. include dual lung and skin involvement, rapid growth of flat dark brown colonies on fungal cultures, and the presence of septate hyphae with characteristic conidiogenous cells (annellides) observed on microscopy

Biography

Dr. Murphy studied Medicine at University College Cork Ireland graduating in 2019. She completed a post graduate Master's in Clinical Research. She is completing her residency training in the Mayo Clinic Rochester Minnesota in the United States. She is returning to Ireland in 2024 to commence Infectious Diseases specialty training. Her interests include bone and joint infections and opportunistic pathogens.

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Native aortic valve endocarditis secondary to streptococcus gordonii: A rare presentation

Streptococcus Gordonii (SG) is an alpha hemolytic gram-positive streptococcus bacterium most commonly present in the oral cavity and gastrointestinal tract. Despite an increase in the incidence of Infective Endocarditis, SG cases reported on a native aortic valve are relatively uncommon. Previous cases of SG have been associated with spondylodiskitis, intraabdominal infection, and oral procedures. We present a case of a 79-year-old male with a native aortic valve SG endocarditis that was admitted for AKI, diarrhea, and dehydration, found have SG bacteremia with endocarditis, 1.7cm vegetation on native aortic valve and subsequent multiple septic emboli on brain MRI. The patient was successfully treated with IV antibiotics and required aortic valve replacement at following hospitalization. The most likely source of the bacteremia was a trigger point injection to the lumbar spine which was consist with MRI lumbar spine findings of spinal abscess. However, other possible sources include oral procedure and colonoscopy with polypectomy within 8 weeks of the hospitalization. This case illustrates the importance of thorough history taking and consideration for echocardiogram to rule out endocarditis if SG bacteremia is present, in addition to close monitoring and outpatient follow up post diagnosis. Considering an increasing number of procedures involving the oral cavity, spine and abdominal area, and we hope that this case will bring awareness in the diagnosis of SG endocarditis.

Audience Take Away Notes

- The audience will be able to understand the clinical significance of ordering echocardiogram for patients diagnosed with Streptococcus Gordonii bacteremia and its related complications such as valvular vegetation and septic emboli. Multiple sources of SG endocarditis are addressed, and this should prompt audience to expand differential diagnosis based on this case presentation

Biography

Dr. Franciela Golden studied Health Science at Merrimack College and graduated in 2017. She completed a Master of Health and Wellness Management in 2018 followed by Medical School Graduation from The Idaho College of Osteopathic Medicine in 2023. She is currently a first year Family Medicine Resident at Mayo Clinic Florida. Aleksandra Murawska Baptista, MD FHM is a consultant in department of Hospital Internal Medicine in Mayo Clinic Florida. She graduated Family Medicine Residency Program in Alabama after which she graduated Fellowship Program in Hospital Medicine in Geisinger Hospital in Pennsylvania. Before she became Mayo Clinic Faculty she was working as a Hospitalist and Instructor of Medicine at Brigham and Women's Hospital in Boston and Harvard Medical School. She is an assistant professor and associate program director for Hospital Internal Medicine Fellowship Program. She is involved in multiple leadership projects including being a President of North Florida Chapter for Society of Hospital Medicine. She is passionate about education and innovation. She is involved in developing curriculum projects for medical students as well as residents. She also is a Mayo Alix School of Medicine Faculty and Society Affair Representative for Association of American Medical Colleges. She is involved in multiple quality improvements projects as well as international collaboration with other hospitals and universities.

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Colonization and infection in admitted patients with vancomycin-resistant Enterococcus in a tertiary hospital

Enterococci are gram-positive, facultative anareobic bacteria that are usually found in gastrointestinal tract of humans, animals and environmental sources. Enterococci can lead to severe hospital-acquired infections and are difficult to treat due to their high level of antibiotic resistance. Vancomycin-Resistant Enterococci (VRE), are strains that developed resistance to vancomycin which is used against gram-positive bacterial infections. VRE are one of the most common nosocomial pathogens that cause colonisation and infection both in hospitalized patients.

We aim to better understand whether the patient is only carrier or infected with VRE by conducting a retrospective study including admitted patients between 2019 and 2024 at Selcuk University Hospital.

1467 rectal swab samples were inoculated onto chromogenic VRE agar and incubated at 37°C. After bacterial growth, identification was performed using the Vitek-2 automated system. The disc diffusion method was used to determine antibiotic susceptibility according to EUCAST guidelines.

Out of 157 rectal swab culture-positive patients, 97 patients (61.7%) were only colonized and 60 patients (38.2%) were infected by VRE. 30 patients (19.1%) had cystitis, 18 patients (11.4%) had blood-stream infection, three patients (1.8%) had meningitidis yet one of them was shunt-associated, two patients (1.2%) had catheter infection, two patients (1.2%) had wound infection, one patient (0.6%) had both cystitis and blood-stream infection, one patient (0.6%) had both cystitis and peritonitis, one patient (0.6%) had both cystitis and catheter infection; one patient (0.6%) had both blood-stream infection and pleuritis, one patient (0.6%) had tissue infection.

In conclusion, we observed a high rate of infection in VRE carriers. The highest percentage of patients had cystitis however life-threatning infections such as blood-stream and meningitis are also observed. Since VRE easily spread among admitted patients, comply with the rules of isolation plays a key role in protecting non-colonized patients. Determining the source is crucial for preventing transmission of VRE by especially the hands of medical staff or devices within the hospital.

Audience Take Away Notes

- The high rate of infection developed in VRE carriers
- Life-threatning infections such as blood-stream and meningitis also observed
- Isolation of colonized patients plays a key role in protecting non-colonized patients

Biography

Prof. Dr. Hatice Turk Dagi graduated as MD in 1999 from Selcuk University/Faculty of Medicine, Turkiye. She received specialization in Medical Microbiology degree in 2009 at the same institution. She worked in Batman State Hospital between 2009-2011. Since 2012 has worked in Selcuk University/Faculty of Medicine. She received her Prof. Dr. degree in 2021. She received her PhD degree in Immunology in 2023 at the same institution.

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Antimicrobial activity of peptides derived from lycosa erythrognatha spider venom against quinolone-resistant Uropathogenic Escherichia Coli (UPECS)

Uropathogenic Escherichia Coli (UPECs) is the leading pathogen involved in urinary tract infection. Although quinolones are widely used in these cases, the resistance of UPECs to this class has been growing significantly, challenging the effectiveness of antibacterial therapy. Thus, the development of novel antimicrobials agents for the treatment of quinolone-resistant UPECs infections is imperative. Herein, arthropod toxin stand out as a promising source of new bioactive compounds against superbugs such as quinolone-resistant UPECs, especially Antimicrobial Peptides (AMPs).

Objectives: To study the antibacterial effect of synthetic peptides derived from a natural compound present in the venom of the spider Lycosa erythrognatha against clinical isolates of quinolone-resistant UPECs.

Methodology: Ten clinical isolates of UPECs were included. The bacteria were identified by biochemical-physiological assay. Antimicrobial resistance profile and the Extended Spectrum Beta-Lactamase (ESBL) production was determined. Next, the antibacterial effect of the peptides was studied by determining the Minimum Inhibitory Concentration (MIC) and Minimum Bactericidal Concentration (MBC). In silico study was performed to determine the mode of action of the peptide against the E. coli adhesins PapG and FimH via ClusPro webserver.

Results: Five compounds were tested, but LyeTx I mnΔK (16 amino acid residues; 1871.32 Da) showed the best activity. The MIC and MBC of this compound was of 2 μM and 8 μM, respectively, to all included isolates. All the isolates were resistant to nalidixic acid, ofloxacin, norfloxacin ciprofloxacin and levofloxacin. In addition, five isolates were ESBL-positive. Peptide showed binding with both of the adhesins, PapG and FimH, that help E. coli in binding to kidney and bladder cells, respectively. Conclusion: The LyeTx I mnΔK peptide is a potential prototype to development of new antimicrobial agents against quinolone-resistant uropathogenic Escherichia coli.

Financial support: CAPES, INCT-TeraNano, CNPq, FAPEMIG.

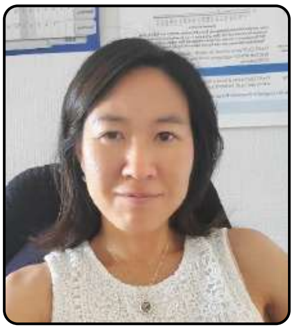
Keywords: E. Coli, Urinary Infection, Drug Resistance, Antimicrobial Peptides, Drug Development.

Audience Take Away Notes

- Audience can see the antibiotic resistance profile of quinolone-resistant uropathogenic Escherichia coli (UPECs)
- Audience can avoid taking the antibiotics which are not effective against quinolone-resistant uropathogenic Escherichia coli (UPECs)
- The antimicrobial peptides can be used for the treatment of several other pathogenic bacteria and fungi
- After some clinical trials we will be able to formulate a new peptide based antibiotic
- It will help in desiging the treatment strategies for quinolone-resistant uropathogenic Escherichia coli (UPECs) infections
- Antimicrobial peptides have captivated the interest of researchers worldwide due to their broad-spectrum antifungal capabilities and the low likelihood of inducing drug resistance. There has been a gradual yet notable advancement in the development of peptides, attributed to their minimal cytotoxicity and hemolytic activity, positioning them as ideal candidates for enriching the arsenal of antibiotic drug classes. On a laboratory scale, peptides have demonstrated significant therapeutic potential in vivo studies

Biography

Mr. Ihtisham Ul Haq is pursuing Joint PhD at Universidade Federal de Minas Gerais, Belo Horizonte, Brazil and Silesian University of Technology, Gliwice, Poland. He is working under the supervision of Prof Maria Elena de Lima and Prof katarzyna Krukiewicz. His main research interests are antimicrobials and antimicrobials peptides. He has 22 publications including 7 book chapters 4 research papers and 11 review papers.



Joo Hee Walzlein*, Andreas Kurth, Susann Kummer
Centre for Biological Threats and Special Pathogens, Robert Koch-Institute, Berlin, Germany

Stability and disinfection studies for risk group 4 pathogens: Improving biosafety measures for laboratories and patient management

Our project highlights the critical need for scientific data in assessing the risks posed by emerging and re- emerging viruses, both during endemic and pandemic outbreaks. It emphasizes the importance of validated decontamination procedures and infection control measures with the aim to minimise person-to-person transmission, as well as transmission through environmental contamination.

There is a general lack of evidence-based scientific data guiding the implementation of infection control measures, particularly in handling infectious patient samples and contaminated materials. This issue extends to the need of improving biosafety measures in high-containment laboratories.

To address this lack of data, this study follows a three-fold approach:

Validation of Sampling Techniques: This involves validating defined sampling techniques to ensure reproducible results for swabs on various surfaces, thereby facilitating accurate assessment of environmental contamination.

Determining Persistence of Infectivity: These studies aim to determine the persistence of infectious particles derived from risk-group 4 pathogens in different (body) fluids and on various relevant surfaces across various environmental conditions. These data are crucial for understanding the longevity of viral presence and transmission potential in field, hospital and laboratory environments.

Validation of Disinfection and Decontamination Procedures: Different commercially available and commonly used disinfectants are tested for their ability to reduce viral load under various conditions including concentration, temperature and exposure time.

