magnus Group

4TH EDITION OF WORLD CONGRESS ON

INFECTIOUS DISEASES

21-22
JUNE, 2023

ROME
ITALY

Venue:
Mercure Roma West, Viale Eroi di Cefalonia, 301,
00128 Roma RM, Italy

BOOK OF ABSTRACTS

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21-22 JUNE

BOOK OF
ABSTRACTS

4th Edition of World Congress on INFECTIOUS DISEASES

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Zsaklin Varga
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Welcome Message

I warmly welcome you to attend the 4th Edition of World Congress on Infectious Diseases to be held in Rome. The sessions cover all aspects of infectious diseases and have attracted speakers from all around the world, willing to share their expertise and experiences. In a world that has been dominated by an infectious disease SARS-CoV-2, it is exciting that those involved in the diagnosis, control and management of infections can once again come together. We look forward to your participation be it in person or virtually.

Wayne Dimech

Wayne Joseph Dimech

National Serology Reference Laboratory, Australia

Welcome Message

Dear Infection 2023 Participants,

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

Ranjan Ramasamy
IDFISH Technology, United States

Welcome Message

It is a great honour for me to be a member of the scientific committee and attend the 4WCID. This event occurs at the end of the pandemic and I am sure we will be offered valuable contributions about this topic, together with others dealing with the infectious diseases issue, coming from all around the world.

Rome, the eternal city, with its monuments, historical buildings, churches, typical quartiers and renowned cooking, in this season offers pleasant warm weather, allowing the attendants and their families to spend some time even on vacation. I welcome you to Rome and I do hope all participants will appreciate this event and those present will enjoy their stay.

Pietro Salvatori

Private Practice, Italy

Welcome Message

Dear congress visitors, it is an honor and pleasure to welcome you in this Congress. At no time in last century had infectious diseases been a more pressing concern. It happens in a time when faster technology has made easier to share information and ideas around the world and digital media has taken the lead at the forefront of global conversation. Nevertheless the opportunity to meet in person will give an incomparable additional value to the planned meetings. This conference will be one for us to share our thoughts and exchange ideas on how to chart our journey forward to reach new heights. I look forward to seeing you in Rome.

Alfonso Recordare

Dell'Angelo Hospital, Italy

Welcome Message

Dear participants, it is a pleasure to welcome you to this Congress focused in this exciting and interesting topic.

Infectious diseases are a major global health problem. The pandemic caused by SARS-CoV-2 has highlighted the fragility of our global health security system, pointing out some major deficiencies of even the most advanced countries in combating infectious diseases and, in particular, viral infections caused by RNA viruses. RNA viruses are a major threat to the human health. They are responsible for infections with high morbidity and mortality rates, and a tremendous socioeconomic burden. SARS-CoV-2 virus has been the latest in a list of RNA viruses responsible of major outbreaks worldwide in recent decades. Human immunodeficiency virus (HIV), hepatitis C virus (HCV), Ebola virus or Zika virus (ZIKV) are just other examples of RNA viruses that have produced important outbreaks in the last 40 years. Researchers around the world have been warning governments about the risk of RNA viruses and the absolute need for an in-depth understanding of the molecular biology of viruses and their interactions with host cells. SARS-CoV-2, in particular, has highlighted the vulnerability of the humanity as a whole to RNA virus infection, regardless of the social group or geographic region. Neither effective treatments nor vaccines have been available in time for any of the above viruses. This has been largely due to the lack of knowledge about RNA viruses. On the other hand, the strategies used to obtain antivirals have provided unacceptably late results and have not always been successful. It is therefore essential to anticipate an infection and develop tools to combat it in advance by exploring innovative strategies. The development of vaccines against SARS-CoV-2 has been an excellent example of the cost-effectiveness of exploring approaches based on new concepts, as was the case with the development of vaccines based on an RNA molecule. sharing of knowledge and advancements in the development of efficient antiviral molecules and therapeutic strategies will undoubtedly contribute to improving human health by effectively combating and preventing future infectious diseases.

Alfredo Berzal-Herranz

Instituto de Parasitología y Biomedicina López-Neyra, (IPBLN) CSIC, Spain

Welcome Message

It is indeed a special privilege to welcome you all on behalf of the organizing committee to this gracious occasion of 4th Edition of World Congress on Infectious Diseases scheduled on 23-24th June 2023, Rome, Italy. The WCID has been organized by Magnus group since 2020 in hybrid mode. The Magnus group has been continuously striving hard to bring expertise from different sectors on one platform of 'One Health'. I thank all the participants for showing their interest in attending the conference and bringing the expertise to this august gathering. This would be the 3rd consecutive successful year of the event and your presence will make it to greater heights.

The workshop's theme is particularly pertinent to professionals in the field of Infectious Diseases. It would be a great moment to network with other professionals around the world. The conference will definitely provide an opportunity for exchange of research experiences among experts from different fields of infectious diseases so that we can move forward into a new era of challenges and opportunities.

A very warm welcome once again.

Gayatri Tripathi

ICAR-Central Institute of Fisheries Education, India

Welcome Message

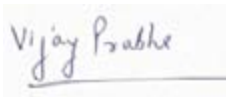
Dear congress attendees, it is an honour and pleasure to write a few welcome words. Cold sterilisation and disinfection technology are now receiving unprecedented attention from researchers. Cold atmospheric plasma is among the cold sterilisation methods showing promising results in the disinfecting and sterilising pathogens that cause infectious diseases. This technique brings about faster, more efficient and more effective ways of preventing the spread of infectious diseases. The cold atmospheric plasma can be utilised to disinfect surfaces, food materials and medical instruments that can all be a source of pathogenic microorganisms. Other advantages of cold atmospheric plasma are; it is an environmentally friendly technique that is easy to operate, can be applied to irregular shapes and surfaces, and is cost-effective. This novel technology could go a long way in preventing and reducing the cases of infectious diseases when utilised properly.

Chunyang Li

Jiangsu Academy of Agricultural Sciences, China

Welcome Message

Dear distinguished Congress visitors, it is my honour and pleasure to extend a warm welcome to each and every one of you. Infections are a ubiquitous phenomenon that can manifest in individuals across all demographics and result from a wide range of pathogenic agents. Emerging and re-emerging infectious diseases have ravaged nations, causing significant disease burden, disability, and loss of life due to their immediate and long-term repercussions. The global propagation of antimicrobial resistance represents a particularly ominous threat, as it renders many infections untreatable. To an unprecedented extent, issues related to infections in the context of global health have become a priority for world leaders and health policymakers alike. To address this problem, an integrated approach combining health promotion, disease prevention, and patient treatment is paramount. Despite the magnitude of the issue, the encouraging fact is that we have an opportunity to significantly improve public health through a better understanding of the threats we face and appropriate scientific and technological advancements.



Vijay Prabha

Department of Microbiology Panjab University Chandigarh, India

Keynote Speakers

Stephen Hsu
Augusta University,
United States

Wayne Joseph Dimech
National Serology Reference Laboratory,
Australia

Ranjan Ramasamy
IDFISH Technology,
United States

Pietro Salvatori
Private Practice,
Italy

Giuseppe Joe Vincini
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Genevieve Inchauspe
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Saurabh Chattopadhyay
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Alfonso Recordare
Dell'Angelo Hospital,
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India

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Vijay Prabha
Department of Microbiology Panjab University Chandigarh,
India

Thank You All...

ABOUT
MAGNUS GROUP

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

Participation from 90 different countries and 1090 different Universities have contributed to the success of our conferences. Our first International Conference was organized on Oncology and Radiology (ICOR) in Dubai, UAE. Our conferences usually run for 2-3 days completely covering Keynote & Oral sessions along with workshops and poster presentations. Our organization runs promptly with dedicated and proficient employees' managing different conferences throughout the world, without compromising service and quality.

ABOUT
Infection 2023

Magnus Group takes the pleasure to announce **4th Edition of World Congress on Infectious Diseases (Infection 2023)** going to be held from June 21-22, 2023 at Rome, Italy and Virtually with the theme Eradicating Infectious Disease through Ascension in Research. Infectious Disease conference will provide all the attendees, the opportunity to network with experts, present their research findings to an international audience and notify the latest scientific developments from world's eminent speakers and contribute to various discussions that will shape future health policies and a proper patient care all around the world. The Conference will have a mix of lectures of keynote addresses, panel discussions, case discussions, current reports of scientific progress featured in oral abstracts and posters. The chosen topics will be of great benefit to practicing clinicians and academicians in the field of infectious diseases, medicine, microbiology, epidemiology, public health, critical care, pulmonology, pharmacology, pathology, pharmacy, nursing, and clinical research. This conference offers an opportunity for faculty, postgraduates, fellows, residents, and undergraduates to present their work, learn and network with the experts.

EXHIBITOR

Clinical Consulting is a full service, progressive, Contract Research Organization (CRO) providing high quality clinical development strategy and management services for clinical trials with extensive experience in infectious diseases including: CAP, HAP, VAP, cUTI, PH, BV. We provide support for biotech and pharmaceutical companies by offering fast, high quality and cost-effective clinical trial management services. They have been operating since 2004 and have established ourselves as a trusted development partner in the field. Clinical Consulting is trusted development partner providing intelligent, comprehensive and cost efficient options, and the high quality service. Our services are based on focus we give to our customers, growing and progressing experience, reliability and resources.

Clinical Consulting prides itself on offering intelligent, comprehensive, and cost-efficient options to its clients. They aim to deliver high-quality services that meet the specific needs of their customers. The company's success is attributed to its customer-focused approach, continuously growing and progressing experience, reliability, and available resources.

Contact Info:
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EXHIBITOR

CATUG Biotechnology provides novel CRDMO services with a particular focus on mRNA vaccines and therapeutics as well as gene and cell therapy (GCT). Plasmid, mRNA, LNP, and analytical QC are our four fundamental technology platforms. Our strong expertise and know-how aim to provide end-to-end solutions to our clients in the life cycle of mRNA therapeutics and GCT product development. We customize unique services and creative solutions to fit each client's needs and timeline.

CATUG is a CRDMO focused on advanced therapy, especially in mRNA & GCT, equipped with novel technologies. Our team has deep expertise in platform research, process development, analytical development and manufacturing, providing end-to-end solutions with quality and efficiency. As a trusted partner, CATUG always put our clients first. We value every client's particular request and customize unique solutions. Our global PM team provides 24-7 client service to guarantee project progress and communication. CATUG is innovative and technology-driven. We constantly develop novel approaches to meet complex challenges. We're flexible, delivering the best possible custom solutions that conform to our client's needs, from single problem-solving to end-to-end solutions.

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21-22 JUNE

DAY 01

IN-PERSON KEYNOTE FORUM

4th Edition of World Congress on

INFECTIOUS DISEASES

MVA-based virotherapies in the treatment of infectious diseases

A famous milestone in the vaccine field has been the first successful vaccination against smallpox in 1798 by Edward Jenner. Using the vaccinia cowpox virus, Jenner was able to protect vaccinees from variola or smallpox. The Modified Virus Ankara (MVA) poxvirus strain has been one of the vaccines subsequently developed to prevent smallpox infection and was selected by the US government in their Biodefense strategy. MVA is a non-propagative virus with a strong established safety profile. Progress in molecular biology as well as in the understanding of the host mounted immune responses after infection by MVA have led to the development of MVA as vaccine platform in the field of preventive and therapeutic vaccination. This later class of therapeutics has witnessed growing interest that has translated into an increasing number of therapeutic vaccine candidates reaching the clinics both in oncology and infectious diseases. Prototype MVA-based therapeutic vaccines have targeted four major chronic infections including viral hepatitis, AIDS, human papillomavirus- linked pathologies and tuberculosis. More recently, we have used MVA to deliver a so-called host-directed therapy i.e. a therapy targeting host pathways rather than directly the pathogen. Specifically, we have developed a recombinant HDT-MVA to deliver the IL-7 immune-modulator with the goal to restore immune homeostasis in critically ill sepsis patients. This lecture will present through specific examples, a review of the growing place taken by MVA-based virotherapies to fight infectious diseases. Both pre-clinical and clinical developments will be discussed.

Audience Take Away Notes

- Presentation will help the audience to get familiar with novel concepts and application of viral-based products
- It will encourage researchers to get involved in the growing field of immunotherapies
- It should reassure the clinicians about safety implementing immunotherapies to treat infectious diseases beyond and/or in complement to more traditional treatments (such as antivirals and antibiotics)
- It could motivate faculty to add to their tutorial a chapter on use of viruses/viral-based platforms in the development of novel weapons to fight infectious diseases

Genevieve Inchauspe

ImmunResQ Department, France

Biography

After obtaining her PhD degree from the University of Toulouse (France), G Inchauspe performed a post-doctoral training at the National Institute of Health (Bethesda USA). She moved in 1989 to the Lindsley Kimball Research Institute of the New York Blood Center as a Member Investigator and in 1995 joined the French National Institute of Health (INSERM) where she continued to pursue research on immunological and vaccine development against hepatitis C virus infection. Since 2005, the department she heads at the biotech Transgene (Lyon, France) has developed therapeutic vaccines against several chronic infectious diseases and more recently a novel immunotherapy to treat sepsis immunosuppression.