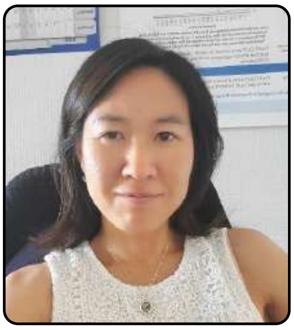
Ultimately, the results from these studies are meant to be used for providing improved evidence for infection control measures in hospital environments, thereby enhancing safety for both patients and healthcare workers. Especially in areas, in which high-risk viruses are endemic, this is of utmost importance in order to prevent disease spreading. In addition, the data are intended to be used for formulating and adjusting validated safety measures in high-containment laboratories. Finally, by filling knowledge gaps and optimising validating protocols, this study aims to contribute to a general pandemic preparedness, therefore minimising the risks of global infectious disease spreading.

Audience Take Away Notes

- Especially doctors and healthcare workers in areas in which high-risk viruses are endemic, will benefit from guidelines based on newly obtained scientific data regarding virus stability and effective disinfection regimes
- The data obtained from these studies will also help to improve biosafety measures in hospital environments as well as in laboratory settings
- The results can further be used in order to correctly set up experiments, for which virus stability and specific decontamination procedures are crucial

Biography

Dr. Joo Hee Walzlein studied Biology at the Eberhard-Karls-University in Tubingen, Germany and graduated in 2003. She then joined the group of Prof. Kettenmann at the Max-Delbruck Center in Berlin, Germany and received her PhD in Medical Neurosciences in 2007. After several postdoctoral positions at King`s College/University College London (London, UK) in the field of prion research, she obtained a position as a research fellow at the Robert Koch-Institute in Berlin and is now working with high-risk viruses.



Joo Hee Walzlein[1]*, Karla A. Schwenke[1], Joy Orezimena Mejedo[1,2], Jenny Ospina Garcia[1,2], Sebastian Reusch[2], Christian Klotz[2], Marc A. Schneider[3,4], Susann Kummer[1]

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Establishment of a human lung organoid method platform for infectious disease modelling

Background: In recent years, organoids have advanced to prominent and versatile tools in 3R research, representing valuable alternatives for animal models and physiologically relevant human disease models at the same time. As the federal Public Health Institute, the RKI aims to establish an in-house multi-species, multi-organ organoid platform. The objective is a broad methodology in order to strengthen the Institute`s pandemic preparedness plans for novel and re-emerging pathogens, which often have to be handled in a BSL4 laboratory. So far, in our group, bronchial and nasal lung organoids have been generated from adult stem cells derived from various primary and commercial cells. Characterisation on mRNA and protein level showed that, with small variances, all organoids consist of a physiologically applicable cell composition.

Methodology: Single-cell RNA sequencing (scRNA sec) should be applied to investigate complex questions like e.g. viral cell tropism, host cell response etc. Less generalized questions regarding differential gene expression during a viral infection can be tackled with the Nanostring method. In order to study inter-organ viral dissemination, as well as inter-species transmission of pathogens, the relatively new multi-organ-chip technology is currently being established. Classic antiviral tests are also included in our method range. Once conditions will be established, these tests will be applied to the multi-organ-chip format, which allows physiologically more relevant tests. Finally, using a fluorescent labelled virus, 4D image data have been generated and with the help of deep learning, will be used for modelling viral replication kinetics.

Results: Quality control scRNA sec runs yielded a good cell viability, sufficing for future runs. Differential gene expression following infection of lung organoids with the BSL4 pathogens EBOV, MARV, NiV and LASV has been studied by a Nanostring host-response panel and is currently being analysed. Preliminary infection of organoids on organ chips with VACV-GFP have been performed and successful inter-organ transmission could be observed. Furthermore, the anti-viral effect of the two clinically licensed drugs itraconazole and fluoxetine has been tested in EBOV-infected organoids. Results are currently being analysed. Lastly, the successfully generated 4D data is currently being processed by our AI department.

Audience Take Away Notes

- On completion of this study a fully characterized novel model system will be available for infectious disease research
- The data will be published open access and freely accessible for the scientific community
- Establishment and optimization of the different methods will facilitate their application in other areas of organoid research
- All methods will be established for application in a high-containment laboratory, which will make tedious and time-consuming adjustments for other research groups working in the same environment dispensable

Biography

Dr. Joo-Hee Walzlein studied Biology at the Eberhard-Karls-University in Tubingen, Germany and graduated in 2003. She then joined the group of Prof. Kettenmann at the Max-Delbruck Center in Berlin, Germany and received her PhD in Medical Neurosciences in 2007. After several postdoctoral positions at King`s College/University College London (London, UK) in the field of prion research, she obtained a position as a research fellow at the Robert Koch-Institute in Berlin and is now working with high-risk viruses.

Julia Nowak[1]*, Jacque Ssanyu[2], Flavia Namiiro[3], Nicola Mountford[4], Avery Parducci[4], Kieran Walshe[5], Peter Waiswa[2], Sean Doyle[1]

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[5]Accuplex Diagnostics Ltd., Maynooth, Ireland

Diagnosis of neonatal sepsis using a rapid lateral flow test to detect serum Amyloid A.

Sepsis is a serious medical condition, and newborns in Low- and Middle-Income Countries (LMICs) are particularly vulnerable. Uganda has one of the highest rates of neonatal sepsis deaths in the world at 17 neonatal deaths per day. Such high mortality rates are largely due to the absence of suitable biomarkers and diagnostic systems to enable early diagnosis. However, Serum Amyloid A (SAA) is emerging as a potential standalone biomarker for the diagnosis of neonatal sepsis. SAA can be detected by laboratory-based tests but these are often unavailable in LMICs.

To address these issues, in an ethically-approved study we deployed a competitive, lateral flow test (NeoSep-SAATM; Accuplex Diagnostics Limited, Ireland) to semi-quantitatively detect SAA in whole blood at patient-side in a LMIC. Our study assessed the performance of NeoSep-SAATM for neonatal sepsis detection. NeoSep-SAATM showed a sensitivity and specificity of 92 % and 73 % with PPV and NPV of 0.78 and 0.90, respectively (n= 714) individuals; 95% CI). NeoSep-SAATM significantly out-performed the currently-available gold-standard biomarker, C-Reactive Protein, for neonatal sepsis detection ($P < 0.0001$, 95% CI). This study demonstrates NeoSep-SAATM can successfully detect sepsis and potentially enable a rapid decision to initiate antibiotic therapy to improve neonatal mortality incidence.

Biography

Julia Nowak studied Biological and Biomedical Sciences at Maynooth University, Ireland and graduated in 2022. She then joined the Science Foundation Ireland- funded research group led by Prof. Sean Doyle at Maynooth University collaborating with Makerere University in Kampala, Uganda working on the NeoSepsis Project. Together, the research group won a prize of 1 million Euro as part of a competitive project scheme funded by Science Foundation Ireland. The NeoSepsis team is working on delivering a SAA-detecting lateral flow test to Ugandan healthcare systems to aid in neonatal sepsis diagnosis.

Kathleen Maguire[1]*, Elizabeth Hastie[2], Ahmed Shabaik[3], Anne Cowell[2]

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Peritoneal coccidioidomycosis presenting as treatment resistant tuberculosis

We present a case of peritoneal coccidioidomycosis in an immunocompetent female patient initially diagnosed with tuberculosis at an outside hospital who presented with suspected RIPE therapy failure. She presented with a history of recurrent ascites, headaches, and shortness of breath. She underwent bronchoscopy, paracentesis, and lumbar puncture, which respectively revealed hilar lymph node aspirate, peritoneal fluid, and cerebrospinal fluid, all positive for Coccidioides and negative for Tuberculosis. Extrapulmonary or disseminated coccidioidomycosis occurs only in approximately 1% of patients and typically involves the skin, bone, or meninges. This case underscores the importance of reconsidering the diagnosis in patients who have seemingly failed RIPE therapy in regions where Coccidioides is endemic. Accurate diagnosis and appropriate antifungal therapy led to inpatient treatment with amphotericin B and plan for indefinite fluconazole and outpatient ID follow up after discharge. Unfortunately, the patient was lost to follow up. Overall, this case contributes to existing literature by highlighting diagnostic challenges and the importance of broadening the differential in endemic regions when treatment is not leading to symptom resolution.

Audience Take Away Notes

- Recognize diagnostic challenges in cases of disseminated fungal infections, especially in areas where multiple fungi are endemic
- Review immune markers thought to play a role in coccidioidomycosis susceptibility and pregnancy as an immunocompromising state
- Discuss treatment of coccidiomycosis and important labs to monitor

Biography

Dr. Maguire received her M.S. in Biology at University of California, San Diego in 2016. She received her M.D. in 2021 at the same institution. She continued her training in Internal Medicine at UCSD and will complete her residency training in June 2024.

Khalid Al Balushi[1]*, Zaaima AL Jabri[2]

[1]Senior medical student, College of Medicine and Health Sciences, Sultan Qaboos University, Muscat, AL-Khoudh, Oman
[2]Assistant professor, Department of microbiology and Immunology, College of Medicine and Health Sciences, Sultan Qaboos University, Muscat, AL-Khoudh, Oman

Prevalence of co-infections among hospitalized patients with COVID-19 at a Tertiary-Care Hospital, Muscat, Oman: A retrospective study

Objectives and Rationale: This study aims to investigate the prevalence, demographics, and risks of co-infections among hospitalized patients at Sultan Qaboos University Hospital (SQUH); a tertiary-care hospital in Muscat, Oman.

Aim: This study aims to identify the most common etiologies of co-infections and the associated pathogens in coronavirus disease 2019 (COVID-19) patients admitted to Sultan Qaboos University hospital (SQUH). In addition, it aims to assess the risk factors and the empirical antimicrobial therapy prescribed during their admission.

Methods: A 2-year retrospective cohort study that included a total of 2000 adult patients admitted with moderate to severe COVID-19 and associated with the presence of co-infection at SQUH from January 2020 to December 2021. All the clinical and demographic data were provided by the electronic medical record. The data were analyzed using the Statistical Package for Social Science Software Version 23 (SPSS).

Results: Out of the 150 co-infected COVID-19 patients, Respiratory pathogens predominated. Bacterial etiologies were the most common; including Klebsiella pneumonia (19%) which was the leading pathogen to cause bacterial co-infections, followed by Pseudomonas aeruginosa (14%) and MRSA (11%). Fungal etiologies were also common and were mostly caused by candida species. Viruses affected 9% of COVID patients and were mostly caused by Rhinovirus, followed by Adenovirus. There is an association between co-infections and the prevalence of older age groups (>50), and ventilation usage (all types of ventilation). More than two-third of the patients were males. The most common empirical antibiotic used was ceftriaxone, followed by Azithromycin and meropenem.

Conclusion: The most common co-infection associated with COVID are bacterial, followed by fungal and, to a lesser extent, viral co-infection. This could help direct the treatment and management of COVID-19 by improving modifiable risk factors that can predispose to these co-infections. Co-infections are common and severe, particularly in ventilated patients who require special attention.

Keywords: Co-infections, COVID-19, Ventilation, Comorbidities, Antibiotics, Management.

Audience Take Away Notes

- Audience will learn through understanding how antibiotics should be used cautiously in such situation, as bacteria is no the only onanism that co-occurs with COVID-19
- As doctors, they will use the antibiotics cautiously in such infections
- Having an idea about what specific organism might be causing the co-infection with COVID-19
- By involving large centers, this research has the potential to be expanded for further understanding

Biography

Khalid Al Balushi is a senior medical student at Sultan Qaboos (SQU) University, he graduated high school from Huntington high school in the US and is now working with Dr. Zaeema from the microbiology department on Infectious diseases researches. He already published a Narrative review about a Immunotherapeutic drug called Tebentafusp that is used in Uveal melanoma, currently is involved in researches about Infectious diseases at SQU.