The rationale of ethanol inhalation for disinfection of the respiratory tract in SARS-CoV-2-positive asymptomatic subjects

The severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) pandemic is a major health concern affecting socio-economic lives. As with other highly contagious diseases, it is of utmost importance to identify and treat the healthy carriers or positive asymptomatic subjects (PAS) early. SARS-CoV-2 entry points are mainly in the respiratory tract. No specific virucidal treatments against SARS-CoV-2 are currently available. Monoclonal antibodies are under evaluation, but high cost and possible ineffectiveness against virus variants could limit their use. Resorting nonspecific drugs is an alternative approach. Among them, ethanol (EtOH) is known to be a powerful, cost-effective, and abundant virucidal agent, now advised for surgical hand and surfaces disinfection. The paper aims to determine the potential role of inhaled ethanol to disinfect SARS-CoV-2 PAS, taking into account the dimension of the problem, ethanol efficiency and other beneficial effects on the respiratory tract, ethanol local and general toxicity and ethanol therapeutic window; consequently, to propose a study in order to verify this hypothesis. Together with the consolidated knowledge, an extensive review of the medical literature has been carried out looking for sound data able to support (or discard) the rationale on which a study could be built up. Evident data supporting the inhaled ethanol potential role on SARS-CoV-2 PAS disinfection have been found and discussed. A clinical trial to test the hypothesis that inhaled ethanol could be rapidly efficient in lowering or eradicating SARS-CoV-2 from the respiratory tract in PAS is advisable. Individual and public health benefits are stressed, together with socio-economic positive fallouts.

Audience Take Away Notes

- Friendly use in daily practice
- When finally proved, Ethanol inhalation will greatly reduce costs for human and health provider resources
- This research can be easily extended in any research center, mostly in low-income countries
- It provides a practical solution for slowing down/blocking SARS-CoV-2 and other enveloped viruses
- It provides new information to assist in pandemic management
- Great potential for saving lives and reduce financial burden

Pietro Salvatori

Head & Neck Surgeon, Private Practice, Milan, Italy

Biography

Dr. Pietro Salvatori graduated at the University of Florence Medical School, Italy. He earned specialization in General Surgery, Otorhinolaryngology, and Maxillo-Facial Surgery. He was Research Fellow at the University of Liverpool, served in several Institutions, and ended his hospital career as Head of ENT-H&N Department of the Humanitas San Pio X Hospital, Milan, Italy. At present, Dr. Salvatori acts as freelance Head & Neck Surgeon. Most of both his work and research dealt with head and neck cancer. Dr. Salvatori published more than 50 papers. During recent pandemic, he made research with international colleagues and published on ethanol inhalation to treat SARS-CoV-2 infection and Covid-19.

BOOK OF ABSTRACTS

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21-22 JUNE

DAY 01

IN-PERSON SPEAKERS

4th Edition of World Congress on

INFECTIOUS DISEASES

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[2]School of Science, Technology and Engineering, University of the Sunshine Coast, Sippy Downs, Queensland, Australia
[3]Australian Infectious Disease Research Centre, University of Queensland, St Lucia, Queensland, Australia
[4]School of Chemistry and Molecular Biosciences, University of Queensland, St Lucia, Queensland, Australia

Rapid, isothermal detection of Zika virus: A potential alternative to RT-PCR

Zika Virus (ZIKV) is a re-emerging flavivirus that poses a significant public health threat. ZIKV exhibits a wide array of non-vector borne human transmission routes, such as sexual transmission, transplacental transmission and blood transfusion. Detection and surveillance of ZIKV is considered paramount in prevention of major outbreaks. With the majority of cases reported in low-resource locations, simple, low-cost detection methods are considered highly desirable. Here we have developed a sensitive and specific ZIKV diagnostic using Reverse Transcription Recombinase-Aided Amplification (RT-RAA) coupled with Lateral Flow Strip Detection (LFD) targeting the ZIKV NS1 gene. This diagnostic provides high throughput performance and speed without compromising sensitivity and specificity, compared to the gold-standard RT-PCR. We show our ZIKV RT-RAA-LFD can detect 500 copies of ZIKV RNA/µL in under 30 minutes. Specificity testing confirmed that our assay does not detect any co-circulating flaviviruses (Dengue, West Nile, Japanese encephalitis and Yellow Fever viruses) or Chikungunya virus. Furthermore, the sample processing employed here results in complete inactivation of ZIKV (MR766 strain) in 5 minutes at RT. In comparison to conventional RT-PCR our ZIKV RT-RAA-LFD does not require expensive machinery, specialised laboratory settings or extensively trained personnel. Current research endeavours are focused on implementation of a one-step sample processing method coupled with our ZIKV RT-RAA-LFD of clinical samples (serum and urine) to assess the rapid, POC usability of our diagnostic in resource limited settings. Collectively, our data suggests that our ZIKV RT-RAA-LFD diagnostic has the potential to become a clinically sensitive and specific alternative to RT-PCR, particularly within resource-limited settings, where ZIKV and several other arboviruses are endemic.

Keywords: Recombinase Aided Amplification (RAA), Zika Virus (ZIKV), Lateral Flow Strip Detection (LFD), Point-of-care (POC)

Audience Take Away Notes

- Viral infection diagnostic technique that is different to conventional methods
- Point-of-Care detection, diagnostics and surveillance of viruses and viral infections
- Emerging arboviruses and viruses of concern

Biography

Completed a Bachelors in Medical Sciences, minoring in chemistry at Dominican University of New York, USA. Then Completed a Master's Degree (University of Queensland, Australia) in Molecular Biology with a particular focus on host-pathogen interactions of Flavivirus infections. Currently a PhD focusing on detection, diagnostics and surveillance of viruses and viral infections at The University of the Sunshine Coast, Australia.

Pau Cistero[1], Sara Sentre Domingo[2*], Gloria Matambisso[3], Henriques Mbeve[3], Nelo Ndimande[3], Alfredo Mayor[1]

[1]Institute for Global Health, Hospital Clinic, Barcelona, Catalonia, Spain
[2]Molecular Diagnostic, CerTest Biotec, San Mateo de Gallego, Aragon, Spain
[3]Centro de Investigacao em Saúde de Manhica (CISM), Maputo, Mozambique

No cold chain molecular workflow for detecting and differentiating *plasmodium*

Background: Malaria (or paludism), is a mosquito-borne parasitic disease caused by *Plasmodium*, is a leading cause of death and disease in many developing countries. The objective of this study was to determine the clinical performance of VIASURE *Malaria* Real Time PCR Detection Kit and VIASURE *Malaria differentiation* Real Time PCR Detection Kit using dried blood spot on filter paper samples. The aim of this retrospective study was to validate and compare the clinical sensitivity and specificity of the VIASURE assays with the reference method used in the laboratory.

Material and methods: The lyophilized Malaria assay and Malaria differentiation assay, which detects the genus *Plasmodium* spp. and the main human pathogenic *Plasmodium* species: *P. falciparum*, *P. ovale*, *P. vivax*, *P. malariae* and *P. knowlesi* respectively, were used in comparison with an 18S rRNA in-house malaria screening and differentiation assays. A total of 300 blood on filter paper collected from 2016 to 2019, from patients with clinical suspicion of malaria in the Manhiça-Magude district of southern Mozambique were analysed. The DNA extraction was carried out using the Chelex® 100 sodium method and the thermocycler employed was Applied Biosystems 7500 Real-Time PCR System.

Results: A total of 77 samples were considered as *Plasmodium spp.*-positive by both assays, 1 false positive result and 15 false negative results for VIASURE were obtained and 207 samples showed to be negative for this target by both assays. Regarding species differentiation: VIASURE assay showed 58 true positive and 3 false negative results for P. falciparum, 2 true positive results for *P. malariae* and 1 true positive and 1 false negative result for *P. ovale*. After data analysis, the sensitivity and specificity values obtained were:

VIASURE target	Sensitivity	Specificity
Plasmodium spp.	0.83 (0.74-0.9)	0.99 (0.97-1)
P. falciparum	0.95 (0.86-0.99)	1 (0.94-1)
P. malariae	1 (0.15-1)	1 (0.94-1)
P. ovale	-	0.98 (0.91-1)

Conclusions: This retrospective study demonstrated the good sensibility and specificity of both VIASURE molecular assays using this extraction method on dried blood spots, which is a workflow that does not require a cold chain to be performed.

Audience Take Away Notes

- Diagnostic workflow where no cold chain is needed as samples, extraction and RT-qPCR are done with material stored at room temperature
- Good sensibility and specificity of both VIASURE molecular assays using this extraction method on dried blood spots

Biography

Sara Sentre Domingo studied a BSc in Biotechnology at the University of Zaragoza. Later on, she studied an MSc in Molecular and Cellular Biology at the University of Zaragoza, graduated in 2019, and a MSc in Bioinformatics and Biostatistics at the Universitat Oberta de Catalunya, graduated in 2022. She is currently a junior researcher at the Molecular Diagnosis department at CerTest Biotec.

Susan Jack[1, 2*], Mike O'Brien[3], James Ussher[4, 5], Richard Egan[2], Ariyapala Samaranayaka[2]

[1]Te Whatu Ora, National Public Health Service, Southern District, Dunedin, New Zealand
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[3]Te Whatu Ora, Southern District, Dunedin, New Zealand
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[5]Southern Community Laboratories, Dunedin, New Zealand

Carriage of neisseria meningitidis among university students living in residential colleges, Dunedin, New Zealand

Invasive meningococcal disease is a severe disease caused by *Neisseria meningitidis* that can present as septicaemia or meningitis and may lead to disability or death. Nasopharyngeal carriage of N. *meningitidis* may occur in up to 15% of the general population with a higher prevalence reported among adolescents and young adults. Longitudinal studies among first year university students have shown increasing prevalence of carriage during the first year of study with those living in shared or crowded accommodation having a higher likelihood of carriage and disease. To date there has been limited N. *meningitidis* carriage data from New Zealand University student populations. In 2018 a series of three cases of meningococcal disease in one university residential college prompted the treatment of all residents with clearance antibiotics. Three months later a carriage survey was undertaken among first year students living in all 14 residential colleges of the university. The objectives of the study were to increase understanding of N. *meningitidis* carriage prevalence among students in their first year in a New Zealand residential college, to examine the presence of risk factors for carriage, and determine the impact clearance antibiotics have on carriage in the student population.

Audience Take Away Notes

- The prevalence of N. *meningitidis* carriage among first year university students living in a residential college in New Zealand
- What risk factors were associated with N. *meningitidis* carriage including whether vaping is an independent risk factor
- Following clearance antibiotics, how quickly does N. *meningitidis* recolonize the nasopharynx

Biography

Susan Jack (MBChB, Dip Paeds, MPH+TM, PhD, FNZCPHM) is a New Zealand public health medicine specialist. She is currently a Medical Officer of Health and Clinical Director of Te Whatu Ora, National Public Health Service, Southern District, New Zealand. Susan is an honorary Senior Lecturer with the Department of Preventive and Social Medicine, University of Otago, Dunedin, New Zealand. Susan worked in Cambodia for many years including with WHO in the areas of child survival, nutrition, maternal and newborn health. Her interests include infectious diseases, effective translation of evidence into policy, strategy, implementation, and evaluation of public health programmes.

Mohammad Mir, PhD
Western University of Health Sciences, United States

Therapeutic intervention of Bunyavirus induced hemorrhagic fever and cardiopulmonary disease

Viruses from different families in the order Bunyavirales contains highly contagious and deadly viruses, having no cure at present. For example, Hantaviruses from the family Hantaviridae are negative stranded emerging RNA viruses and category a pathogens that cause serious illness when transmitted to humans through aerosolized excreta of infected rodents. Hantavirus infections cause Hemorrhagic Fever with Renal Syndrome (HFRS) and Hantavirus Cardiopulmonary Syndrome (HCPS) with mortality rates of 15% and 50%, respectively. Annually 150,000-200,000 cases of Hantavirus infections are reported worldwide, and there is no treatment for this viral illness. The mortality rate of rift valley fever virus from the family Phenuiviridae can go as high as 60% in certain out breaks. The mortality rate of Heartland virus, another member of the family Phenuiviridae is 30%. Crimean Congo Hemorrhagic Fever Virus (CCHFV) (Nairoviridae) has a mortality rate of 40%. La Crosse virus from the family Peribunyaviridae, especially the California serogroup, causes very serious encephalitis that changes the mental status in most infected patients. There are numerous other Bunya viruses that cause serious human illnesses with bad prognosis because of the lack of vaccine and antiviral therapeutics. Thus, the need of the hour is to develop a broad spectrum antiviral therapeutic that selectively targets Bunya viruses and improves the prognosis of their deadly diseases. Through our basic research efforts we identified the interaction between Hantavirus nucleocapsid protein and viral mRNA 5' UTR as a novel target for therapeutic intervention of Hantaviruses. Using a high throughput screening approach, we identified a lead inhibitor that binds to the nucleocapsid protein, disrupts the N protein-UTR interaction and inhibits Hantavirus replication in cells. The recent X-ray crystal structure revealed that Hantavirus N protein shares structural homology with other Bunya viruses nucleocapsid proteins. Consistent with the structural conservation of the target (N protein), we asked whether the identified lead inhibitor inhibits the replication of other Bunya viruses. To this end, NIH tested our lead inhibitor against multiple viruses from diverse virus families. Interestingly, the lead inhibitor specifically inhibited all the tested viruses from the order Bunyavirales, such as Rift valley fever virus, Heartland virus, Lacrosse virus, and Hazara virus, which is a model virus used for studying CCHFV disease. The lead inhibitor did not show any effect upon the viruses from nine other families, demonstrating its specificity for Bunyaviruses Our research program is focused to use a combination of approaches including medicinal chemistry, X-ray crystallography, biochemistry, in vivo reporter assays and anti-viral testing to synthesize the derivatives of the lead inhibitor, having high target binding affinity and improved antiviral efficacy. The goal is to identify several drugs like candidates that have strong and broad spectrum anti-viral activity. This drug like candidates will be tested for anti-Bunyavirus activity in animal models.

Walter Fabricio Silva Martins[1, 2*], Martin Donnelly[2], David Weetman[2]

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Insecticide resistance and use of household insecticides for personal protection: Insights from vector-borne disease outbreaks

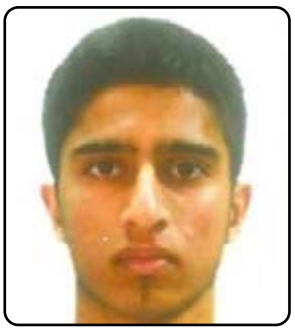
Aedes aegypti is the most important vector of at least four fatal and/or debilitating arboviruses (dengue, chikungunya, yellow fever and Zika). Insecticide-based approaches remain the major intervention to minimize vector-borne disease burden across the diseases. In Brazil insecticide resistance is increasing, likely as a result of overuse or misuse of insecticides. One major source of selection may come from unregulated and increasing use of household insecticides, but the contribution this makes is very poorly understood. We have investigated the mechanisms of resistance and cross-resistance between household and public health insecticides in Brazilian *Ae. Aegypti* to demonstrate how household insecticides could contribute to the broad evolution of insecticide resistance.

Audience Take Away Notes

- Over the talk, I will address new approaches relevant to the detection and monitoring of the evolution of insecticide resistance driven by my unregulated usage of household insecticides. The audience will have an opportunity to further discusses the impact of personal protection against mosquitos and threats to public health ant-vector interventions
- The usage of household insecticides and their association with the evolution of insecticide resistance in vector mosquitos have been poorly investigated. In my talk, I will provide insights for further research underlying a timely issue for public health
- We have developed new approaches for testing and monitoring evolving resistance driven by household insecticides, which will be addressed during the talk. See manuscript pre-printing: https://doi.org/10.21203/rs.3.rs-2451023/v3
- In our current research project, we developed improved methods based on the WHO guideline for testing household insecticides. Our approach provides a high-throughput and reproducible approach method, which would assist further study design
- List all other benefits
    - Discuss the timely problem of global increasing of vector-borne diseases transmission
    - Further discuss the risk for public heath of unregulated usage of household insecticides
    - Share with the audience our expertise for testing and monitoring efficiency of special repellents and aerosol formulations against mosquito vector of infection diseases

Biography

Dr Fabricio Silva Martins graduated in Animal Biology (MSc) from the Federal University of Pernambuco, Brazil. He received his PhD in Tropical Medicine at The University of Liverpool / Liverpool School of Tropical Medicine, United Kingdom. He re-joins LSTM in 2018 in the department of vector biology as an associated researcher working in the Welcome Trust funded project to identify the drivers of insecticide resistance in Brazilian *Aedes aegypti.*



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Control of *C. difficile*-associated disease using a multimodal intervention

Clostridioides difficile has been recognized as the most common cause of hospital-acquired diarrhoea. The symptoms vary from mild diarrhoea to fulminating infection, leading to pseudomembranous colitis and death. Since 2003, *C. Difficile*-Associated Disease (CDAD) has been a part of mandatory surveillance in the UK; mandatory surveillance in Northern Ireland was introduced in 2004. The UK Department of Health has published guidelines on the control of CDAD and has also developed a 'care bundle' to reduce the risk of acquiring *C. difficile*.

Since 2008, The Southern Health & Social Care Trust (SHSCT) noticed a rise in the number of new cases of CDAD. As a result, our trust's infection prevention control and senior management team developed a comprehensive intervention plan which included early diagnosis, prompt isolation of all patients with diarrhoea in a single room or cohort ward, implementation of contact precautions with a campaign to promote hand hygiene, implementation of an antibiotic stewardship Programme, education and training of all clinical staff, enhanced environmental cleaning with compliance monitoring, enhanced surveillance and feedback via an e-dashboard and root cause analysis for all patients.

Implementing a multimodal intervention strategy has proven very effective. We have since noted a reduction in the incidence of *C. difficile* cases from February 2009 onwards in all the healthcare facilities within the SHSCT, both in hospital and community cases. Following the intervention, the reduction of CDAD fell in patients aged ≥65 years from 164 cases in 2008-09 to 37 cases in 2009-10, a reduction of 77% within one year. However, what was particularly notable was that following the intervention, we started to see a reduction in CDAD after six weeks, and a 65% reduction in cases which continued till 2021/2022 (Fig 1). In conclusion, it is possible to reduce hospital-acquired CDAD via the implementation of a multimodal intervention strategy.

Fig 1: No. of cases of hospital inpatient episodes of C. difficile ≥ 65 years

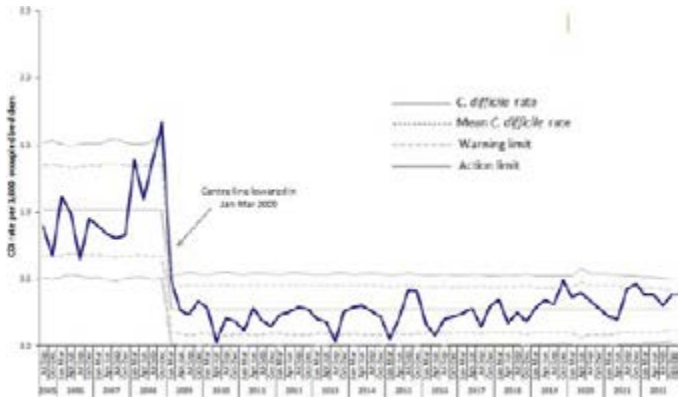

Figure 1: Statistical Process Control Chart of reduction in C. difficile in Southern Health and Social Care Trust. Source. Northern Ireland Public Health Agency, Quarterly Report, Nov 2022.

Biography

Dr Damani studied medicine at the University of Malta, having graduated in 2019 and is currently working as an internal medicine in the UK. Dr Damani has done presentations at infection prevention and control conferences, both nationally and internationally. Most recently, he has led a quality improvement project involving 3 PDSA cycles on improving compliance with local antibiotic guidelines at a regional level.

Ali Amoushahi[1], Elham Moazam[2], Amin Reza Tabatabaei[3], Golnaz Ghasimi[3], Ian Grant-Whyte[4], Pietro Salvatori[5*], Ahmed Ragab Ezz[6]

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Efficacy and safety of inhalation of nebulized ethanol in COVID-19 treatment a randomized clinical trial

Background: This study was designed to evaluate the efficacy and safety of nebulized ethanol (EtOH) in the treatment of COVID-19.

Methods: A RCT of 99 symptomatic and RT-PCR-positive patients admitted to a hospital receiving Remdesevir-Dexamethasone was conducted. They were randomly assigned to receive distilled water spray (Control Group, CG) or 35% EtOH spray (Intervention Group, IG). Both groups inhaled three puffs of spray (nebulizer) every 6 h for a week. Primary outcome: Global Symptomatic Score (GSS) between the two groups at the first visit and on days 3, 7, and 14. Secondary outcomes: Clinical Status Scale (CSS, a 7-point ordinal scale ranging from death to complete recovery) and readmission rate.

Results: Forty-four and 55 patients were enrolled in the intervention and control groups, respectively. Although there was no difference at admission, the GSS and CSS improved significantly in the IG ($p=0.016$ and $p=0.001$, respectively). The IG readmission rate was significantly lower (zero vs. 10.9%; $p=0.02$).

Conclusions: Inhaled-nebulized EtOH is effective in rapidly improving the clinical status and reducing further treatment. Due to its low cost, availability, and absent/tolerable adverse events, further research is recommended on curative and preventive EtOH effects.

Audience Take Away Notes

- Friendly use in daily practice
- Ethanol inhalation will greatly reduce costs for human and health provider resources
- This research can be easily extended in any research center, mostly in low-income countries
- It provides a practical solution for fast recovery from Covid-19 at negligible toxicity
- It provides new information to assist in pandemic management
- Great potential for saving lives and reducing financial burden

Biography

Dr. Pietro Salvatori graduated at the University of Florence Medical School, Italy. He earned specialization in General Surgery, Otorhinolaryngology, and Maxillo-Facial Surgery. He was a Research Fellow at the University of Liverpool, served in several Institutions, and ended his hospital career as Head of the ENT-H&N Department of the Humanitas San Pio X Hospital, Milan, Italy. At present, Dr. Salvatori acts as a freelance Head & Neck Surgeon. Most of both his work and research dealt with head and neck cancer. Dr. Salvatori published more than 50 papers. During the recent pandemic, he made research with international colleagues and published on ethanol inhalation to treat SARS-CoV-2 infection and Covid-19.

Patricia Marques Moralejo Bermudi[1,2] *, Francisco Chiaravalloti-Neto[1], Raquel Gardini Sanches Palasio[1], Marta Blangiardo[2], Monica Pirani[2]

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Spatio-temporal patterns of dengue incidence and their associated factors, Brazil, 2000-2018

Dengue is a neglected tropical disease. This arbovirus is an important public health problem and has a great economic impact, especially in emerging countries. Globally, the incidence of dengue has expanded abruptly in recent decades, potentially associated with climatic factors. Here, we study the spatio-temporal dynamics of dengue incidence in Brazil, which has experienced severe and extensive epidemics over the past years. We use an ecological design and carry out spatio-temporal mapping of the disease distribution; we also investigate the effect of important risk factors for dengue incidence, including climate, environmental and socio-economic variables. All data are obtained from freely accessible sources, such as: Notifiable Diseases Information System – SINAN (Dengue cases), Brazilian Institute of Geography and Statistics - IBGE (demographic and socioeconomic information), and Global climate and weather data – WolrdClim (climate variables). Then, under different scenarios of changes in greenhouse gas emission, we predict the dengue incidence over the entire Brazil. We consider 19 years, from January 2000 to December 2018 and the spatial unit of analysis is micro region (set of municipalities with similar specificities, regarding the organization of space; there are 558 in Brazil). Using the R language and INLA package, we quantify the risks of dengue incidence associated with the covariates of interest, by building hierarchical models, within a Bayesian framework, taking into account latent spatio-temporal patterns. Preliminary analyses show evidence of an association between dengue dynamics and drought index, precipitation, temperature, urban infrastructure, biome, Normalized Difference Vegetation Index (NDVI), deprivation and elevation. In addition, there is a residual spatio-temporal dependence, in which distinct temporal patterns and unequal distribution of dengue incidence risk are observed through the Brazilian microregions. Understanding the spatial and temporal patterns and the factors associated with dengue is important for its surveillance and control.

Audience Take Away Notes

- Understand the importance of studying the Spatio-temporal dynamics of dengue incidence in the past years, in order to inform surveillance and control measures for future scenarios
- Understand the Spatio-temporal patterns of the disease in Brazil, a continental country
- Understand the relationship between climatic and socio-environmental factors and dengue incidence in Brazil

Biography

MSc Patricia Marques Moralejo Bermudi is a PhD student at the School of Public Health at the University of Sao Paulo, Brazil (FAPESP: 2020/12371-7). Currently she is undertaking a research internship at the School of Public Health at Imperial College London, England (FAPESP: 2021/11721-7). She completed her master's and undergraduate degree in Public Health at University of Sao Paulo. She has taught two short courses and has 10 scientific articles published, two scientific articles accepted for publication and one book chapter published.