Kristine Mae D. Barredo, MD, MPH

Department of Pediatrics, Zamboanga City Medical Center, Zamboanga City,
Zamboanga del Sur, Philippines

Epidemiological and clinical features of COVID-19 among the pediatric patients admitted in the Zamboanga City Medical Center and other facilities handling Covid patients

Introduction: Defining the epidemiological and clinical features of COVID in pediatric patients can aid in the control of spread and improve the curative rate.

Objectives: This study determined the epidemiological and clinical characteristics of COVID confirmed children admitted at Zamboanga City Medical Center and other facilities handling COVID-19 patients.

Methodology: This is a descriptive study among RT-PCR confirmed COVID-19 children, less than 18 years, who were admitted at ZCMC and other facilities handling COVID patients from March 2020 to September 2021. The outcome included the incidence and survival rates. The variables studied included demographic data, clinical status, clinical symptoms, complications, treatment done, and clinical outcome. Data entry was performed and was analyzed using counts or frequencies and percentages.

Results: A total of 2,025 patients were admitted to hospitals (n=141, 7%) and quarantine facilities (n=1884, 93%) within Zamboanga City. 72 out of the 141 respondents were admitted to Zamboanga City Medical Center, the apex tertiary hospital in the region. The mean age of the respondents was 9.94±5.78 years old.

Six hundred seventy-six (33.3%) were considered as direct contacts of index cases. Two hundred ninety-nine (14.76%) were symptomatic, with fever (66.1%) as the most common symptom. One hundred forty-one (6.9%) were admitted to hospitals, while the remaining 1,844 (91.05%) were admitted to quarantine facilities. Most patients (44.7%) were classified with moderate COVID. However, there were 23 (1.13%) deaths reported. Majority (66.7%) did not necessitate oxygen support. Nevertheless, 67.7% received IV antibiotics – most commonly Ceftriaxone (49, 52.17%) and Gentamycin (21, 22.34%).

Conclusion and Recommendation: While COVID-19 infection in the pediatric age group was generally mild with low mortality rates, infections in this age group should not be overlooked. With the emergence of more virulent variants and with many unvaccinated, the pediatric population continuous to be a vulnerable group that requires special attention.

Audience Take Away Notes

- Many may consider COVID-19 now as a thing of the past. However, the threat continues as more virulent variants are emerging. With this presentation, the audience will have an additional insight on the epidemiological features and clinical presentation of COVID- 19 in children. They will also learn how these children were treated, and their outcome, despite being in a province of a third world country
- Though COVID-19 infection is generally mild in the children population, it should always be considered as a diagnosis as its clinical presentation is vast and erratic. In addition, having data on

the epidemiological and clinical features of COVID-19 can help administrations/offices assessing the health of the community and amending their policies on the control of spread and treatment of this infection

- COVID-19 is a relatively new disease; and with the emerging virulent variants and its varying presentations, further research on the treatment, management, and its complications will be of great help in combating and controlling this disease. In addition, with the advent of COVID vaccination in children, further studies may also compare the disease course between the vaccinated and unvaccinated children
- This does not provide a practical solution to a problem that could simplify or make a designer's job more efficient
- This study can be used as a benchmark for similar studies

Biography

Dr. Kristine Mae D. Barredo is a graduate of Doctor of Medicine at the Ateneo de Zamboanga University, Philippines in 2016. The year after, she received her Masters in Public Health at the same institution. Thereafter, she went into her pediatric residency training at Zamboanga City Medical Center and graduated last April 2023. She is currently working at the same institution as a junior consultant, and as a part-time instructor at her alma mater, the Ateneo de Zamboanga University.

Lauren Panny*, Ashley Piper, Christina Gardner, Crystal Burke
Division of Virology, US Army Medical Research Institute of Infectious Diseases,
Frederick, MD, United States

Improved techniques for validation of inactivated virus and RNA of positive sense RNA viruses for containment research

Alphaviruses, such as Eastern Equine Encephalitis Virus (EEEV), are genetically encoded by a single positive sense RNA genome. Following glycoprotein-assisted entry into the cells, fusion with the endosomal membrane, and capsid release, translation of the non-structural proteins is rapidly initiated by the host cell ribosome. With initiation of viral replication being driven by the host cell, functional alphavirus RNA that successfully enters a permissive host cell can result in production of progeny virions. This presents a challenge when there is a desire to remove samples from containment spaces as proof of viral RNA inactivation is required in addition to inactivation of infectious virus. Many laboratories validate inactivation of alphavirus RNA by merely adding the viral RNA to a media overlay on cells. However, this methodology does not provide entry of the RNA into cells where replication occurs, therefore, it does not validate that the RNA is inactivated rather that the RNA is not entering into cells. Alphaviruses are responsible for numerous severe human diseases that can cause neurological complications (new world alphaviruses) or debilitating arthritis (old world alphaviruses). Therefore, it is essential from both a biodefense and public health perspective to validate that viral RNA present in samples removed from the containment environment is inactivated and unable to produce infectious virions. The research proposed in this abstract aims to demonstrate these points using methods that ensure viral RNA enters into cells during a series of experiments aimed at validating inactivation of EEEV RNA by chemical means.

Audience Take Away Notes

- The audience will learn how to best validate the inactivation of RNA from positive sense RNA viruses. This knowledge will help better mediate the removal of potentially infectious genomic material from laboratory facilities. This knowledge will help scientists ensure the safety and mediation of infectious viral pathogens

Biography

Dr. Panny received her B.S. in General Biology in 2015 while researching in Dr. David Donze's genetics laboratory. She then worked at clinical research organizations performing biopharmaceutical testing for 2 years. Dr. Panny received her PhD degree and graduate certificate in public health at Virginia Polytechnical Institute in 2023 while researching Venezuelan equine encephalitis virus under Dr. Kylene Kehn-Hall. Currently, Dr. Panny is working as a postdoctoral fellow funded by the National Research Council. Her research is performed at the US Army Medical Research Institute of Infectious Disease where she works with numerous viral pathogens under the mentorship of Dr. Crystal Burke.

L. Gounder[1,2]*, M Pillay[1,2], S Manyana[1], S Govender[1], A Khan[1,2], K Francois[1,2], P. Moodley[1,2], N. Msomi[1,2], K. Govender[2], R Parboosing[2,3], K Naidoo[4], B Chimukangara[2,4,5]

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[4]Centre for the AIDS Programme of Research in South Africa (CAPRISA), Durban, South Africa
[5]Critical Care Medicine Department, NIH Clinical Center, Bethesda, Maryland, United States

Assessing HIV-1 drug resistance in patients with virological failure amid the rollout of dolutegravir in hyperendemic Kwazulu-Natal, South Africa

Background: HIV Drug Resistance (HIVDR) remains a major threat to achieving sustainable viral suppression in patients on Antiretroviral Therapy (ART). In South Africa, since its rollout in December 2019, Dolutegravir (DTG) has been the preferred ART backbone.

Methods: We curated HIVDR genotypic data obtained from the National Health Laboratory Service (NHLS) for ART-experienced patients with virological failure (i.e., consecutive viral loads ≥1,000 copies/mL) receiving HIV care at public-sector healthcare facilities in KwaZulu-Natal (KZN), South Africa. We estimated the levels of HIVDR from genotypes collected between January 2020 and June 2022, and assessed temporal trends in HIVDR across 11 districts of KZN following DTG-rollout in South Africa.

Results: Of the 2,380 genotypes curated, 2,049 (86.1% CI 84.6–87.5) had HIVDR mutations, with most resistance mutations occurring among adult females aged >19 years, ($p=0.01$). Protease inhibitor (PI)-specific mutations were present in one-third of genotypes, including 671 (28.2%) with additional resistance to nucleoside, and non-nucleoside reverse transcriptase inhibitor (NNRTI) mutations. Only 39 genotypes had integrase resistance data, 9 (23.1%) of which had intermediate to high levels of resistance to DTG. Overall, compared with densely populated peri-urban and urban districts, rural districts had fewer HIVDR genotypes (369/2380, 15.5%) but more HIVDR (86.4% CI 82.5–89.8).

Conclusions: Six out of seven genotypes from patients with virologic failure had HIVDR mutations despite DTG-rollout, with persistent NNRTI resistance. Thus, while the introduction of DTG is expected to alleviate the HIVDR burden, a sub-population of people may not fully benefit from DTG-use due to multi-drug resistance, at which point PI-based ART may be warranted. There were higher proportions of HIVDR in rural districts and among adult women, highlighting regions and individuals needing priority HIV care. Overall, these findings urge the strengthening of HIV services in public healthcare systems to ensure sustainable DTG-use in first-line and subsequent ART regimens.

Audience Take Away Notes

- Our research highlights the importance of monitoring trends in HIV drug resistance, especially during programmatic changes in drug regimens. Such information is crucial in evaluating the success of HIV treatment programmes, considering that expanded access to antiretroviral therapy has been suggested as a strategy to eliminate HIV in South Africa
- Mapping the proportions of resistant patients at public-sector healthcare facilities in a hyperendemic

province in South Africa, provides a basis for targeted spatial health systems strengthening, particularly in rural areas

- We describe HIV-1 drug resistance mutations to integrase strand transfer inhibitors, thus adding to the growing body of knowledge on dolutegravir-related resistance. This knowledge is valuable to scientists, clinicians, pharmacists and policymakers for planning interventions and optimizing service delivery in sub-Saharan Africa

Biography

Dr. Lilishia Gounder is a South African clinical virologist and an emerging researcher whose interests include HIV drug resistance, geospatial analysis, and data science. She is currently in her 3rd year of PhD training, which focuses on monitoring and analysing HIV drug resistance in the province of KwaZulu-Natal, South Africa, the epicentre of the HIV pandemic.

Dr. Luis F. Vargas Garcia[1]*, Dr. Angelina Espino Barros Palau[2], Dr. Marcos Ibarra Flores[3]

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Diseminated lyme disease: A rare presentation of bilateral optic neuritis and sinus bradycardia without any conduction defects

Lyme disease (Lyme borreliosis) is a multisystem zoonotic disease caused by the spirochete Borrelia burgdorferi. Individuals without treatment may progress to a disseminated stage having cardiac, neurological or another systemic manifestations. We present a rare case of a 40-year-old white woman from Monterrey, Mexico without medical history. She presented to the emergency department with progressive onset of bilateral vision loss, headache and tingling/numbness of her bilateral lower and upper extremities. She also reported episodes of sudden loss of consciousness for 8 weeks. In the emergency room, sinus bradycardia without evident metabolic alterations is detected and dilated fundus exam demonstrated bilateral optic head edema, hyperemia, and optic nerve elevation. After extensive workup and ruling out other neurological and cardiac alterations, she was diagnosed with Lyme Disease with elevated serum IgM antibodies of 30.55 UR/mL (reference 0.00- 22), and the Western blot was positive for serum IgM Lyme antibodies but negative for IgG antibodies. More specifically, 2 bands (P21 IgM and P25[Osp C] IgM) were positive in addition to the positive Western blot, which fulfilled the Centers for Disease Control and Prevention (CDC) recommendation for a positive Lyme test. Due to the persistence of symptoms a lumbar puncture was performed, and showed normal opening pressure; glucose and protein levels were within normal limits but there was mild Cerebrospinal Fluid (CSF) pleocytosis with lymphocyte predominance. She was treated with doxycycline for 2 weeks. She was discharged home in stable condition with outpatient neuro- ophthalmology and cardiology follow-up.

Audience Take Away Notes

- Increase awareness to include Lyme disease in the differential diagnosis of optic neuritis
- This research could be used among clinicians to expand their research or teaching about zoonotic infections and their diverse clinical manifestations
- Learning about this case could simplify or make a clinician job more efficient by speeding the diagnosis of Lyme disease and prevent complications

Biography

Dr. Vargas studied Medicine at the Universidad de Monterrey, Mexico and graduated in 2010. He then joined the Internal Medicine Residency at the Hospital Christus Muguerza Alta Especialidad in Mexico and graduated in 2014. After 2 years he received his degree as Infectious Diseases M.D in Guadalajara, Mexico and in 2017, after one year of medical fellowship he obtained the degree of Neuro-infectiologist by the Universidad Autonoma de Mexico, one the most prestigious Universities in the country. He has published case reports as well as original researches in the field of Infections of the CNS in local and international journals.

Dr. Maria Aguilar Amaya*, Kenneth Rocko Cook
Southwest Interdisciplinary Research Center, Arizona State University, Phoenix, Arizona, United States

Advancing sexual health education: A methodological triangulation in the development and impact of the DISH-AZ academic detailing program

During this poster presentation, the presenter will discuss the development of the Academic Detailing (AD) DISH-AZ (Detailing for Improved Sexual Health in Arizona) program and will explain the methodological triangulation approach that is being used in Arizona. By employing a methodological triangulation approach consisting of academics, a provider/healthcare staff, and public health experts, the DISH-AZ program offers invaluable benefits for enhancing the quality and effectiveness of academic detailing to connect, educate, and support better health outcomes for LGBTQ+ patients and people living with HIV (PLWH), while also providing a more comprehensive understanding of healthcare topics. This approach not only increases the credibility of the information presented but also allows for tailored educational strategies that address the diverse needs and preferences of the target audience. Furthermore, methodological triangulation enables the cross-validation of key messages and recommendations, reinforcing their validity and relevance. Ultimately, this collaborative and multidisciplinary approach fosters innovation, promotes evidence-based practice, and contributes to improved healthcare delivery and patient outcomes.

The presenter will also discuss the methodology used for whole clinic assessment and pathways for AD sessions in order to meet the needs of the entire clinic. DISH-AZ uses AD strategies to address the gaps in knowledge and methods to assist healthcare staff to improve equity in patient care, especially for LGBTQ+ patients and PLWH, through comprehensive clinic-wide connection, education, and support. DISH-AZ is an AD program launched in 2021 by Arizona State University (ASU) in collaboration with the Arizona Department of Health Services (ADHS). Targeting health care staff caring for individuals living with and at risk for HIV, DISH-AZ emphasizes a holistic approach to improve care and patient outcomes using AD sessions to promote evidence-based and status neutral practices. In 2023, 250 sessions were held with 144 providers in Arizona and Nevada and 18 group presentations had 500+ attendees. The strategy involves developing programs and education with a status-neutral and pleasure-based biomedical approach, addressing outreach methods, protocols, and clinical practices. Lastly, while the focus of the program has been on status neutral approaches and practices, Pre-Exposure Prophylaxis (PrEP) and non- occupational Post Exposure Prophylaxis (nPep) to prevent HIV transmission, Rapid Start implementation for rapid initiation of antiretroviral therapy for persons diagnosed with HIV, hepatitis C treatment, and drug user health, since then, the program has expanded to include other topics such as mpox, gender-expansive care, and syphilis. The DISH-AZ Academic Detailers have expertise from each of the focus topics as well as lived experiences, which has proven to be impactful when establishing credibility with physicians and clinical staff. The lived experiences of our Academic Detailers enrich the educational exchange between detailers and physicians and their staff, leading to more meaningful discussions, enhanced learning outcomes and ultimately, improved patient care.

Audience Take Away Notes

- The development and methodology of the DISH-AZ (Detailing for Improved Sexual Health in Arizona) academic detailing program, including the utilization of methodological triangulation involving academics, providers/healthcare staff, and public health experts
- The benefits of employing a methodological triangulation approach to academic detailing, such as enhancing the quality and effectiveness of educational interventions for LGBTQ+ and people living with HIV (PLWH) and providing a more comprehensive understanding of healthcare topics
- The significance of tailored educational strategies that address the diverse needs and preferences of the target audience, resulting from the collaborative efforts of academics, physicians, and public health experts
- The impact of the DISH-AZ program on healthcare delivery and patient outcomes, demonstrated through the number of sessions conducted, the range of topics covered and the expertise and lived experiences of the academic detailers involved in the program

Biography

Dr. Maria Aguilar-Amaya is Director of the Office of Evaluation and Partner Contracts and at Arizona State University, Southwest Interdisciplinary Research Center (SIRC). She is Faculty Associate in the School of Social Work. Her current research focuses on health equity using community-based participatory research. Previous research focused on substance use/abuse and recidivism. She is a bilingual and bicultural researcher; a citizen of Mexico and the USA with ancestral roots from Apache and Tarasco tribes in Mexico. She received her MA (2005) and doctorate degree (2013) from the University of Phoenix (AZ, USA) in Organizational Management and Leadership.

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A snapshot of a representative Brazilian state of illegal mining in indigenous areas during the era of malaria elimination

Malaria is a public health problem and the cases diagnosed in the capital of Roraima have the potential to characterize the burden of the disease in the state. This study aimed to describe the epidemiological, clinical and laboratory aspects of malaria cases diagnosed in Boa Vista. For this purpose, a descriptive, cross-sectional study was carried out in two health units in the city, with individuals diagnosed with malaria and who agreed to respond to the questionnaire. Of the total of 206 participants, 96.1% (198) reported gold mining activity, characterized as men, mixed race and young. Of the group of miners, 66.2% (131) came from other states of Brazil or other countries. The mines were mainly located in the Yanomami Indigenous Territory in Roraima. P. vivax infection occurred in 74.3% (153) of participants. In the miner's group, there were reports of hospitalizations for severe malaria, reports of previous episodes of malaria and delays in treatment after the onset of symptoms. Although 73.2% (145) of miners reported knowing how malaria was transmitted, only 54% (107) took precautions with mosquito nets or repellents. The use of Artecom® and chloroquine was reported by miners as a way of relieving symptoms before returning to work, which highlights the importance of molecular surveillance of antimalarial resistance. Miners are considered a vulnerable population and impact to perpetuate malaria in Roraima. Therefore, access to diagnosis and treatment in gold mining areas and integrated surveillance of this population's mobility routes are important strategies to achieve the goal of eliminating malaria in the state.

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Use of intravenous immunoglobulin in neonatal enteroviral sepsis

A 4-day-old term infant with a low EOS risk score originally presented to the ED with six hours of lethargy and poor feeding. Initial work-up was demonstrated acute liver failure (PT/INR 18.5, ALT>90, AST>300), hypoglycemia, hyperferritinemia (ferritin >44,000), severe thrombocytopenia, and hypoxia concerning for enteroviral sepsis. Her hospitalization was complicated by hyperinsulinemia, hypoxic respiratory failure, severe pulmonary hypertension, and decreased systolic biventricular function (concerning for myocarditis). The patient required mechanical ventilation as well as vasoactive support with epinephrine and milrinone.

Management of her severe enteroviral sepsis was primarily supportive; however, the patient was initially treated with 2 g IVIG. Existing literature demonstrates some level of evidence in favor of using IVIG for the treatment of severe enterovirus infection. Despite her complications, the patient showed remarkable improvement after treatment with IVIG. At time of discharge, she was tolerating enteral feeds and was weaned off both heart failure therapies and sildenafil. Her echocardiogram showed mildly diminished systolic function and mild mitral valve regurgitation.

This case presentation will further contribute to the literature addressing the utility IVIG use in neonates with enterovirus infection. We aim to complete a comprehensive literature review and identify the most recent evidence and consensus on guidelines about the use of IVIG in the fetus and neonate.

Audience Take Away Notes

- This case expands on the current limited evidence about the utility of IVIG in neonatal enteroviral sepsis
- This case reviews a broad spectrum of clinical syndromes associated with enterovirus
- The literature review aims to provide the most recent evidence and consensus on guidelines about the use of IVIG in infants

Biography

Dr. Michele de Leon Jauregui graduated in 2011 from the University of Utah with degrees in Chemistry and Psychology. She earned her Doctor of Medicine at Rush University. She is currently a third year Triple Board Resident (pediatrics, psychiatry, and child psychiatry) at the University of Utah. She has presented at multiple conferences and published in both psychiatric and pediatric journals.

Dr. Melanie Rosado graduated in 2012 from the University of Michigan with a degree in Psychology. She completed her Doctor of Medicine at Rush University. She is currently a second year Internal Medicine and Pediatrics resident at the University of Utah. Her current interests include heart failure, cardiogenic shock, clinical reasoning, and intensive care. Dr. Rosado has presented at the Society of General Internal Medicine and has published in the journal, Pediatrics.

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Designing a Pre-Exposure Prophylaxis (PrEP) training for providers to increase PrEP awareness and prescription for black cisgender women

Background: Awareness and uptake of HIV Pre-Exposure Prophylaxis (PrEP) remains low among Black/African American cisgender women at risk for HIV acquisition. Primary care appointments present a valuable opportunity for introducing PrEP to clients; however, Primary Care Providers (PCPs) report minimal comfort level and low familiarity with PrEP. Ensuring PCPs are properly trained on PrEP is crucial as increased PrEP knowledge is associated with higher rates of PrEP prescription and future intent to prescribe. We conducted focus groups with medical providers at Community Health Centers (CHCs) across the Southern and Midwestern United States to identify themes informing the content, design, and delivery of a PrEP provider education aiming to increase PrEP utilization among Black women.

Methods: Focus group discussions occurred with providers at three healthcare organizations in the Midwest and South from August 2022 to February 2023. Providers were asked for input on content and design of provider education regarding PrEP and feedback on preliminary visuals and case scenarios. Transcripts underwent rapid qualitative content analysis using the Stanford Lightning Report Method via Dedoose software. Emergent themes were identified and presented under the domains of the Consolidated Framework for Implementation Research (CFIR).

Results: 10 providers (n=10) completed four focus groups. Themes emerged related to the individual characteristics of providers (limited PrEP knowledge, low comfort initiating PrEP discussions), the outer setting of client needs (perceptions of provider bias in identifying women who are at risk for HIV, varying levels of HIV risk self-perception), and attributes of the inner setting (need for support from the implementing center). Key opportunities were identified to maximize the benefit of training material, design, and delivery (i.e., developing specific case scenarios to enhance providers' cultural competency with Black women and their overall knowledge regarding PrEP).

Conclusion: A comprehensive PrEP training for providers should feature a combination of didactic material and interactive role-plays to equip providers with knowledge relevant to PrEP prescription for women while building their comfort initiating PrEP discussions with clients. Centers should implement effective and sustainable initiatives to support providers in prescribing PrEP following training completion, such as sharing updated PrEP guidelines and creating quick reference guides.