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Molecular screening for intestinal protozoan and fungal pathogens and first subtyping of *blastocystis* spp. in hemodialysis patients in Slovakia

Blastocystis spp., *Cryptosporidium spp.*, *Giardia intestinal* is and *Microsporidia* spp. are protozoan and fungal intestinal pathogens in immunocompromised individuals, causing symptomatic or asymptomatic infections, which are usually undiagnosed. Uremia in hemodialysis patients with CRI induces a state of immunosuppression. Diarrhea is also one of the most important clinical manifestations. The aim of this study was to perform molecular screening and subtyping of *Blastocystis spp.*, *Cryptosporidium parvum/hominies*, *Giardia intestinal* is and *Microsporidia* spp. in hemodialysis patients, to help assess risk factors contributing to the infection and the distribution of circulating genotypes. From 53 stool samples, zoonotic Blastocystis subtypes were identified in 13 patients (24.5%), with a dominant prevalence of ST 3 (n=9), followed by ST 1 (n=3) and ST 2 (n=1). Molecular panels for the diagnosis of *C. parvum/hominies*, *G. intestinal* is and *Microsporidia* spp. was negative.

All Blastocystis subtypes identified in patients in this study, revealing possible animal sources of infection, but due to the immunosuppression condition in these patients, contact with nursing staff and contaminated surfaces or objects while undergoing therapy may also be an important transmission route.

Acknowledgement: This study was supported by grant VEGA 1/0359/21

Audience Take Away Notes

- Molecular methods are more accurate than conventional microscopic diagnostic of protozoan and fungal infections, especially when the load of pathogens in the sample is low, revealing undiagnosed infections with moderate manifestations. It is necessary to keep in mind, that the population of immunocompromised individual's increases each year, therefore, we aim to draw attention to novel methods to be applied for diagnosing emerging opportunistic pathogens in this group of patients
- From a clinical perspective, the possible application and introduction of novel diagnostic methods for opportunistic pathogens in immunocompromised patients, especially in patients, in which diarrhea is a result of another ongoing disease or therapy and opening a path for targeted antimicrobial therapy leading to the increase of the quality of life
- Subtyping and phylogenetics reveals the distribution of individual subtypes of pathogens. Zoonotic subtypes should be the focus from both an epidemiological perspective, but also an epizootiological view and environment control

Biography

Elena Hatalova, D.V.M., Ph.D. studied at the University of Veterinary Medicine and Pharmacy in Kosice, Slovakia, where she also received her Ph.D. in 2019. She currently works at the Department of Epidemiology, Pavol Jozef Safarik University, Faculty of Medicine, in Kosice, Slovakia as a researcher. Her research is focused mainly on molecular diagnostic and typing of bacterial and viral pathogens and parasites.

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[2]Department of Chemistry, Indian Institute of Technology, Delhi, India

Inhibitory effects of limonene on *candida albicans* virulence-related traits

A major global problem is the severe toxicity of conventional antifungal medications and multidrug resistance. Investigation of new substances with outstanding therapeutic potential is necessary. In this work, the antifungal potential of limonene, a secondary metabolite present in numerous essential oils derived from citrus plant, is assessed. It was tested for antifungal susceptibility, hydrolytic enzyme secretion, morphological transition, adhesion, and biofilm formation in *in-vitro anti-Candida* research. Further testing was conducted using docking tools, followed by MD simulations employing five main antifungal targets related with pathogenicity (Als3, Bcr1, Plb1, Sap2 and Tec1). It only results in 1% RBC cell lysis at MIC of 300 µg/ml. To buccal epithelial cells, limonene drastically decreased adherence. As well as being reduced by 73% and 53%, respectively, at MIC, were the hydrolytic enzymes proteinases and phospholipases. It was observed under a microscope that limonene administration prevents morphological change in C. *albicans*. Also decreased by 91% and 87%, respectively, were adhesion and biofilm development. Stable hydrophobic contacts with all of the target proteins, with the exception of Bcr1, are confirmed by docking and MD modelling experiments. According to the current research, C. *albicans* is inhibited by limonene's main virulence factors. Limonene is an excellent candidate to be researched as an antifungal medicine due to its low toxicity, ease of availability, and great antifungal potential. To comprehend the present work's mode of action and precise target sites, molecular and in vivo research are required.

Keywords- biofilms, Candida albicans, hydrolytic enzymes, Limonene

Biography

Saiema earned a master's degree in Biochemistry from the University of Delhi. Currently working on deciphering the antifungal activity of selected natural compounds and studying their mechanistic mode of action against human fungal pathogen Candida albicans. She has employed a variety of biochemical and molecular biology techniques to find potential drug targets in Candida.

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Onchocerciasis drug development: From pre-clinicals to humans

Twenty diseases are recognized as Neglected Tropical Diseases (NTDs) by World Health Assembly resolutions, including human filarial diseases. The end of NTDs is embedded within the Sustainable Development Goals for 2030, under target 3.3. Onchocerciasis afflicts approximately 20.9 million people worldwide with>90% of those infected residing in Africa. Control programs have made tremendous efforts in the management of onchocerciasis by mass drug administration and aerial larviciding; however, disease elimination is not yet achieved. In the new WHO roadmap, it is recognized that new drugs or drug regimens that kill or permanently sterilize adult filarial worms would significantly improve elimination timelines and accelerate the achievement of the program goal of disease elimination. Drug development is, however, handicapped by high attrition rates, and many promising molecules fail in preclinical development or in subsequent toxicological, safety and efficacy testing; thus, Research and Development (R&D) costs are, in aggregate, very high. Drug discovery and development for NTDs is largely driven by unmet medical needs put forward by the global health community; the area is underfunded and since no high return on investment is possible, there is no dedicated drug development pipeline for human filariasis. Repurposing existing drugs is one approach to filling the drug development pipeline for human filariasis. The high cost and slow pace of discovery and development of new drugs has led to the repurposing of old drugs, as this is more cost-effective and allows development timelines to be shortened. However, even if a drug is marketed for a human or veterinary indication, the safety margin and dosing regimen will need to be re-evaluated to determine the risk in humans. Drug repurposing is a promising approach to enlarging the pool of active molecules in the drug development pipeline. Another consideration when providing new treatment options is the use of combinations and de novo discovery from medicinal plants. My talk will summarize recent advances in the late preclinical or early clinical stage in the search for a potent macroflaricide, including drugs against the nematode and against its endosymbiont, Wolbachia pipientis.

Audience Take Away Notes

- The different onchocerciasis animal models used to assess the efficacy of drugs
- The two arms of onchocerciasis drug research; direct (against the adult worm and microfilariae) and indirect (against the endosymbiont, Wolbachia pipientis)
- Knowledge of drugs under development which will aid in achieving elimination targets
- This talk will add more knowledge to the different drug discovery platforms that are available for researchers to use
- Provide existing knowledge for the different drug combinations that can be formulated to guide policies and decision makers
- For elimination to be achieved at a faster rate, so this will add more impetus for suitable, safe and cost-effective macroflaricides to be developed, and this is one of the top priority goals for all onchocerciasis researchers
- Yes, This can be used to train students in clinical research how drugs are being developed and guide them on preclinical platforms of this disease model

- Yes, Currently the Onchocerca adult parasite is not susceptible to any approved WHO drugs. Developing a macrofilaricide is of utmost importance to kill the adult worm and halt the parasite lifecycle which can in turn reduce elimination timelines Sure. Combining the macrofilaricides under clinical trials with the approved drug ivermectin will have a marked effect on the parasites lifecycle and aid in elimination of these infectious agents

Biography

Dr Ngwewondo Adela is a holder of a Ph.D. in Biochemistry from the University of Buea since 2019 and has keen interest in drugs and diagnostic research. The WHO/TDR Clinical Research and Development Fellowship was just the right opportunity to foster her understanding of the Drug Discovery and Development pipeline. She actively led the writing of an expert review while actively taking part in the two clinical trials on Emodepside and Flubentylosin at DNDIGeneva Switzerland. Her focus is to work towards the discovery of new therapeutic options and diagnostic biomarkers for onchocerciasis, schistosomiasis and has authored 7 publications.

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Diagnosis of suspicious skin lesions in Mpox times

Background: The appearance of skin lesions of viral nature can be a symptom of infection or reactivation of the Herpes Simplex Virus type 1 (HSV-1), Herpes Simplex Virus type 2 (HSV-2), Varicella Zoster Virus (VZV), T. *pallidum* or mpox virus infection. Given the ability of these pathogens to easily spread by contact, an accurate and fast diagnosis, such as PCR-based tests, is crucial for a successful epidemiological management. In the present study, the aim was to determine the clinical performance of three qPCR assays, as well as their usefulness for the joint characterisation of samples.

Material and methods: A total of 334 cutaneous swabs samples collected from patients with suspicion of infection attended at the Hospital Universitario Miguel Servet were analysed using the three assays under study: VIASURE *Herpes virus* 1, *Herpes virus* 2 & *Varicella Zoster Virus* Real Time PCR Detection Kit, VIASURE *Treponema pallidum* Real Time PCR Detection Kit and VIASURE *Mpox* Real Time PCR Detection Kit. Samples were collected between December 2021 and November 2022. These samples were requested through the Biobanco del Sistema de Salud de Aragón (BSSA) and the study has the authorization of the Aragón Ethics Committee (PI22/409). DNA/RNA extraction was performed using the automated extraction method magLEAD® 12gC instrument with the MagDEA Dx SV kit (Precision System Science Co.) and amplification was performed using CFX96™ Real-Time PCR Detection System (BioRad). The obtained results were compared with the reference assays RealStar® Orthopoxvirus PCR Kit 1.0 (Altona) for mpox virus detection and Allplex™ Genital ulcer assay (Seegene®) for HSV-1, HSV-2, VZV and T. *pallidum* detection.

Results: Based on the data analysis, a very good overall agreement was obtained for all the studied targets.

	Overall agreement	TP	TN	FP	FN	Sensitivity	Specificity	PPV	NPV
HSV-1	1 (0.98-1)	49	285	0	0	1 (0.92-1)	1 (0.98-1)	1 (0.92-1)	1 (0.98-1)
HSV-2	1 (0.98-1)	50	284	0	0	1 (0.92-1)	1 (0.98-1)	1 (0.92-1)	1 (0.98-1)
VZV	1 (0.98-1)	30	304	0	0	1 (0.88-1)	1 (0.98-1)	1 (0.88-1)	1 (0.98-1)
T. pallidum	1 (0.98-1)	35	299	0	0	1 (0.90-1)	1 (0.98-1)	1 (0.90-1)	1 (0.98-1)
Mpox virus	1 (0.98-1)	38	295	0	0	1 (0.90-1)	1 (0.98-1)	1 (0.90-1)	1 (0.98-1)

Conclusions: The assays under study prove to be a suitable tool for differential analysis in patients presenting skin lesions associated with suspected HSV-1, HSV-2, VZV, T. *pallidum* or mpox virus infection. Moreover, the shared thermal protocol of the assays allowed for the simultaneous detection in the sample, creating a customized panel option for the user, in contrast to the reference assays employed, which required two separated analyses, taking longer to reach the complete evaluation of the sample.

Audience Take Away Notes

- A new faster strategy for suspicious skin lesion swab diagnosis that provides a simultaneous differential analysis of HSV-1, HSV-2, VZV, T. *pallidum* or mpox virus infection
- User can create personalized panel options by combining the different assays

Biography

Sara Sentre Domingo studied a BSc in Biotechnology at the University of Zaragoza. Later on, she studied a MSc in Molecular and Cellular Biology at the University of Zaragoza, graduated in 2019, and a MSc in Bioinformatics and Biostatistics at the Universitat Oberta de Catalunya, graduated in 2022. She is currently a junior researcher at the Molecular Diagnosis department at CerTest Biotec.

Aws Sami Al-Farsi[1*], Zaid Alhinai[1], Hanan Al Khatri1, Abdul-Aziz Al Hinai[1], Fatma Ba Alawi[2], Khuloud Al Maamari[2], Laila S. Al Yazidi[3]

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The burden of human parechoviruses on children in Oman

Objectives: To study the burden, clinical and laboratory features and outcome of Human Parechoviruses (HPeVs) infection among children managed at a tertiary hospital in Oman.

Methods: This is a retrospective study of children (< 18 years of age) with molecular proven HPeV infection managed at our centre between January 2017 and December 2019. Data was collected from patients' medical records and analyzed to describe the demographic, clinical and laboratory features, management and outcome.

Results: HPeV infection was detected in 61 patients, 72% of whom were males. The median age of these patients was 9 months (IQR, 6-15 months). HPeV was detected throughout the year with no significant peaks. Forty-eight (79%) patients were hospitalized and their median hospital length of stay was 5 days (IQR, 3-8 days). A history of premature birth (16%) was the most common comorbidity seen among this group. The majority of our patients (84%) had co-infection with other viruses. Fever (41 patients; 67%) and cough (41 patients; 67%) were the most common presenting symptoms. Two-thirds of children with HPeV infection in this cohort were managed for lower respiratory tract infection and none for meningitis. Diarrheal illness was not common (8 patient, 13%). All patients had full recovery.

Conclusion: HPeVs does not show a clear seasonality in Oman. Most of the children were younger than 2 years of age and had a viral co-infection. Outcomes of HPeVs were favorable, with no mortalities, but thorough follow-up of neurological outcomes was lacking.

Audience Take Away Notes

- This is the first study of HPeVs infection among children in Oman
- This study focused on assessing the burden of HPeVs infection among children in Oman and describe their clinical and laboratory features
- This study's findings will help pediatricians understand the complete clinical picture and outcomes of this virus in Oman and the region

Biography

Mr. Aws is a final year medical student at Sultan Qaboos University.

M Paz Peris[1], Blanca Dehesa[2*], M Esperanza Teresa-Rodrigo[2*], Henar Alonso[2]

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Clinical evaluation of MPOX virus detection by real time PCR

Background: In an increasingly globalized and interconnected world, the outbreak of an infectious disease in one country can become a worrying health emergency for the whole world. A recent example is the 2022 Mpox outbreak affecting multiple areas across the world. In this context, Global health systems need to develop effective strategies to interrupt transmission as soon as possible by identifying cases, clusters, and sources of infection. The aim of this retrospective and collaborative study was to perform the external clinical validation of a ready-to-use reagent product designed by Certest Biotec for the detection of Mpox virus by QPCR.

Methods: A total of 165 samples suspected of Mpox virus were used for this analysis. The standard procedure of the Microbiology Laboratory of the Miguel Servet University Hospital was considered as reference techniques (RealStar Orthopoxvirus PCR kit 1.0, Altona Diagnostics and bidirectional sanger sequencing). The use of all data and samples was approved by the research ethics committee of Aragon (CEICA) (PI22/412; 5 Oct 2022).

Results: Accuracy tests showed good clinical validation values (Table 1): Sensitivity 1 (0.97-1); Specificity 1 (0.98-1); Positive predictive value 1 (0.93-1) and Negative predictive value 1 (0.95-1). Strength of agreement was almost perfect (K=1; P<0.001) and spearman correlation test yielded strong correlation (rs=0.78; P<0.001). All positive samples were sequenced and all generated sequences with suitable sizes were blasted for species classification confirming Mpox virus presence.

TP	TN	FP	FN	Sensitivity	Specificity	PPV	NPV	K
69	96	0	0	1 (0.97-1)	1 (0.98-1)	1 (0.93-1)	1 (0.95-1)	1

Conclusions: This retrospective study demonstrates the good clinical parameters and the strong overall agreement between the VIASURE® *Monkeypox virus* Real Time PCR detection kit (CerTest Biotec) compared to both the RealStar Orthopoxvirus PCR kit 1.0 and the Sanger sequencing results. The added value observed is the useful support to clinicians in their specific diagnosis of Mpox virus infections due to the diagnostic specificity data obtained.

Furthermore, the stabilized and ready-to-use format allows storage at room temperature, enabling a longer shelf life. This is an important advantage in laboratories where refrigerated storage space is limited. It also facilitates transport, so there is no need for special cold packaging, making it environmentally safe and reducing additional costs.

Audience Take Away Notes

- A new tool for molecular diagnosis of Mpox virus is presented in a stabilized and ready-to-use format
- The format of the test allows storage at room temperature and a longer shelf life. This is an important advantage in laboratories where refrigerated storage space is limited. It also facilitates transport, so there is no need for special cold packaging, making it environmentally safe and reducing additional costs
- The clinical performance of the test is equivalent to reference methods currently used in health systems for Mpox virus detection

Biography

Blanca Dehesa studied Biotechnology at the Zaragoza University and graduated in 2018. Then, she studied a master's degree in Biomedicine with a cancer research focus at the University of Barcelona. She joined the Clinical evaluations department of the molecular diagnostics division of CerTest Biotec, S.L. in 2020 and since then she has taken part in several clinical evaluation studies in collaboration with different hospitals and research centers.

Khalid E. Ibrahim, Abdulaziz S. Alsheikh, Salah A. Ramadan, Abdulaziz M. Alshehri, Basel N. Aljohani, Abdulaziz A. Rami, Mohsin M. Khared*, Abdulaziz A. Alzahrani

King Abdulaziz Hospital, Jeddah, Saudi Arabia

Sternal wound infection following open heart surgery: Incidence, risk factor, pathogen, and mortality

Introduction: Surgical Site Infections (SSI) are a significant cause of morbidity and mortality after surgery. Due to its high morbidity and mortality rates after open-heart surgery, Sternal Wound Infection (SWI) is one of the most important consequences to avoid and manage. *Staphylococcus* species (mainly S. aureus and coagulase-negative *staphylococci*) are the most frequently reported bacteriological pattern in SWIs cases with positive culture following open-heart surgery. Our aim in this study is to assess the incidence, risk factors, causative organisms, and mortality rates of SWIs in patients who had open-heart surgery over a 9-year period between January, 2011 to December, 2019 at King Abdulaziz University Hospital, Jeddah, Saudi Arabia.

Methods: A retrospective study was done on 634 patients who underwent open heart surgery. Data was collected including patient demographics, BMI, blood groups, history of chronic diseases such as Diabetes, COPD, and Hyperlipidemia, previous cardiac surgery, previous myocardial infarction, duration of the operation, blood transfusion during the operation, length of hospitalization, and bypass time with each type of sternal wound infection.

Results: The incidence of Superficial Sternal Wound Infections (SSWI) and Deep Sternal Wound Infections (DSWI) was 8.6% and 4.1%, respectively. Coagulase-negative staphylococcus was the most frequently isolated organism from SSWI and DSWI patients. A concomitant Diabetes Mellitus that necessitates blood transfusion was identified as one of the risk variables for SSWI in a multivariate regression study. While concomitant Diabetes, being a woman, and a lengthy hospital stay were independently linked with DSWI. Compared with the SSWI group, the 30- day mortality rate for DSWI patients was 3.8% as opposed to 3.7%. The difference in the survival was not statistically significant. Having an older, longer bypass time and postoperative problems were independent risk factors for 30-day mortality.

Conclusion: This study found an incidence of SSWI and DSWIs of 8.6% and 4.1% respectively. Multivariate regression analysis showed that risk factors for SSWI were having a comorbid diabetes mellitus, requiring blood transfusion. While DSWI independently was associated with the female gender, comorbid diabetes, and long hospitalization period. The 30-day mortality was 3.8% for DSWI patients compared with 3.7% for SSWI group. Future studies in various healthcare settings are required in order to generalize the results because this was a single center study.

Audience Take Away Notes

- The importance of surgical site infections and the associated morbidity and mortality rates
- Incidence, risk factors, and mortality rate of surgical wound infections in patients who had open-heart surgery
- It will help them recognize what are the microorganisms following open-heart surgery
- The difference between the risk factors and the incidence of superficial sternal wound infections and deep sternal wound infections after open-heart surgery

Biography

I am Mohsin Khared, a sixth-year medical student at King Abdulaziz University. I am interested in in Internal Medicine especially infectious diseases. I love going to medical conferences that are related Infectious diseases and Internal Medicine in general and present my abstracts there.

Ruta Plepyte[1], Emilija Sereikaite[1], Aurelija Petrutiene[2], Aurelija Zvirbliene[1], Milda Pleckaityte[1*]

[1]Institute of Biotechnology, Life Sciences Centre, Vilnius University, Vilnius, Lithuania

[2]Department of Bacteriology, National Public Health Surveillance Laboratory, Vilnius, Lithuania

Predicted coverage by 4CMenB and MenB-fhbp vaccine against invasive serogroup B neisseria meningitidis isolated from 2017-2019 in Lithuania

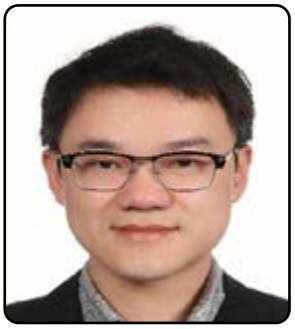
The incidence of Invasive Meningococcal Disease (IMD) in Lithuania was among the highest in Europe during the past two decades reaching an average of 2.24 cases/100,000 population. The vast majority of IMD cases were caused by serogroup B meningococcal. In 2018, the only four-Component Meningococcal B vaccine (4CMenB) was introduced to Lithuania's National Immunization program. The two- component meningococcal B vaccine (MenB-Fhbp) is registered for the vaccination of individuals 10 years and older, but the cost of the vaccine is not reimbursed. Studies on the potential coverage of Men B vaccines in Lithuania would contribute to better monitoring of vaccination impact and planning of future prophylactic strategies. We genotyped 60 serogroup B isolates collected in Lithuania between 2017-2019. The clonal complexes most frequently identified were cc32 (78.3%) and cc41/44. Vaccine relates antigens were obtained, as follows: targeted gene amplification and sequencing were provided for 37 isolates recovered in 2017, whereas whole genome sequencing was performed for 23 isolates recovered in 2018-2019. Meningococcal strain coverage by 4CMenB and MenB-Fhbp vaccine was predicted using the genetic Meningococcal Antigen Typing System (gMATS) and Meningococcal Deduced Vaccine Antigen Reactivity (MenDeVAR) Index methods, respectively. Vaccine coverage using gMATS was estimated for 58 MenB isolates (2017-2019), as PCR of vaccine antigens was not obtained for two isolates. gMATS predicted 53 (91.4%, CI 81.4-96.3%) covered isolates, 1 (1.7%) non-covered isolate, and 4 (6.9%) unpredictable isolates. Most serogroup B isolates (87.9%) were covered by a single vaccine antigen, most commonly Fhbp peptide variant 1 (84.5% of isolate), which is linked with cc32. The overall level of strain coverage by the 4MenB vaccine was 94.8% (CI 85.9-98.2%). The Fhbp peptides included in the MenB-Fhbp vaccine were not detected among the analyzed invasive isolates; however, the identified predominant variant 1 was considered cross-reactive. In total, 88.1% (CI 77.5-94.1) of isolates were predicted to be covered by the MenB-Fhbp vaccine. In conclusion, both serogroup B vaccines demonstrate the potential to protect against IMD in Lithuania.

Audience Take Away Notes

- Genetic tools to estimate meningococcal B vaccine coverage successfully replace sophisticated assays which require trained personnel and cultivable meningococcal strains
- Molecular data on vaccine coverage is currently sparse for Eastern European countries
- Estimation of potential coverage of meningococcal B vaccine is relevant to determine the right target age group for vaccination
- Other faculty could use the results of this study to expand their research or teaching to address public health interventions

Biography

Dr. Milda Pleckaityte studied Biochemistry at the Vilnius University, Lithuania and graduated as MS in 1990. She then joined the research group at the Institute of Biotechnology, Vilnius. She received her PhD degree in 2006. She was a research scientist at R&D, Sicor Biotech (member of Teva group) from 2003 to 2008. She joined the Department of Immunology at the Institute of Biotechnology, Vilnius University in 2008 and appointed senior scientist position in 2015. She has published 26 research articles in SCI (E) journals.



Jeng-How Yang[1*], Zhong-Fu Lin[1], Chun-Wen Cheng[2, 3], Po-Yen Huang[2, 3], Ting-Shu Wu[2, 3]

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Lack of association between yeastone antifungal susceptibility of *cryptococcus meningitis* cerebrospinal fluid isolates and risk factors for poor prognosis

Background: Cryptococcal Meningitis (CM) is associated with high mortality. The relation between antifungal susceptibility and treatment outcomes is not well characterized. There is paucity of surveillance data of Cerebrospinal Fluid (CSF) isolates of cryptococcus investigated with YEASTONE colorimetric broth microdilution susceptibility testing.

Methods: This was a retrospective study of laboratory-confirmed CM patients at a single-center between 2010 and 2016. Antifungal susceptibility of CSF isolates was determined by YEASTONE colorimetric broth microdilution. Clinical parameters, CSF laboratory indices, and antifungal susceptibility results were analyzed to identify risk factors for mortality.

Results: There were 53 isolates. High rates of resistance to fluconazole and flucytosine were observed in this cohort. Voriconazole showed the lowest MIC (0.06 μg/mL) and lowest rate of resistance (3.8%). There was no significant correlation between antifungal susceptibility and mortality. On univariate analysis, hematological malignancy, concurrent cryptococcemia, high Sequential Organ Failure Assessment (SOFA) score, low Glasgow Coma Scale (GCS) score, low CSF glucose level, high CSF cryptococcal antigen titer, and high serum cryptococcal antigen burden were associated with mortality. On multivariate analysis, meningitis with concurrent cryptococcemia, GCS score, and high CSF cryptococcus burden, were independent predictors of poor prognosis.