Audience Take Away Notes

- Our findings contribute to existing literature indicating comfort discussing sexual health and PrEP as a key training need among primary care providers in the United States. In particular, our research is valuable for primary care providers looking to gain self-efficacy with discussing and prescribing PrEP, particularly for cisgender women, as this work will contribute to our research team's development of a comprehensive PrEP educational training consisting of a combination of didactic and interactive material. We believe this training will play a role in bridging inequities in PrEP distribution in the United States by increasing provider PrEP knowledge and confidence and, subsequently, PrEP awareness and uptake among Black cisgender women

Biography

Nikki Kasal received her Bachelor of Arts in Biological Sciences from the University of Chicago in 2021. She currently attends the University of Chicago Pritzker School of Medicine and will receive her MD in 2026.Dr. Melanie Rosado graduated in 2012 from the University of Michigan with a degree in Psychology. She completed her Doctor of Medicine at Rush University. She is currently a second year Internal Medicine and Pediatrics resident at the University of Utah. Her current interests include heart failure, cardiogenic shock, clinical reasoning, and intensive care. Dr. Rosado has presented at the Society of General Internal Medicine and has published in the journal, Pediatrics.

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Does switching from triple (or quadruple)-drug regimen to double-drug regimen with oral INSTIs reduce Drug-Related Adverse Events (DRAES) and toxicity in virologically suppressed people with HIV? Satisfaction study

Background: Triple- or quadruple Drug Regimens (3 or 4DR) remain the gold standard for HIV treatment. However, there is currently a trend towards a reduction in the number of drugs from 3 or 4DR to Double-Drug Regimens (2DR) based on Integrase Strand Transfer Inhibitors (INSTIs). Switching to 2DR is not based on increased efficacy, as studies suggest non-inferiority of 2DR, but aims to reduce adverse events and long-term toxicity associated with prolonged exposure to current antiretroviral drugs. However, to date, neither clinical trials nor real-world data have confirmed this hypothesis.

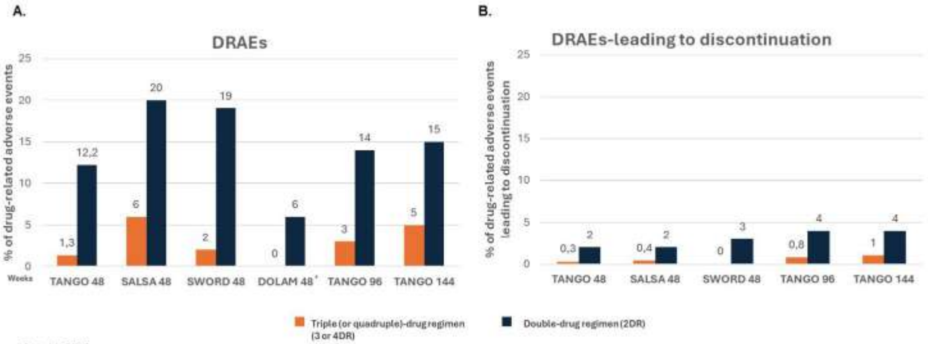
This study aims to describe the proportion of DRAEs reported in phase III and IV studies in virologically suppressed people with HIV (PWH) on 3 or 4DR and those who have switched from 3 or 4DR to 2DR with second-generation oral INSTIs at ≥ 48 weeks.

Methods: A systematic literature review was conducted, searching the main databases (PubMed, ClinicalTrials.gov, EU Clinical Trials Register, Cochrane, and Embase) from March 2014 to March 2024 and the main conferences from March 2022 to March 2024. We included phase III clinical trials and phase IV studies evaluating the switch from 3DR or 4DR to 2DR based on oral second-generation INSTIs in virologically suppressed PWH, with ≥ 48 weeks of follow-up.

Results: Nine publications met the inclusion criteria. Eight publications corresponded to three phase III clinical trials (TANGO, SALSA and SWORD) at different follow-up periods and one to a phase IV study (DOLAM), with a 48-week follow-up.

The percentage of DRAEs and DRAEs leading to discontinuation increased in patients who switched to 2DR ([6-20%] and [2-4%], respectively) compared to those who remained in 3DR or 4DR ([0-6%] and [0-1%]) at 48 weeks in all studies analyzed (Figure 1). A similar trend was observed with longer follow-up times. Differences observed in laboratory parameters when switching from 3DR or 4DR to 2DR were not clinically relevant.

Figure 1



*Probable DRAEs.
DRAE: Drug related adverse events

Conclusions: Therapy simplification from 3DR or 4DR to 2DR with oral second-generation INSTIs in virologically suppressed PWH at ≥ 48 week did not enhance the safety and tolerability profile compared with 3DR or 4DR continuation, according to data reported in phase III clinical trials and phase IV studies.

Financial support: Gilead Sciences

Audience Take Away Notes

- The audience will gain a comprehensive understanding of the safety and tolerability profile of switching from complex (3- or 4-drug regimens) to a reduced double therapy using oral second-generation INSTIs in virologically suppressed patients with HIV
- This knowledge will help clinicians in making informed decisions regarding treatment strategies for virologically suppressed patients
- This systematic review serves as a resource for other researchers and clinicians in the field of HIV treatment. It provides a basis for further research on optimizing treatment regimens and understanding patient outcomes
- These findings may contribute to refining treatment guidelines and protocols, leading to more effective and safer management strategies for HIV patients globally
- Yes, this study shown that the reduction in number of drugs from double to triple (or quadruple) regimens did not enhance the safety and tolerability profile, contrary to prevailing belief
- Other benefits
    - This SLR summarizes all currently available evidence related to switching therapy from triple (or quadruple) drug regimen to dual drug regimen with oral INSTIs, which helps clinicians keep up to date with the latest research

Biography

Dr. Pere Domingo Pedrol is an Internal Medicine specialist who graduated from the University of Barcelona. He is currently the Director of the HIV/AIDS Program at the Infectious Diseases Unit of Hospital de la Santa Creu i Sant Pau in Barcelona. Dr. Domingo has authored more than 800 scientific papers and 100 book chapters and has spoken at over 600 conferences. He reviews for more than 60 journals or serves on editorial boards. His research mainly focuses on antiretroviral therapy and its complications, and he collaborates with the Spanish and European Medicines Agencies.

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Catheter-related atlantibacter hermannii sepsis in a hemodialysis patient

Background: Atlantibacter hermannii, previously known as Escherichia hermannii is a rare causative agent of human infections. Several reports testify that the most frequently infected patients are immunosuppressed, especially those undergoing hemodialysis.

Materials and Methods: A 34-year-old man with an end-stage renal disease complained of chills, fever and general fatigue at the end of a regular hemodialysis session. The blood cultures were performed using BD BACTECTM Plus Aerobic/F and BD BACTECTM Plus Anaerobic/F bottles incubated in BACTEC 9120 Blood Culture System. Semiquantitative (roll-plate) culture of a segment from the replaced catheter tip was performed. The bacterial isolate was identified using Vitek 2 Compact. Verification of the automated identification was performed using 16S sequencing. The antimicrobial susceptibility test was performed by using ATS-N222 card on a Vitek 2 compact and minimum inhibitory concentrations were reported by the system automatically.

Results: Physical examination demonstrated that the patient was febrile (39.2°C) with a normal pulse rate (80/min) and arterial pressure (140/80 mm/Hg). The laboratory tests were as follow: white blood cells 7.2 x 109/l with 89% neutrophils, C-reactive protein 145 mg/l, hemoglobin 89.0 g/l, erythrocytes 2.7 x 1012/l, hematocrit 0.28 l/l platelets 184 x 109/l and creatinine clearance < 5 mL/min. The echocardiographic examination showed a vegetation located on the dialysis catheter in the right atrium. Empirical therapy was initiated with intravenous gentamicin and after the isolation of the agent, the treatment was continued with intravenous imipenem/cilastatin. The blood cultures and the tip of the replaced catheter were positive for A. hermannii. The 16S sequence product was used to query the NCBI bacterial database and revealed 99.75% identity to that of A. hermannii strain CIP 103176 16S ribosomal RNA in the NCBI GenBank database. The antimicrobial susceptibility results revealed resistance to aminopenicillins and susceptibility to all other tested antimicrobials.

Conclusions: To our knowledge, this is the first report of catheter-related vegetation with echocardiographic confirmation and the successful eradication of A. hermannii infection in a patient undergoing hemodialysis with imipenem/cilastatin.

Key word: Hemodialysis, Atlantibacter Hermannii, Catheter-Related Bloodstream Infection.

Audience Take Away Notes

- The audience will learn more about the role of an unusual bacterial human pathogen called Atlantibacter hermanii. The number of presented clinical cases associated with this bacterium is still limited. At the same time, A. hermanii is involved in the pathogenesis of quite serious infections. The audience will have a chance to study more about the methods in the bacterial diagnostic process, e.g. clinical, echocardiographic, microbiological, genetic methods and to understand more about antimicrobial susceptibility of A. hermanii

- Our work will help the audience in their job in the accurate clinical and microbiological diagnosis of catheter-related A. hermanii sepsis and also in the treatment of the current bacteria
- This research could be used to expand the researches or teaching of other faculty
- This provides a particular solution in the treatment of catheter-related A. hermanii sepsis in patient undergoing hemodialysis, using a successful antibiotic combination with imipenem/cilastatin
- It will improve the accuracy of a design and also will provide new information to assist in a design problem
- Other benefits
    - First report of catheter-related vegetation with echocardiographic confirmation
    - First report of a successful eradication of A. hermannii infection with imipenem/cilastatin

Biography

Dr. Preslava Hristova studied Medicine at the Medical University-Pleven, Bulgaria and graduated as MD in 2015. She then joined the Department of Microbiology and Virology, Medical University-Pleven as an Assistant professor and also join the Microbiology laboratory at UMHAT “Dr. G. Stranski”, Pleven. In 2020 she has become specialist in Medical Microbiology. She defended her PhD thesis in 2023 at Medical University-Sofia. In February 2024 she became a Senior Assistant professor in the Department of Microbiology and Virology, Medical University-Pleven. She has published more than 10 research articles in SCI(E) journals. Her scientific interests are associate with antimicrobial resistance, vancomycin-resistant enterococci, unusual pathogens and gut microbiota.

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Kluyvera cryocrescens central line associated bacteremia in a hemodialysis patient: A case report and review of literature

Kluyvera sp., an opportunistic Gram-negative bacillus found in clinical specimens such as sputum, urine, bile, peritoneal fluid, and blood, rarely causes significant infections. This case report manages a rare Kluyvera cryocrescens bacteremia in a female patient with chronic kidney disease due to IgA Nephropathy undergoing hemodialysis, highlighting the critical recognition of rare pathogens in patients with complex medical histories.

A 29-year-old female with end-stage kidney disease from IgA Nephropathy, polycystic ovary syndrome, and hypertension presented with weakness, lightheadedness, and generalized tremors three days post-hemodialysis. Despite the lack of fever or hemodynamic instability, symptoms such as weakness, malaise, pleuritic chest pain, and pain at the IJ catheter site suggested a systemic infection. Blood cultures from peripheral and central lines were obtained. Empiric therapy with Piperacillin-tazobactam was initiated. The isolates were identified as Kluyvera cryocrescens, sensitive to the administered antibiotics, which were therefore continued. The IJ catheter was temporarily removed and later re-inserted at a different site. After clinical improvement, IV antibiotics were switched to oral Ciprofloxacin, resulting in symptom resolution and the patient's stable discharge.