Conclusion: Concomitant cryptococcemia, low CSF glucose level, high CSF and serum cryptococcus antigen burden were risk factors for mortality. CM patients with fluconazole MIC ≥64 μg/mL showed extremely high mortality. However, both early and late mortality rates were not significantly different between CM wild type and non-wild type species.

Audience Take Away Notes

- It is an emerging critical issue about *Cryptococcus meningits*, which is a high mortality disease, happened on not only immunocompromised but also immunocompetent hosts. Second, Cryptococcus fungemia is a difficult-to-treat issue because of high morbidity and mortality
- Very few reports discussed about the using Thermo Scientific Sensititre Yeast ONE susceptibility testing to correlate with the treatment outcome of cryptococcus
- Our study revealed the *in vitro* antifungal susceptibility test did not correlate treatment outcome very well. Concomitant cryptococcemia, low CSF glucose level, high CSF and serum cryptococcus antigen burden were predictors for mortality. We think it is an important information for not only clinicians but also clinical microbiologist

Biography

Jeng-How, Yang Attending physician Division of Infectious disease, Department of Internal Medicine, Chang Gung Memorial Hospital, Taoyuan, Taiwan.

Hany Sady Shokry Redah[1,2*], David Chaima[3], Lotta Hallamaa[1], Emma Kortekangas[1], Ulla Ashorn[1], Jomo Banda[3], Charles Mangani[3], Kenneth Maleta[3], Per Ashorn[1,4] & Yue-Mei Fan[1]

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[2]Faculty of Medicine and Health Sciences, Hodeidah University, Yemen
[3]Kamuzu University of Health Sciences, Blantyre, Malawi, College of Medicine, University of Malawi
[4]Department of Paediatrics, Tampere University Hospital, Tampere, Finland

Effect of dietary intervention on the prevalence of asymptomatic malaria among 6-18-month-old children in rural Malawi

The complex interaction between malaria and undernutrition leads to increased mortality and morbidity rate among young children in malaria-endemic regions. Results from previous interventions suggest that improving nutritional status of young children may reduce the burden of malaria. This study tested a hypothesis that provision of Lipid-based Nutrient Supplements (LNS) or Corn-Soy Blend (CSB) supplementation to 6-18 -month-old children in Malawi would reduce the prevalence of asymptomatic malaria among them.

Methods: A total of 840 6-month-old children were enrolled in a randomized trial. The participants received 12-month supplementation with three different daily dietary supplementations: CSB, soy-LNS, or milk-LNS, and one control group without supplementation. The prevalence rate of asymptomatic *Plasmodium falciparum* (*P. falciparum*) was determined by real-time PCR from the participant's Dried Blood Spots (DBS) collected at the baseline and every three months after. The global null hypothesis was tested using modified Poisson regression to estimate the Prevalence Ratio (PR) between the control group and three intervention groups at all ages combined. All the models were adjusted for malaria at baseline, season of DBS sample collection, site of enrolment, and household asset Z-score.

Results: In all children combined, the prevalence of *P. falciparum* was 14.1% at enrollment, 8.7% at 9 months, 11.2% at 12 months, 13.0% at 15 months and 22.4% at 18 months of age. Among all samples that were taken after enrolment, the prevalence was 12.1% in the control group, 12.2% in the milk-LNS, 14.0% in soy-LNS, and 17.2% in the CSB group. Compared to children in the control group the prevalence ratio of positive malaria tests was 1.19 (95% CI 0.81 - 1.74; P=0.372) in the milk-LNS group, 1.32 (95% CI 0.88 - 1.96; P=0.177) in the soy-LNS group and 1.72 (95% CI 1.19 - 2.49; P=0.004) in the CSB group.

Conclusion: The sample findings do not support a hypothesis that LNS or CSB supplementation would reduce the prevalence of asymptomatic malaria among Malawian children. In contrast, there was a signal of a possible increase in malaria prevalence among children supplemented with CSB.

Keywords: Asymptomatic malaria, Children, Dietary Intervention, Malawi, Prevalence rate

Biography

Hany Sady, PhD in Molecular Parasitology from the University of Malaya (UM), Malaysia in 2016. I joined as a researcher Prof. Dr. Per Ashorn's research group at the Center for Child, Adolescent, and Maternal Health Research, Faculty of Medicine and Health Technology, Tampere University. I am an assistant professor at Hodeidah University in Yemen. I was born in Hodeidah, Yemen.During my PhD degree, I worked as a research assistant, and I managed to publish 19 research articles (Tier 1). I got a dean's award in Academic Session 2010/2011 as an appreciation certificate for my excellent achievements in the master`s academic grade in the master's degree of Health Science (Biomedical Sciences) at Universiti Kebangsaan Malaysia (UKM), Malaysia.

BOOK OF ABSTRACTS

magnus Group

21-22 JUNE

DAY 01

IN-PERSON POSTERS

4th Edition of World Congress on

INFECTIOUS DISEASES

Dong Yang[1], Yi Xue[3], Shannon Taylor[1], Elizabeth A. Ihms[2], Kathrin Weyer[4]*, Lillian Zalduondo[1], Bernd Seilheimer[4], Elizabeth Fitzpatrick[1,3], Colleen Jonsson[1,3]

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Engystol may reduce lung pathology in SARS-CoV-2 infected hamsters: A pilot study

Despite the introduction of vaccines and new anti-viral therapies, the COVID-19 pandemic, caused by Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) continues to be a serious global public health crisis. The emergence of new viral variants that escape protection from vaccines is a continuing problem throughout the world and it is imperative to develop new therapeutics to treat the disease. Immunomodulatory drugs are an effective therapeutic approach to treat COVID-19 patients and reduce morbidity and mortality. Engystol (EGY-2) is a multicomponent drug made from natural ingredients that has anti-viral properties and shows beneficial immunomodulatory activity in upper respiratory tract infections. In this pilot study, we used a low and a high dose of daily subcutaneous EGY-2 beginning 7 days prior to infection through to 3 days post-infection to measure the ability of EGY-2 in reducing disease severity in a SARS-CoV-2 hamster model. This pilot study shows that EGY-2 (1, 6 mL/kg), when given prophylactically, qualitatively reduces lung inflammation and its associated histopathology in SARS-CoV-2-infected Syrian hamsters. Interestingly, histopathological manifestations caused by progressive SARS-CoV-2 infection may predict COVID-19 severity better than individual measures such as viral load. EGY-2 appeared not to affect body weight loss, blood cell parameters or viral load. Supported by previous studies, these results suggest that EGY-2 may have immunomodulatory effects that may reduce disease severity alone or as part of a combination therapy in COVID-19 patients. Further investigations are needed.

Audience take away Notes

- Presentation will encourage researchers on immunomodulatory strategies against COVID-19
- It underlines the importance of the histopathological manifestations caused by SARS-CoV-2 infection as they may be improved, although individual measures such as body weight loss, blood cell parameters or viral load appeared not being affected
- It will introduce the multicomponent drug Engystol which consists of natural ingredients, and which may be beneficial in reducing disease severity when used alone or as part of a combination therapy in COVID-19 patients

Biography

Dr. Kathrin Weyer studied Biology at the Ruhr University Bochum in Germany and graduated as MS in 2010. She then joined the Developmental and Cellular Biology Group headed by Prof. Dr. Jens Schwamborn at the Luxembourg Centre for Systems Biomedicine (LCSB), Luxembourg and received a PhD degree from the University of Luxembourg in 2015. After three years of a postdoctoral research associate at the same institution, she joined as a preclinical project manager at Heel GmbH in Germany where she conceptualizes, initiates, plans, implements and evaluates preclinical research projects on amongst others respiratory infections in cooperation with scientific partners.

Raquel Gardini Sanches Palasio[1*], Patricia Marques Moralejo Bermudi[1], Fernando Luiz de Lima Macedo[2], Lidia Maria Reis Santana[2,3], and Francisco Chiaravalloti-Neto[1]

[1]Laboratory of Spatial Analysis in Health (LAES), Department of Epidemiology, School of Public Health, University of Sao Paulo (FSP/USP), Sao Paulo, SP, Brazil
[2]Epidemiological Surveillance Center (CVE) Prof. Alexandre Vranjac, Coordination of Disease Control, Health Department of the State of Sao Paulo, Sao Paulo, SP, Brazil
[3]Federal University of Sao Paulo (Unifesp), Sao Paulo, SP, Brazil, Lidia

Comparing climatic and socioeconomic factors inside and outside the high-risk spatial clusters of Chkiungunya and Zika in Brazil

Chikungunya and Zika diseases are caused by viruses from the families Togaviridae and Flaviviridae, respectively. These diseases are subject to climate change, as temperature and precipitation variations can affect the survival, reproduction and distribution of the virus and its vector. Chikungunya and Zika have been reported in over 115 and 92 countries, respectively. The Brazilian Ministry of Health has reported continuing transmission in Brazil, and when comparing 2022 and 2021, there was an increase in chikungunya and Zika cases of 78.9% and 42.0%, respectively. The objectives are identifying high-risk areas for these arboviruses in the 5,570 Brazilian municipalities between 2015 and 2021 and their relationship with climate and socioeconomic factors. The databases were obtained from the Brazilian Notifiable Diseases Information System. High-risk spatial clusters were identified based on scan statistics using sex and age indirectly standardized data and the Poisson probability distribution. The maximum size of the cluster population was obtained with the Gini index. We used the mean t-test to compare the temperature, precipitation, and socioeconomic variables between the inside and outside municipalities of the high-risk spatial clusters. We identified 38 (accounting for 707 municipalities) and 53 (accounting for 520) high-risk clusters for chikungunya and Zika, respectively. Zika clusters were distributed mainly in the center-west Brazilian region, and chikungunya clusters were the most spread in the northeast. The t-test showed that municipalities included in high-risk clusters for both diseases had higher maximum and minimum temperatures than those not included. This corroborates other studies that show temperature influencing Aedes distribution patterns and, consequently, the diseases incidence. The probable temperature increase in the future may indicate an increased in the occurrences of these diseases. Municipalities included in chikungunya high-risk clusters had lower proportions of households with water supply, sewage systems, and garbage collection, and worse socioeconomic level than those not included. The municipalities in high-risk spatial clusters presented lower precipitation levels for chikungunya and higher level for Zika. This contradictory result may be a consequence of a stronger relationship of chikungunya with the socioeconomic level than Zika. The lower level of precipitation in the chikungunya high-risk clusters could be related to areas with extremely dry conditions and harmful socioeconomic levels, favoring the inadequate water storage. Both conditions lower and higher precipitation levels, favor the increase of the number of artificial and/or natural breeding sites and the occurrence of arboviruses. Find Zika clusters mainly in the center-west could be related to the highest proportion of municipalities with disposal of solid waste in dumps in this region. Furthermore, this region is presenting the most significant increase in the infestation of Ae. albopictus, which is considered a secondary vector of Zika virus. In conclusion, it was possible to select areas at high-risk for arboviruses for directing and optimizing the implementation of surveillance and control measures. This is important because the vector control and medical costs associated with these diseases are high. In addition, our results indicate that climate change and socioeconomic factor had to be taken into account for disease control.

Audience Take Away Notes

- The importance of climate and socioeconomics in the distribution of arbovirus diseases
- Zika and Chkiungunya have different distributions in Brazil
- The municipalities inside the high-risk clusters for both arboviruses had higher maximum and minimum temperatures than the outside
- The municipalities inside the chikungunya high-risk clusters had worse socioeconomic levels and lower precipitation levels
- The municipalities inside the Zika high-risk clusters had higher precipitation levels and the highest proportion of municipalities with disposal of solid waste in dumps

Biography

Dr. Raquel Gardini Sanches Palasio graduated as a biologist in 2007 at University Center Foundation Santo Andre. She was a trainee in Superintendence for Endemic Disease Control at the Laboratory of Biochemistry and Molecular Biology, Brazil, in 2009-2011. She graduated as master's degree in 2013 from the State University of Campinas, Brazil. She received her Ph.D. degree in 2019 at the University of Sao Paulo. In 2022, she began postdoctoral fellowship supervised by Dr. Francisco Chiaravalloti-Neto at the Laboratory of Spatial Analysis in Health at same University.

Sheeba S Sawant*, Ayesha Rahman, Timothy Baldwin, Habib Khan
University of Wolverhampton, United Kingdom

Exploring the impact of *plectranthus amboinicus L.* extracts on antioxidant system and cell membrane integrity of *P. aeruginosa* PA01 and *S. aureus* NCTC8325

Background: Medicinal plants have drawn attention due to their antibacterial properties against several disease-causing bacteria. *Plectranthus amboinicus* has been studied to possess various biological properties that can be explored to attain new therapeutics to combat such diseases. This study investigated the effect of *Plectranthus amboinicus* leaf extracts on catalase activity, reactive oxygen species and lipid peroxidation activity, cytoplasmic membrane permeability and efflux pump mechanisms in *S. aureus* and *P. aeruginosa*.

Materials and methods: The effect of *P. amboinicus* extracts on the catalase activity of *P. aeruginosa* and *S. aureus* was screened using 30% hydrogen peroxide. The impact of extracts on the concentration of lipid peroxidation product (malondialdehyde) was spectrophotometrically determined. The total intracellular ROS concentration after exposure to the extracts was evaluated using 2′,7′-dichlorodihydrofluorescein diacetate (H2DCFDA, which is oxidized to 2′,7′-dichlorofluorescein (DCF) by ROS. The influence of extracts on the cytoplasmic membrane permeability was spectrophotometrically determined using diSC3-5 dye. Similarly, using the Rhodamine-6-G uptake assay was used to study the effect of extracts on the efflux pumps.

Results: The catalase activity in *P. aeruginosa* and *S. aureus* decreased by 60% and 20% respectively after exposure to the extracts. The generation of ROS can cause reaction with the polyunsaturated fatty acids of lipid membranes and induce lipid peroxidation. Demonstrating this phenomenon, there was an increase in ROS activity in *P. aeruginosa* and *S. aureus* after exposure to *P. amboinicus* extracts. Additionally, the concentration of lipid peroxidation product (malondialdehyde) increased by 42.38% and 42.5% in *P. aeruginosa* and *S. aureus* respectively. Both *P. aeruginosa* and *S. aureus* cells showed alteration in cytoplasmic permeability after treatment with *P. amboinicus* extracts. The extracts altered the permeability of *P. aeruginosa* by 58% and S. aureus by 83%. The efflux pump mechanisms were investigated using Rhodamine-6-uptake assay and displayed decrease in efflux by 25.5% in *P. aeruginosa* and 24.2% in *S. aureus* after treatment with extracts.

Conclusion: The combination of different techniques in association with the bacterial virulence factors offers additional value in understanding the influence of *P. amboinicus* extracts on *P. aeruginosa* and *S. aureus*

Audience Take Away Notes

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

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

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

- In addition, my research can provide new perceptions into the potential risks and benefits associated with phytochemicals and their cytotoxicity. This information could be used to inform the design of safer products, and to help designers make more updated findings about the products they use.
- *Plectranthus amboinicus* also known as Indian borage has been used since ancient times for its antimicrobial activities. Some of the advantages of working with this plant are as follows,

1. Natural antimicrobial activities: Indian borage plant is reported to consist of phytochemicals such as thymol, carvacrol, eugenol which display a variety of bioactivities and are known to inhibit a range of microbes. The broad range of activity against fungi, Gram negative and Gram-positive bacteria, makes this plant an ideal candidate for treating infections
2. Low toxicity and side-effects: Indian borage was reported to be safe and non-toxic home remedy for decades and can be an alternative to synthetic drugs which have negative side effects
3. Synergistic effects: Indian borage contains multiple bioactive compounds that could work together with existing antibiotics to provide synergistic effects, potentially increasing its antimicrobial activity

Biography

Sheeba S Sawant completed her bachelor's degree in microbiology at Mumbai University, India in 2016. She subsequently obtained her master's degree in microbiology from St. Xavier's Autonomous College, Mumbai University, India. Currently, she is pursuing her Ph.D. in Pharmaceutical Microbiology at the University of Wolverhampton, United Kingdom. She has published a review article, and a results paper.

- Evaluation of the effect of leaf development in *Plectranthus amboinicus* l. on antimicrobial activity and virulence factors of *Pseudomonas aeruginosa* PA01 and *Staphylococcus aureus* NCTC8325
- *Staphylococcus aureus* Biofilm: Morphology, Genetics, Pathogenesis and Treatment Strategies

Raquel Gardini Sanches Palasio[1*], Patricia Marques Moralejo Bermudi[1], Fernando Luiz de Lima Macedo[2], Lidia Maria Reis Santana[2,3] and Francisco Chiaravalloti-Neto1

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Chkiungunya and Zika high-risk co-occurrence clusters in Brazil: Is there a perfect overlap?

Chikungunya and Zika diseases are transmitted by the same vectors, Aedes aegypti and Ae. albopictus, and possibly the transmission is related to the same environmental and socioeconomic factors. In other words, a simultaneous space and time occurrence is expected. In addition, these arboviruses have similar signs and symptoms, making clinical and laboratory diagnosis difficult. Consequently, the simultaneous circulation of these diseases can impact the overload of assistance services. The Pan American Health Organization and the Brazilian Ministry of Health have warned of an increase in the number of chikungunya and Zika cases and death in America and Brazil above those reported in recent years, 2019-2023. This study aimed to do scan multivariate analyses and find high-risk temporal, seasonal, space, and space-time clusters for the Zika and chikungunya co-occurrence in Brazilian municipalities between 2015 and 2021. We used the municipality of residence, age group, sex, symptom onset month, and year of the Zika and chikungunya confirmed cases. We also considered the centroid coordinates and population of the municipalities, and a significance level of 5%. The purely temporal analysis revealed a high-risk co-occurrence cluster between January and May 2016. Seasonal analysis revealed a high-risk cluster between January and June, during summer and autumn. The spatial analyses identified 20 clusters, including 103 municipalities in the central-west Brazilian region, 63 in the southeast, 11 in the north, eight in the northeast, and one in the south. The space-time analysis revealed 13 high-risk clusters, including 803 municipalities in the northeast, 146 in the north, 41 in the southeast, two in the south, and, contrary to the spatial analysis, none in the central-west. Most of these clusters began between January and April, from 2015 to 2017, except one that began in November 2015 (in the northeast) and three that started in 2021 (two in the northeast and one in the south). The spatial and space-time clusters with the highest relative risk for chikungunya and Zika co-occurrence happened in Bahia state. Despite some common areas, we observed the absence of a perfect overlap between spatial and space-time clusters for Zika and chikungunya in the present study. One hypothesis for these patterns includes the degree of susceptibility of populations in different Brazilian regions. Furthermore, this may also be related to socioeconomic factors, which were more associated with chikungunya than Zika, making their spatial pattern unequal. Other studies have indicated that vector differences, virus genetic mutation, and precipitation levels may influence the distribution pattern for each disease. In conclusion, we observed a dispersion of arboviruses from northeast to central-west, first for Zika in 2016 and chikungunya in 2018; their resurgence in the northeast in 2021; and the same seasonality. Identifying the high-risk areas of co-occurrence is essential to alert the health services to avoid a system collapse

Audience Take Away Notes

- Temporal, seasonal, space, and space-time multivariate cluster analyses of the co-occurrence of Zika and chikungunya in Brazil between 2015 and 2021
- Simultaneous temporal and seasonal analyses

- Spatial clusters were not perfectly overlapping, however presented an area in common
- High-risk space-time clusters was found in the central-west region, but not in the same period
- Resurgence of Zika and chikungunya cases in the northeast Brazilian region in 2021

Biography

Dr. Raquel Gardini Sanches Palasio graduated as a biologist in 2007 at University Center Foundation Santo Andre. She was a trainee in the Superintendence for Endemic Disease Control at the Laboratory of Biochemistry and Molecular Biology, Brazil, in 2009-2011. She graduated as master's degree in 2013 from the State University of Campinas, Brazil. She received her Ph.D. degree in 2019 at the University of Sao Paulo. In 2022, she began a postdoctoral fellowship supervised by Dr. Francisco Chiaravalloti-Neto at the Laboratory of Spatial Analysis in Health in the same University.

Sheema Mir
Western University of Health Sciences, United States

Development of a syndromic molecular diagnostic assay, using barcoded magnetic bead technology for tick-borne pathogens

The infectious disease diagnostics often depends on costly serological testing with poor sensitivity, low specificity, and long turnaround time. Here In this manuscript, we demonstrate the proof of the principle for simultaneous detection of two tick-borne pathogens from a single patient sample using barcoded magnetic bead technology on the BioCode® 2500 system. Specific primer sets complementary to the conserved genes of *Anaplasma phagocytophilum* and *Borrelia Burgdorferi* were used in PCR amplification of the target, followed by the hybridization of the resulting biotinylated PCR products with specific probes tethered to the barcoded magnetic beads for simultaneous detection, using a fluorophore with high quantum yield. The assay has extremely high signal to background ratio and detects up to two copies of the target in a test reaction with high sensitivity and specificity. The assay demonstrated 100 percent positive and negative agreements on performance evaluation using patient specimens and blood samples spiked with tittered pathogens. No cross reactivity was observed with other related tick-borne pathogens and genomic DNA of human, cattle and canine origin. The assay can be upgraded to a sensitive and cost-effective multiplex diagnostic approach that can simultaneously detect all clinically important tick-borne pathogens in a single sample with a short turnaround time.

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The activity of PHMB and other guanidino contain in compounds against acanthamoeba

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

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

Audience Take Away Notes

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

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

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

Biography

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

Rege Anna Marton[1*], Csilla Sebok[1], Mate Mackei[1], Patrik Traj[1], Julia Voroshazi[1], Agnes Kemeny[2], Zsuzsanna Neogrady[1], Gabor Matis[1]

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Investigation of the immunomodulatory effects of cecropin a on a primary hepatic co- culture of chicken origin

The indiscriminate use of conventional antibiotics has contributed to the global spread of antibiotic resistance; therefore, there is an urgent demand to search for alternatives that can provide a novel antimicrobial mode of action. Finding a potential replacement is crucial for livestock farming, where animals are largely exposed to pathogens, while production efficiency, as well as animal health and well-being, have to be maintained. In this field, Antimicrobial Peptides (AMPs) have recently aroused great interest. Besides owning the ability to directly attack microbes, it has attracted increasing attention that AMPs are able to influence the host immune response, thereby being promising candidates for designing new antimicrobial agents. Despite being a thoroughly investigated molecule, only a few studies are available concerning the effects of the AMP cecropin A on cellular level in production animals, and to date, none of them were carried out on the liver. However, the liver plays a key role in maintaining local and systemic homeostasis by regulating loads of inflammatory processes. In our research, the effects of cecropin A were investigated on cell viability and inflammatory response in a chicken primary hepatocyte-non-parenchymal cell co-culture. The peptide was used alone and in combination with polyinosynic-polycytidylic acid (poly I:C, 50 μg/ml)- induced inflammation at concentrations of 1, 3.125, 6.25, 12.5 and 25 μg/ml. Cell viability was determined by colorimetric measurement of Extracellular (EC) Lactate Dehydrogenase (LDH) activity, which indicates the extent of cell membrane damage. To monitor the inflammatory state, the level of Transforming Growth Factor (TGF)-ß1 was measured by ELISA, and the concentrations of Interleukin (IL)-6, IL-10, and Interferon (IFN)-γ were assayed by Luminex method. In our study, we found that the three lowest concentrations of cecropin A did not affect extracellular LDH activity alone or in poly I: C-induced inflammation, however, the solely applied 12.5 and 25 μg/ml concentrations contributed to significantly increased membrane leakage. Based on these results, inflammatory markers continued to be examined only in treatment groups below these latter concentrations. When measuring TGF-ß1, we found that the sole dose of cecropin A at 6.25 μg/ml could decrease the level of the cytokine. In the case of IL-6, IL-10 and IFN-γ, cecropin A significantly reduced their production when applied alone at 1 μg/ml, furthermore at 1 and 6.25 μg/ml – and also at 3.125 μg/ml when assaying IL-6 – in poly I: C-induced inflammation, respectively. According to our results, the treatment of cells with cecropin A at lower concentrations did not result in a change in cell viability, suggesting its safe application. However, from a hepatic perspective, avoiding its higher concentrations might be advisable to consider. In addition, we found that the peptide might display immunomodulatory activity, as when used solely it could affect the production of TGF-ß1, IL-6, IL-10 and IFN-γ. Furthermore, it could also affect the levels of IL-6, IL-10 and IFN-γ during poly I: C-induced inflammation. Thus, our results suggest that cecropin A might be a promising molecule for the development of new antibiotic-substitutive agents; however, there is still a lot to clarify regarding its cellular effects.

Audience Take Away Notes

- The spread of antibiotic resistance contributed to the global aspiration for the reduction of the use of conventional antibiotics. Therefore, finding new agents that might serve as potential replacers for them became increasingly important, and AMPs are especially worth to investigate in this regard. Still, for the future application of AMPs, it is crucial to thoroughly investigate their cellular effects on various cell types.
- Our study provides useful results regarding the potential cytotoxic effect and role of cecropin A in inflammatory processes to consider for the subsequent design of cecropin A-based drugs
- Determining an optimal dose for a future drug candidate is of great importance, which might be also supported by our research, where different concentrations of cecropin A were tested
- In *in vitro* experiments on cell cultures, evoking inflammation is a common part of various types of research. The results of our study might provide additional useful information about poly I: C, which has been of great interest in recently developed inflammatory models
- To date, limited data are available on poultry or chicken cell cultures. However, they might provide novel and valuable information about physiological and pathological processes on cellular level that could be taken into account from a veterinary aspect

Biography

Rege Anna Marton conducted her studies at the University of Veterinary Medicine in Budapest, Hungary, and graduated as a Doctor of Veterinary Medicine in 2021. Thereafter, she joined the research group of the Division of Biochemistry, Department of Physiology and Biochemistry at the same university and started her Ph.D. fellowship in 2022.