Kluyvera cryocrescens poses a risk for opportunistic infections in immunocompromised individuals. Though this infection may be uncommon, documented cases reveal a spectrum of clinical presentations, such as peritonitis, cholecystitis, wound infections, and complications related to indwelling devices. Our literature review, supported by findings from the present case, highlights bacteremia in the context of indwelling catheters as a notable risk factor. Empirical therapy, guided by the organism's susceptibility profile, typically include extended-spectrum cephalosporins, carbapenems, fluoroquinolones, and tetracyclines. Furthermore, this case emphasizes the importance of vigilance for infectious risks associated with hemodialysis and indwelling catheters, advocating for a cautious approach in similar patient populations.

Audience Take Away Notes

- Our case will detail the antibiotic sensitivity profile of the rare pathogen Kluyvera cryocrescens, to choose the most appropriate initial therapy, potentially leading to better patient outcomes
- This presentation will illustrate the clinical variability and potential outcomes of Kluyvera cryocrescens infections through a review of case reports in adult humans
- The discussion will highlight the implications of underlying conditions and indwelling devices in infection risk, particularly in hemodialysis patients
- The detailed case comparison can serve as a starting point for further research into the pathogenesis, treatment, and prevention of Kluyvera cryocrescens infections, as well as antibiotic resistance patterns
- Educators can utilize these tables as teaching tools to demonstrate the complexity of treating infections with variable antibiotic susceptibilities and the importance of considering individual patient histories and comorbidities

Biography

Dr. Quennie studied Doctor of Medicine at University of the East Ramon Magsaysay Medical Center, Philippines and graduated as MD in 2020. She then joined the Internal Medicine residency program at St. Luke's Medical Center, Taguig City Philippines and is currently on her 3rd year the program.

Amna Ahli, MD; Reem al Saadi*, MD; Ady Assaf, MD

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Disseminated Echinococcus infection with Cardiopulmonary involvement

Our presentation is about a challenging case of a 28-year-old male, previously healthy and a nonsmoker, from India and working as a security guard. He was referred to our facility for evaluation of disseminated Echinococcus infection affecting the lung and heart, presenting with hemoptysis, melena, unintentional weight loss, and cardiopulmonary symptoms. Diagnostic findings included positive Echinococcus and Strongyloides antibodies, imaging revealing lung and cardiac masses, and pathology confirming Echinococcus infection. Treatment involved a combination of albendazole and praziquantel therapy, followed by successful surgical resection of cardiac and pulmonary lesions.

Audience Take Away Notes

- The clinical manifestations and diagnostic challenges of disseminated Echinococcus infection with cardiopulmonary involvement
- The importance of a multidisciplinary approach involving medical, surgical, and pathology teams in managing complex parasitic infections
- The role of imaging modalities, serological tests, and pathological analysis in establishing a definitive diagnosis and guiding treatment decisions
- The efficacy of combined medical and surgical interventions in achieving favorable outcomes and preventing disease recurrence
- The significance of long-term pharmacological therapy with albendazole in preventing relapse and ensuring patient recovery
- Enhancing diagnostic acumen in identifying rare infectious diseases, particularly those with atypical presentations
- Implementing a comprehensive treatment strategy involving pharmacotherapy and surgical intervention for complex parasitic infections
- Improving patient care through interdisciplinary collaboration and tailored management plans
- Expanding research endeavors in tropical medicine and parasitology to explore innovative diagnostic modalities and therapeutic interventions
- Providing practical solutions for clinicians encountering similar cases, thereby optimizing patient outcomes and reducing morbidity associated with neglected tropical diseases
- In summary, our presentation offers valuable insights into the diagnosis, management, and treatment outcomes of disseminated Echinococcus infection with cardiopulmonary involvement, equipping healthcare professionals with the knowledge and tools necessary to address similar clinical challenges effectively

Reem Alblooshi, MD
Cleveland Clinic Abu Dhabi, United Arab Emirates

When dengue disguises itself: Uncommon presentation resembling hemophagocytic lymphohistiocytosis in a young adult

We describe a case of a 24-year-old male who presented with fever associated with flu-like symptoms that progressed to skin involvement with a diffuse erythematous and painful rash necessitating inpatient admission for further management. His physical examination was notable for widespread maculopapular rash of the trunk, upper and lower extremities as well as splenomegaly. Extensive investigations were remarkable for elevated liver function tests, ferritin, lactate dehydrogenase, and a peripheral smear revealing ovalocytes with reactive lymphocytes. Brucella antibodies but dengue and cytomegalovirus antibodies were still pending during his inpatient stay. Other autoimmune and infectious investigations and imaging were negative. Multidisciplinary discussions between Rheumatology, Dermatology, and Haematology resulted in primary differentials of hemophagocytic lymphohistiocytosis (HLH), drug eruption rash, and viral illness. He was started on methylprednisolone 80 mg, followed by a gradual taper in light of the differentials. A bone marrow biopsy was scheduled but patient's family declined and he was discharged home. Upon follow-up two weeks post-discharge, the patient received a diagnosis of dengue fever based on the identification of elevated IgM and IgG levels in the initial laboratory tests conducted during the inpatient admission.

Biography

Reem Alblooshi, MD is an Internal Medicine Doctor who graduated from Internal Medicine Residency program at Cleveland Clinic Abu Dhabi institution. She qualified from RAK Medical Health Science University. She then completed her internship at Cleveland Clinic Abu Dhabi. She joined the same center for Internal Medicine residency program. She worked as a junior internal medicine resident then senior resident. Dr. Alblooshi`s academic career includes a number of publications in peer reviewed journals. She was an active member of the medical education community. She is a member of American college of physician for internal medicine. She navigated the rigorous training, showcasing exceptional diagnostic acumen and empathy. Her journey is marked by tireless nights, hands-on experience, and a commitment to staying at the forefront of medical advancements.

Marcela Antonini[1], Mario Vianna Vettore[2], Anita Ogard Repal[2], Daniel de Macedo Rocha[1], Karyanna Alves de Alencar Rocha[1], Henrique Ciabotti Elias[1], Ana Luiza Carsoni Alves de Almeida[1], Marina Andreoli Trigo[1], Julia Freitas Gomes[1], Felipe Barufaldi[3], Rodrigo Carvalho Santana[3], Elucir Gir[1], Bruno Spire[4], Renata Karina Reis[1]*

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Patterns of chlamydia trachomatis and neisseria gonorrhoeae in different anatomical sites among Pre-Exposure Prophylaxis (PrPE) users in Brazil

Introduction: The presence of an untreated STI significantly increases the chance of acquiring HIV. In Brazil, CT/NG testing among PrEP users is insufficient and syndromic treatment is a priority in clinical practice. Multi-site testing for CT/NG improves screening of asymptomatic cases and timely treatment. So, it’s essential for HIV prevention.

Objective: This study aimed to test the importance of multisite testing for better screening of these pathogens and to test the presence of symptoms as an indicator for CT/NG infection.

Methods: This is a cross-sectional study carried out in four public infectious diseases clinics in the city of Ribeirao Preto, São Paulo, Brazil between January 2022 and March 2023. All participants had an anal swab and a first-pass or mid-stream urine collected for Chlamydia Trachomatis (CT) and Neisseria Gonorrhoeae (NG) analysis by Polymerase Chain Reaction (PCR). Data about sociodemographic, sexual behavioural and clinical aspects were collected. Pathway analysis was used to examine the direct and indirect relationships between variables according to the theoretical model.

Results: We screened 171 PrEP users which had two samples collected (urine and anal swab), resulting in 342 samples. Comparing the anatomic sites, the urine samples showed lower sensitivity for CT and NG than anal samples. Gonorrhoea was directly linked to lower age (β= -0.161, p=0.001). Time of PrEP use was directly associated with CT infection (β=0.202; p=0.042) and inversely associated with dysuria (β= -0.121, p=0.009). Lower occurrence of yellow-green secretion was linked to the detection of CT (β= -0.089, p=0.005) and NG (β= -0.048, p=0.002) infections. Foul-smelling discharge was directly associated with CT (β= 0.275, p=0.004) and NG (β= 0.295, p= 0.037) infection.

Conclusion: The symptoms are a bad indicator of CT and NG infection, and the screening must be done in multiple sites since most of the positive results would be missed if only urines were tested. In the case of testing only one anatomical site, specifically the urethra, the CT/NG incidence and prevalence would be underestimated. Multisite testing improves detection rates of CT/NG, and PrEP follow-up benefits people offering STI testing.

Descriptors: Chlamydia trachomatis; Neisseria gonorrhoeae; Sexually Transmitted Infections; Prevalence; Pre-Exposure Prophylaxis; HIV prevention.

Our findings call the attention of health authorities supporting their decisions over public health policies focused on offering CT/NG testing. Our study is about the prevalence of CT/NG by multi-site testing in PrEP users and about the symptoms as a bad indicator of CT/NG infections. This will help the audience understand that multisite testing improves the chance of detecting pathogens. Further, our evidence contributes to the discussion about reducing syndromic diagnosis. Finally, it contributes to the discussion that PrEP benefits their users because it makes it easier to access STI testing, early diagnosis and quick treatment.

Biography

Dr. Renata Karina Reis. Nurse. Master and PhD in at the University of Sao Paulo, Ribeirao Preto College of Nursing. Post-Doctorate at Aix-Marseille Universite, France (2017). Associate Professor at the University of Sao Paulo at EERP since 2018 (PhD, MNSc. RN) with the General and Specialized Nursing Department, Graduate Program in Fundamental Nursing. Coordinator of NAIDST and RENAIDST research group. She has published more than 137 research articles about HIV/aids and sexually transmitted infections.

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Predictors of vaccination rates in people living with HIV/AIDS followed at a specialty care clinic Ribeirao Preto, Sao Paulo, Brazil

Introduction: Vaccine hesitancy was considered by the World Health Organization as one of the 10 threats to global public health in 2019. In Brazil, the National Immunization Program offers the population vaccines free of charge through the Unified Health System. However, people living with the human immunodeficiency virus (PLHIV) may have a worse prognosis for diseases prevented by vaccination and therefore have a special indication for vaccination.

Objective: This study aimed to explore patient-specific predictors that influenced vaccination rates in people living with HIV/AIDS (PLWHA).

Methods: This single-center retrospective cohort review of all cases of PLWHA reported in Notifiable Diseases Information System (SINAN) for HIV/AIDS from the Ribeirão Preto, São Paulo, Brazil to explore patient-specific predictors that influenced vaccination rates in PLWH. The data were collected from the SINAN, which consolidates the registration of notifiable diseases and conditions nationwide. Information regarding the CD4 T-cell count and viral load was collected from the Laboratory Test Control System (SISCEL), while vaccination coverage indicators were obtained from the Computerized Outpatient Care System (Hygia-RP System), specifically from records related to immunization actions. Information about vaccine registration was accessed from the National Immunization Program Information System (SI-PNI Web) and VaciVida System. Univariate and multivariate logistic regression analyses expressed as crude odds ratios (cORs) and adjusted odds ratios (aORs), each with 95% confdence intervals (95% CI), were performed to compare the proportional diferences of factors associated with vaccine coverage.

Results: Our sample included data 645 people living with HIV/AIDS aged 14 to 72 years old and the mean age of the individuals was 32.1 years (SD+/- 11.1). Individuals aged 13 to 19 years had a better vaccination rate (12.8%, p=0.005), and none of those aged 50 years or older had completed the vaccination schedule. Receiving the last vaccine doses at the Specialized Assistance Service (SAE) was associated with completing the vaccination schedule compared to receiving vaccines at Basic Health Units (p=0.009), as well as demonstrating good adherence to antiretroviral therapy (p=0.003). Individuals vaccinated at SAE 4 had a higher rate of being adequately vaccinated; however, there was no association of this variable with the appropriate vaccination schedule (p=0.078). Considering the nine vaccines evaluated, individuals aged 40 years or older were 87.0% (aOR: 0.13, 95%CI: 0.02 – 0.72; p=0.020) less likely to be adequately vaccinated compared to individuals aged 10 to 19 years. With regard to the health facility where the last doses of the vaccine were received, individuals vaccinated in other health units were 10 times more likely to be adequately vaccinated compared to those who received their last vaccine doses at the SAE (aOR: 10.44, 95%CI: 1.35 – 80.83; p=0.025).

Conclusion: The decision to vaccinate is individual, and as such, it is necessary for vaccines to be available in healthcare services where the person receives follow-up care and easily accessible to the population, along with having trained healthcare professionals. Therefore, multifactorial health interventions are needed to address factors influencing vaccine coverage among PLHIV to improve vaccination rates.

Key Words: Vaccines. HIV. Acquired Immunodeficiency Syndrome. Vaccination. Vaccination Coverage.

Audience Take Away Notes

- Our study addresses various factors that may be related to confidence in the safety and efficacy of immunobiologicals, both for those who will receive them and for those who will indicate or administer vaccines. Vaccine coverage in adult individuals is unknown, with few studies conducted to assess vaccination rates in this population and in groups more vulnerable to vaccine-preventable diseases that have special vaccination schedules. This study definitively contributes to understanding the low vaccine coverage in PLHIV. It is hoped that by addressing various factors, ranging from issues related to services to those related to individuals themselves, it will be possible to achieve vaccine coverage not only in PLHIV but also in the entire population

Biography

Dr. Renata Karina Reis. Nurse. Master and PhD in at the University of São Paulo, Ribeirão Preto College of Nursing. Post-Doctorate at Aix-Marseille Université, France (2017). Associate Professor at the University of São Paulo at EERP since 2018 (PhD, MNSc. RN) with the General and Specialized Nursing Department, Graduate Program in Fundamental Nursing. Coordinator of NAIDST and RENAIDST research group. She has published more than 137 research articles about HIV/aids and sexually transmitted infections.

Lic. Rigoberto Fimia Duarte[1]*, Ph.D, Lic. Ricardo Oses Rodriguez[2], MSc, Prof. Paul Robert Vogt[3], MD

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[2]Forecast Department, Meteorological Center of Villa Clara, Cuba
[3]President of EurAsia Heart Foundation, Suiza

Objective regressive regression methodology in terms of infectious entities and more

The methodology of Regressive Objective Regression (ROR) is based on a combination of Dummy variables with ARIMA modeling, where only two Dummy variables are created, and the trend of the series is obtained. It requires few cases to be used, and also allows the use of exogenous variables, with the possibility of modeling and forecasting in the long, medium and short term, depending on the exogenous variable. This methodology has a wide and proven range of applicability in the field of biomedical sciences, ranging from: a) the ROR methodology applied to the control of culicid larval populations (larval densities, both general (DLG) and specific (DLE) (mosquitoes of the genus Anopheles), as well as for the mosquito species Aedes aegypti and Ae. albopictus, involved in the transmission of the arboviral entities Dengue, Yellow Fever, Chikungunya and Zika), b) The ROR methodology and its impact on fluvial and terrestrial malacofauna of veterinary medical interest, c) The ROR methodology and its application in transmissible infectious entities (mainly in transmissible infectious entities, both of viral and parasitic etiology, such as HIV, Leptospirosis, Cholera, Dengue, Chikungunya, Yellow Fever and Zika, and the case of Malaria, as the main parasitic entity), d) ROR methodology applied to Acute Respiratory Infections and Bronchial Asthma Crisis, up to e) ROR methodology and its application in the COVID-19 pandemic (the modeling of SARS-CoV-2, virus causing COVID-19 through the methodology of the Regressive Objective Regression (ROR), both in Santa Clara municipality and Villa Clara province and for Cuba, which made it possible to make short, medium and long term forecasts according to COVID-19. On the other hand, with this methodology, it was possible to make forecasts of deaths and new cases weeks in advance, as well as forecasts for deaths, critical, severe, confirmed and new cases of COVID-19; In addition to the application of this methodology to vaccination against COVID-19 in Cuba, and the comparison of the ROR methodology as a linear model with the non-linear Weibull model for COVID-19), and the possibility of forecasting extreme meteorological disturbances (earthquakes, cold fronts, cyclones and hurricanes), as well as seismic events (earthquakes). Evidently, the ROR Modeling and Prediction methodology is novel, since it allows modeling an immense set of natural, biological, biomedical and social processes and phenomena with great simplicity and economy of resources. By working with exogenous variables, it allows the modeling and prediction of events, phenomena and processes over time, both in the short, medium and long term. Undoubtedly, it also constitutes a contribution to the science of modeling and forecasting variables to know the future, as well as the impact that different variables contribute to an event or phenomenon, and because it is universal, it can be applied anywhere in the Universe.

Audience Take Away Notes

- On a novel methodology, Objective Regressive Regression (ORR), and its multiple possibilities of application in the field of biomedical sciences, and in the forecasting of extreme weather disturbances (earthquakes, cold fronts, cyclones and hurricanes), as well as seismological events (earthquakes)
- It can be used to know the future, as well as the impact that different variables contribute to an event or phenomenon, and because it is universal, it can be applied anywhere in the Universe

- As it requires few cases to be used, it enables the use of exogenous variables, with the possibility of modeling and forecasting in the long, medium and short term, depending on the exogenous variable. This methodology has a wide and proven range of applicability in the field of biomedical sciences
- Yes, this research that other faculty could use to expand their research or teaching
- Of Course this provide a practical solution to a problem that could simplify or make a designer's job more efficient
- Yes, it improve the accuracy of a design, or provide new information to assist in a design problem
- Other benefits.
    - This methodology has a wide and proven range of applicability in the field of biomedical sciences, ranging from: a) ROR methodology applied to the control of culicid larval populations (the mosquito species Aedes aegypti and Ae. albopictus, involved in the transmission of the arboviral entities Dengue, Yellow Fever, Chikungunya and Zika), b) ROR methodology and its incidence in fluvial and terrestrial malacofauna with veterinary medical interest, c) ROR methodology and its application in transmissible infectious entities (mainly in transmissible infectious entities, both viral and parasitic etiology), d) ROR methodology applied to Acute Respiratory Infections and Bronchial Asthma Crisis, e) ROR methodology and its application in the COVID-19 pandemic and f) The possibility of forecasting extreme meteorological disturbances (earthquakes, cold fronts, cyclones and hurricanes), as well as seismic events (earthquakes)

Biography

Rigoberto Fimia Duarte was born in 1966 in the current province of Sancti Spiritus, Cuba. He was Graduated in 1989 in Biology Science. Currently works at the University of Medical Sciences of Villa Clara (UCM-VC), Cuba. He has to his credit, 579 scientific results/publications, of which, he is the author of 398 scientific articles in specialized journals of recognized prestige and impact, as well as 31 books.

Silvia Giono Cerezo[2]*, Julia Moreno M[1,2], Maria Dolores Alcantar Curiel[1]*

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Acinetobacter baumannii blaOXA-143-like and blaOXA-72 with global international clone (IC) 2 and the Latin America endemic Ic5 exhibiting strong biofilm formation in a Mexican Hospital

Acinetobacter baumannii is an opportunistic pathogen responsible for Healthcare- Associated Infections (HAIs) and outbreaks. Antimicrobial resistance mechanisms and virulence factors allow it to survive and spread in the hospital environment. However, the molecular mechanisms of these traits and their association with international clones are frequently unknown in low- and middle-income countries. Here, we analyze the phenotype and genotype of seventy-six HAIs and outbreak-causing A. baumannii isolates from a Mexican hospital over ten years, with special attention to the carbapenem resistome and biofilm formation. The isolates belonged to the global International Clone (IC) 2 and the Latin America endemic IC5 and were predominantly extensively Drug-Resistant (XDR). Oxacillinases were identified as a common source of carbapenem resistance. We noted the presence of the blaOXA-143-like family (not previously described in Mexico), the blaOXA-72 and the blaOXA-398 found in both ICs. A low prevalence of efflux pump overexpression activity associated with carbapenem resistance was observed. Finally, strong biofilm formation was found, and significant biofilm-related genes were identified, including bfmRS, csuA/BABCDE, pgaABCD and ompA. This study provides a comprehensive profile of the carbapenem resistome of A. baumannii isolates belonging to the same pulse type, along with their significant biofilm formation capacity. Furthermore, it contributes to a better understanding of their role in the recurrence of infection and the endemicity of these isolates in a Mexican hospital.

Biography

Dr. Silvia Giono Cerezo PHD National School of Biological Sciences Instituto Politecnico Nacional- IPN Chemist Bacteriologist Parasitologist Doctor of Science Member of the National Academy of Medicine Member of the Mexican Association of Infectious Diseases Collegiate Member of the Postgraduate Studies Professor of Medical Bacteriology and Host-Parasite Relationship Theory and laboratory also Problems of Medical Bacteriology Tutor, Director Advisor of Bachelor's, Master's and Doctorate students Lines of research: Diagnostic Medical Microbiology and Antimicrobial Resistance of the ESKAPE group diagnosis and analysis of the genome of Helicobacter pylori MLST of Stenotrophomonas spp several publications.

Simona Yoffe Deri
Sheba Medical Center, Israel

Early versus late onset necrotizing enterocolitis in very low birth infants in the neonatal intensive care unit

Background: Necrotizing Enterocolitis (NEC), one of the most severe emergencies in neonates, is a multifactorial disease with diverse risk factors.

Objectives: To compare between the clinical and laboratory characteristics of premature infants diagnosed with Early-Onset NEC (EO-NEC) and those with Late-Onset NEC (LO-NEC).

Patients and Methods: Enrolled infants were identified from prospective local data collected for the Israel National Very Low Birth Weight (VLBW, <1500 grams) infant database and from the local electronic patient files data base for the period 1996-2017.

Results: Overall, 95 VLBW infants (61, 64.21% EO-NEC and 34, 35.87% LO-NEC) were enrolled. EO-NEC infants had higher rate of IVH grade 3 and 4 (26.2% vs 2.9%, p=0.005). LO-NEC infants had a higher incidence of previous bloodstream infections (35.3% vs 8.2%, p=0.002) compared with EO-NEC. EO-NEC infants were more likely to undergo surgery (49.2% vs 26.5%, p=0.031), less likely to receive postnatal steroids (8.2% vs 20.6%, p=0.109) and had a higher risk of death (59% vs 41%, p=0.095) than LO-NEC. In multivariable analysis models surgical intervention was associated with EO-NEC (OR: 4.627, p=0.013) as well as PDA and positive blood culture prior to the NEC episode.

Conclusions: Our data support the hypothesis that EO-NEC has significant different clinical and microbiological attributes compared with LO-NEC.

Key Words: Prematurity, Mortality, Bacterial Sepsis.

Biography

Simona Yoffe Deri is from Sheba Hospital, Israel.

Simona Yoffe Deri
Sheba Medical Center, Israel

The presentation of rhabdomyolysis in influenza B patients – A case series

Influenza B-associated rhabdomyolysis is relatively rare. Herein, we describe a retrospective case-series of five children hospitalized in a single institution for rhabdomyolysis from PCR-confirmed Influenza B. Viral sequencing revealed a novel deletion of one amino acid in the viral hemagglutinin, potentially explaining the unusual cluster of cases. Altogether, this work expands current knowledge on Influenza B-associated rhabdomyolysis in children.

Biography

Simona Yoffe Deri is from Sheba Hospital, Israel.

Sneha Thatipelli[1]*, Megan Grabill[2], Kayla Harrell[3], Nia Bhadra Heintz[4], Sara Solomon[5], Shimrit Keddem[6], Florence Momplaisir[7]

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Perspectives of OBGYN clinicians on integrating PrEP in routine women's health care: A qualitative analysis

Background: Human Immunodeficiency Virus (HIV) continues to be a major public health problem in the United States. Pre-Exposure Prophylaxis (PrEP) is highly effective in preventing HIV, but uptake remains low, especially among women. Furthermore, HIV prevention in pregnant individuals provides protection for both the mother and fetus. Research demonstrates OBGYN providers play an important role in HIV prevention care, but OBGYN perspectives around this have not been surveyed.

Methods: We conducted qualitative interviews with OBGYN providers, medical directors, and PrEP navigators in 2 academic OBGYN clinics in Philadelphia to understand facilitators and barriers for PrEP uptake among cisgender women.

Results: We completed 16 interviews: 12 physicians, 2 PrEP navigators, and 2 Advanced Practice Providers. Participants were mostly female (88%). The most common barriers identified included 1) decreased risk perception (provider for the individual or the individual for themselves) 2) Provider inexperience with PrEP Provider discomfort with prescribing and monitoring individuals on PrEP 4) Lack of a streamlined workflow for PrEP 5) Time and personnel limitations and 6) HIV stigma. Facilitators included 1) a strong desire to provide HIV preventative care services 2) an interdisciplinary care team including pharmacists, PrEP navigators, and social workers and 3) Having an infectious diseases expert liaison. Participants suggested education, improvements in workflow, and utilizing the electronic medical record (EMR) for HIV screening and PrEP care.

Conclusions: Understanding barriers and facilitators can help guide implementation of PrEP strategies in the OBGYN setting. Our study demonstrates OBGYN providers view HIV prevention within their scope of practice, however there are key clinic infrastructure and personnel limitations to provide this care. We highlight interdisciplinary teams as a facilitator for this work. Participant feedback suggests care can be improved through a multifactorial intervention including PrEP education, utilizing the EMR for prompts for screening and monitoring, team-based care, and a clear workflow.

Audience Take Away Notes

- Use qualitative interviews to identify key facilitators and barriers for HIV Prevention care among OBGYN providers in an urban healthcare setting
- Use the consolidated framework for implementation research (CFIR) to categorize barriers and facilitators into CFIR domains
- Link barriers and facilitators to implementation strategies in different CFIR domains to improve overall PrEP uptake
- Identify multi-level barriers and facilitators to PrEP uptake in the prenatal care setting
- Describe strategies to improve conversations about the benefits of using PrEP for HIV prevention in pregnancy
- PrEP care can be integrated in routine prenatal care

Biography

Sneha Thatipelli, MD is an infectious disease physician at the University of Pennsylvania. Dr. Thatipelli's clinical interests include general infectious disease with an emphasis on the HIV care continuum. She hopes to work towards improving the health of safety net populations with an interest in combatting health disparities.

Veronika Nemethova[1]*, Petra Babiakova[1], Michal Selc[2,3], Kristina Jakic[2], Lucia Uhelska[1], Boglarka Teglasova[1], Alexandra Poturnayova[4], Lubos Drgona[5], Andrea Babelova[2,3], Filip Razga[1]

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An unconventional therapeutic oligonucleotide effectively reduces SARS-CoV-2 RNA levels in preclinical animal studies

Since the emergence of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) in 2019, the number of confirmed cases worldwide exceeded 770 million in 222 countries by March 2024, with more than 7 million confirmed deaths, according to the statistics from the World Health Organization. In addition to quarantine measures, preventive measures, immunization of the population with vaccines, prophylaxis, symptomatic treatment, or secondary-use medications have become the main tools of prevention and therapeutic intervention against the virus.

Therapeutic oligonucleotides have attracted great interest due to their potency and potential to change the therapeutic landscape of many pathological conditions, including those of viral origin. Targeting the conserved SARS-CoV-2 RNA sequences essential for viral replication offers a rational approach to inhibiting viral infection and thereby halting disease progression.

Following the successful in vitro validation of a tailor-made therapeutic oligonucleotide with an unconventional structural design, called ASC1R, which was shown to be remarkably effective in transfected cell lines, we report here the results of subsequent preclinical animal studies of this active pharmaceutical substance. ASC1R has demonstrated excellent tolerability without any observed behavioural changes or mortality in acute and subacute toxicology studies in C57BL/6 mice, even at doses exceeding 100 times the therapeutically effective concentration. Functional studies showed effective reduction of target RdRp RNA levels in the liver of transfected mice by 95.1 (median (N=9), Q25-Q75=77.7-97.5) and 98.1% (median (N=9), Q25-Q75=94.1-98.8) after single application of ASC1R at doses of 1 and 10 mg/kg, respectively.

The therapeutic potential of ASC1R could translate into substantial clinical benefits for patients with COVID-19. Furthermore, in the context of infectious diseases, our results provide implications for the research and development of analogous antivirals for other diseases of viral origin. The findings could help meet the global challenge of developing new and safe treatment modalities.

This work was supported by the Slovak Research and Development Agency under Contracts No. PP-COVID-20-0007 and APVV-21-0220.

Audience Take Away Notes

- Oligonucleotide-based antisense strategies represent the most powerful approach to blocking target RNAs
- Therapeutic oligonucleotides have attracted much interest due to their potency and potential to change the therapeutic landscape of many pathological conditions, including those of viral origin

- ASC1R has demonstrated excellent tolerability in preclinical acute and subacute toxicology studies
- ASC1R reduced RdRp RNA levels with a remarkable efficiency of >98% after a single dose

Biography

Dr. Nemethova holds an honors degree in Molecular biology and genetics, and Macromolecular chemistry, and has >15 years of professional background in clinically oriented research. After gaining extensive experience working as a specialist at the Center of Molecular Biology and Gene Therapy (CZ), she later became a leader for early-stage validation of therapeutic oligonucleotides at the Slovak Academy of Sciences. As Head of the Therapeutics department at Selecta Biotech SE, she currently coordinates the development and preclinical studies of therapeutic leads for multiple diseases. She has published more than 20 research papers and is the author of several granted patents.

Yen Chin Liu[1,2,3]*, Chih Ching Wu[1,2,3,4], Chun Ju Chang[1,2,3], Shin Ru Shih[1,2,3,5,6], Rei Lin Kuo[1,2,3]

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SARS-CoV-2 omicron nucleocapsid effectively suppresses interferon beta expression via interaction with host HSPA4

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) can dysregulate host antiviral responses, including interferon production, to facilitate viral replication and spread via interacting with their hosts; however, the impact of the SARS-CoV-2 Omicron nucleocapsid protein on the innate immune response remains unclear. In this study, FLAG-tagged nucleocapsids of SARS-CoV-2 were first overexpressed in HEK293T cells, after which anti-FLAG immunoprecipitation and Western blotting assays were performed. Nucleocapsid-associated protein complexes in human cells were identified using co-immunoprecipitation and were combined with in-gel digestion and ultra-high-pressure liquid chromatography coupled to tandem mass spectrometry. We discovered that the nucleocapsid of SARS-CoV-2 could specifically interact with cellular Heat Shock Protein Family A member 4 (HSPA4) in the cytoplasm. The nucleocapsid of the SARS-CoV-2 Omicron variant exhibited a heightened interaction with HSPA4 compared to other variants. Downregulation of HSPA4 expression in A549-ACE2-TMPRSS2 cells decreased the innate immune responses and significantly increased the viral titers, suggesting that HSPA4 was an antiviral regulator in the SARS-CoV-2 life cycle. We further demonstrated that the nucleocapsid inhibited the phosphorylated-interferon regulatory factor 3 protein, interferon beta mRNA, and interferon-stimulated genes; however, HSPA4 overexpression could recover them. Moreover, HSPA4 is involved in the upregulation of innate antiviral immunity. Our data suggests a novel mechanism by which the SARS-CoV-2 nucleocapsid hijacks cellular HSPA4 to suppress the host innate immune response and facilitate viral replication.

Audience Take Away Notes

- The cellular innate immune response of SARS-CoV-2 infection
- The cellular and viral protein-protein interaction
- The variants of SARS-CoV-2 Nucelocapsid proteins

Biography

Dr. Yen Chin Liu received her PhD degree in 2014 from Graduate Institute of Biomedical Sciences, Chang Gung University, Taiwan. The findings reveal a novel mechanism of viruses attacking hosts whereby picornaviral polymerase (3Dpol) enters the nucleus and targets the central pre-mRNA processing factor 8 (Prp8) to block pre-mRNA splicing and mRNA synthesis. This work has been published in PLoS Pathogens. Dr. Liu worked as post-doctoral fellow from 2014 to 2019 in Department of Microbiology, the University of Hong Kong. She identified a novel virus host interaction mediated by XRN1 in influenza virus infection. This work has been accepted by mBio.

Yuanbin Wang*, Thomas Wilson Ph.D, Nicholas Orfan MD

Population Health Impact Inst, United States

Association between COVID-19 infection and myocarditis

Introduction: This study focuses on the relationship between COVID-19 infection and myocarditis across different age groups. Previous studies have indicated that both natural Covid-19 infection and MRNA Covid vaccination might trigger subsequent myocarditis especially in younger adults.

Methods: Insurance claims data from the Colorado all payers claims data set (July 1, 2017 to December 31, 2022) were examined. We used SAS to analyze ICD-10 diagnostic codes for COVID-19 and myocarditis. We excluded cases of myocarditis that occurred more than 5 days before a diagnosis of Covid-19 infection. These samples were grouped into several two by two tables by the two diseases and stratified by five age groups (0 to 17, 18 to 29, 30 to 44, 45 to 64, and 65+).

Results: Our data set included 3,209,252 people, 222,555 with documented cases of COVID-19 infection. There were 143 documented cases of myocarditis. 11 cases of myocarditis were excluded based on occurrence prior to Covid-19 infection as described above. In the COVID-19 group, the rate of myocarditis per ten thousand was 1.123. In the non-COVID group, the rate of myocarditis per 10,000 was 0.358. Patients who were diagnosed with COVID-19 experienced a 3.166 {2.048, 4.895} times increased risk for developing myocarditis than those not diagnosed with COVID-19. (P <.0001) The risk difference varied between age groups. The risk was highest for age groups 0 to 18, 18 to 30 years and 30 to 45 years, with OR's 3.923, 4.288 and 4.969 respectively. The lowest OR'a occurred in the age groups 45 to 65 years and greater than 65 at 2.042 and 2.044.

Conclusions: Our data shows a significant association between COVID-19 infection and the incidence of concurrent or subsequent myocarditis which is most pronounced from ages 0 to 45 years.

Biography

Yuanbin Wang is a student at Brookline High School in Boston, Massachusetts who works as an intern for the Population Health Impact Institute (PHII). PHII uses epidemiological data for large populations to investigate and offer insights on human disease.2014 to 2019 in Department of Microbiology, the University of Hong Kong. She identified a novel virus host interaction mediated by XRN1 in influenza virus infection. This work has been accepted by mBio.

Notes:

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