Luis Vitor Medeiros Lustosa Barbosa[1], Vinicius de Morais Santos[1]*, Ana Laura de Sene Amancio Zara[2]

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Fatal case due to neonatal sepsis in Brazil: Exorbitant cost for society

Context: Estimating the costs of illness and making efficient management of the available health resources is fundamental in a scenario with scarce and finite resources. In Brazil, the indirect costs for early death due to neonatal sepsis are still unknown.

Objective: To analyze the trend of indirect costs of fatal cases from neonatal sepsis in Brazil.

Methods: A time series analysis of costs per fatal case due to neonatal sepsis in children aged up to 28 days was performed. The cases were notified with the ICD-10 P36 in the Mortality Information System (SIM) of the Unified Health System (SUS), in the period from 2000 to 2021. We estimated the cost of fatal cases of neonatal sepsis using the human capital approach to determine the lost income from premature death. We estimated the remaining working life expectancy at their age of death considering the minimum age of retirement of 65 years and 60 years for males and females, respectively. We calculated the years of life lost and used a standard discount rate of 3% per year. We multiplied the discounted years by Brazil Gross Domestic Product (GDP) per capita each year according to sex. GDP values were updated by national inflation until March/2023. Costs were estimated in Reais and converted to International Dollars in 2022 (1Int$=R$2,530). Secondary data were extracted from the Department of Informatics of the SUS using TabWin program, version 4.1.5, and trends were analyzed using the Prais Winsten regression method ($p<0.05$), in the Stata program, version 14.

Results: From 2000 to 2021, 71,853 fatal cases due to neonatal sepsis in children aged up to 28 days were reported, 56.3% of which were male, with a total of 854,938 years of working life lost. The total lost income was Int$13.2 billion, with an average cost of Int$183,662.9 (standard deviation ± Int$44,350.8) per fatal case. The number of deaths due neonatal sepsis decreased by 2.83% annually (95%CI -3.42- -2.23; $p<0.001$) and, consequently, the sum of years of working life lost also decreased annually (average annual incremental rate= -2.82%; 95%CI -3.41 - -2.23; $p<0.001$). Over the 22 years, the cost per early death due to sepsis remained stable (average annual incremental rate= 0.50%; 95%CI -0.30 - 1.31; $p=0.212$). With the maintenance of the total cost and the reduction in the number of deaths, the average cost increased over time, at an average annual incremental rate of 3.38% per year (95%CI 2.45 – 4.32; $p<0.001$).

Conclusion: Even with the reduction in the number of deaths due to neonatal sepsis, the costs remained the same over time. The economic burden of neonatal sepsis is substantial, considering the cumulative total indirect cost in the period, and the increasing average cost per early death. This reflects the opportunity cost implicit in the resources lost by society.

Audience Take Away Notes

- This research has as its central argument the idea that the costs arising from a disease of high morbidity and mortality, such as neonatal sepsis, goes beyond those that can be directly measured, such as those dispensed in beds, hospital supplies or medicines

- By learning about how significant the economic impact of indirect costs is resulting from early death from neonatal sepsis, the public will be able to apply this concept in other research in health economics, observing how the indirect costs of a disease or aggravation contribute to increase the impact of a morbid condition on society
- This research has as its object the evaluation of the indirect costs resulting only from early death by neonatal sepsis (ICD-10 P36). However, sepsis is a disease that also affects other age groups, so that the economic and health assessment of the impact of this disease, including other less restrictive ICDs-10, can benefit from the information exposed in this work. Research that focuses on the evaluation of indirect costs arising from early death from other diseases related to sepsis can also benefit from the results of this work, including neonatal sepsis in its evaluation
- Understanding how neonatal sepsis economically impacts society is fundamental for research in the Health Economics area to be more assertive in the elaboration of strategies aimed at mitigating this public health problem. The new information exposed by this research allows us to understand what are the indirect costs that affect the Brazilian Economy because of early death from neonatal sepsis. By providing a better understanding of the costs of the disease, this subject will allow health resource management projects to act in a more efficient and proportional way, correctly allocating the financial resources where they are most necessary
- List all other benefits
    - This research is of singular importance since it is set in Brazil, a country still in development, with serious health problems and which suffers socioeconomic impacts arising from diseases with high morbidity and mortality, such as neonatal sepsis, greater than their global peers already developed. Thus, elucidating the indirect economic burden of neonatal sepsis in Brazil allows assessing the impact that this condition has on an underdeveloped country, while at the same time opening space for future research that compares the indirect cost of this disease in developed and developing countries. Another significant benefit of this research is that its results serve as an argument for health managers of the need to invest resources in health policies that mitigate the significant morbidity and mortality of sepsis. The evaluation of the indirect costs of this disease must be understood by the amount of capital that was no longer produced by the citizen because of early death from neonatal sepsis. Thus, by becoming aware of the financial loss that these deaths bring to society, health management programs will be able to act to reduce the impact of neonatal sepsis, especially from the point of view of the economy that an early intervention can provide

Biography

Luis V. M. L. Barbosa is a sixth-year medical student, class 2017-2022, at Federal University of Goias.

Marina Nick[1*], Frederick A Partridge[2], Ruth Forman[3], Kathryn Else[3], Carole JR Bataille[4, 5], Angela J Russell[4, 5], David B Sattelle[1]

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Screening the Medicines for Malaria Venture (MMV) pandemic response box chemical library on caenorhabditis elegans identifies re-profiled candidate anthelmintic drug leads

The 3 major classes of soil transmitted helminths (whipworm, hookworm and Ascaris) affect 1.5 billion people worldwide mostly in poor countries, where they have adverse effects on child development, nutrition, and the work capacity of adults. Although there are drugs effective on Ascaris, notably the benzimidazoles, those same drugs show poor efficacy particularly against whipworm (*Trichuris trichiura*) and to a certain extent hookworm. Parasitic nematodes also infect farm livestock and companion animals. Resistance to currently deployed human and veterinary anthelmintic drugs is a growing problem. Therefore, new chemical anthelmintic lead compounds are urgently needed. One of the fastest routes to a novel therapeutic lead is to screen libraries of drugs which are either already approved for human use or have already been part of clinical trials. We have pursued this approach to anthelmintic lead discovery using an Invertebrate Automated Phenotyping Platform (INVAPP) for screening chemicals and the well-established nematode genetic model organism Caenorhabditis elegans2. The 400 compound Medicines for Malaria Pandemic Response Box library was screened with each compound tested initially at 1.0 x 10-4 M. We identified 6 compounds (MMV1593515 (vorapaxar), MMV102270 (diphyllin), MMV1581032 (ABX464), MMV1580796 (rubitecan), MMV1580505 and MMV1593531) active in both an L1-L4 growth / motility assay and in an L4 motility assay. For vorapaxar, an EC50 of 5.7 x 10-7 M was observed, a value comparable to some commercial anthelmintic.

Although not a parasite, the ease with which high-throughput screens can be pursued on the free-living nematode *C. elegans* makes this a useful approach to identify chemical leads and complement the often lower-throughput experiments on parasitic nematode models.

Audience Take Away Notes

- The global burden of soil-transmitted helminths and the urgent need for effective anthelmintic drugs
- The use of high-throughput screening of drug libraries for anthelmintic lead discovery
- The identification of six compounds, including vorapaxar, which showed activity against soil-transmitted helminths, particularly whipworm
- The potential of using the free-living nematode C. elegans as a model organism for high-throughput screening
- The audience will be able to use this knowledge to better understand the challenges in developing effective anthelmintic drugs and to consider the potential of using high-throughput screening to identify new chemical leads. This could be particularly relevant for those working in drug discovery and development, as well as researchers interested in parasitic nematodes and neglected tropical diseases

- The findings of this research could be useful for other faculty looking to expand their research or teaching in the areas of anthelmintic drug discovery, parasitic nematodes, and drug screening methods
- The identification of new compounds active against soil-transmitted helminths could provide a practical solution to a significant public health problem, particularly in low-income countries where these infections are prevalent. This could potentially simplify or make the development of anthelmintic drugs more efficient and improve the accuracy of drug discovery efforts
- Other benefits of this research include the potential to improve child development, nutrition, and work capacity in affected populations, as well as the ability to address the growing problem of anthelmintic drug resistance in both humans and livestock

Biography

Ms Marina Nick is studying in the final year of Division of Medicine PhD under supervision of Professor David B Sattelle at University College London University (UCL), London, UK. She collaborates with Professor Else and Dr Forman of Manchester University, Professor Russell and Dr Bataille of Oxford University, Dr Partridge of university of Westminster. She has published 3 papers and the abstract presented here is part of the other paper which will be published soon. She studied physiology and pharmacology at University of Westminster, London, UK before getting her Medical Genetics and Genomes MSc at Oxford Brooks University, Oxford, UK.

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Concept elicitation, cognitive debriefing and usability testing of COVID symptoms diary

Objective: COVID-19, caused by a coronavirus, SARS-CoV-2, has been the cause of the global pandemic from 2020-2022. Due to COVID-19's novelty, there exist no validated Patient Reported Outcome (PRO) tools that allow for proper evaluation of patient infection severity based on symptom reporting. The aim of this study was to elicit the symptoms profile experienced with COVID-19 using a qualitative approach and develop an initial Patient Reported COVID-19 Sign and Symptom Diary (PRO COVID-19) (electronic diary; eDiary).

Methods: Leveraging research regarding signs and symptoms of COVID-19 around the world, an electronic Patient Reported Outcome (ePRO) tool was developed and utilized among adult COVID-19 patients enrolled in a COVID-19 interventional trial in the US. Upon study exit, a subset of patients opted into an exit interview regarding use of the ePRO where three key processes were executed to support validation of the tool, 1) Concept Elicitation (CE) to encourage spontaneous responses regarding how participants characterize their symptoms of COVID-19, 2) Cognitive Debriefing (CD) using a think-aloud method to explore the relevance, clarity, and understandability of the ePRO, and 3) Usability Testing (UT) to determine ease or difficulty of use of the tool interface in its electronic format.

Results: Twenty-one patients (n=21) completed the exit interview. In the CE, the most common symptom reported was fatigue/tiredness (76%), followed by loss of sense of smell (71%), and body aches (67%). Overall, 23 symptoms were identified in CE, 12 symptoms occurred in approximately 29% to 76% of the participants, nine symptoms reported in 10% to 24% and two symptoms occurring in 5%. The CD portion of the interview found that ePRO elements were well understood. Findings supported maintaining the items as written and adding head congestion as a symptom which was frequently reported by patients, as well as loss of appetite (52% each). Twenty (20) symptoms were included in the final eDiary. For UT, 100% of patients responded favorably to the ease of use of the ePRO, with 95% patients seeing no issues during use.

Conclusions: The initial Patient Reported COVID-19 Sign and Symptom Diary (PRO COVID-19) in electronic format was demonstrated to be a valid PRO tool for clinical diagnostic and investigation use among COVID-19 patients to help clinicians assess severity of infection.

Audience Take Away note

- Introduction to a validated patient reported outcome tool for COVID-19 infection
- Report on COVID-19 symptomology and quality of life impact

Biography

CEO of SPRIM US LLC, with over 28 years of experience as a scientist in clinical technologies, clinical trials, decentralized clinical trials, digital training/innovations/integrations and clinical science consulting. Significant experience in eClinical technologies, eCOA/COA, Patient Reported Outcomes (PRO), electronic Patient Reported Outcomes (ePRO), and rater training for patients, caregivers and site raters. Author of 35 publications, 4 patents, >150 posters, >250 oral presentations, 53 webinars, 30 white papers, and 20 awards focused on clinically innovative improvements in data quality and increased sensitivity of efficacy and safety outcomes for clinical trials and healthcare.

Anderson da Silva Rego*, Luisa Filipe, Joao Apostolo, Pedro Parreira, Anabela Salgueiro-Oliveira

The Health Sciences Research Unit: Nursing, Nursing School of Coimbra, Coimbra, Portugal

Advancing infection control and pressure ulcer prevention: Developing an innovative antibacterial pajama with dual benefits

CPressure Ulcers (PUs) are characterized as localized defects in the skin or underlying soft tissue caused by shear, friction, or prolonged and unrelieved pressure on bony prominences. They present a significant global health challenge, with prevalence rates ranging from 7% to 23% in Europe and higher rates observed in the USA (9% to 29%). Prevention and treatment strategies for PUs primarily focus on managing skin lesions to prevent their progression and mitigate inflammatory processes. Complications associated with PU development, such as chronic pain and cutaneous injuries, can lead to increased inflammation and a heightened risk of mortality. PUs are prone to polymicrobial infections, as they create a favorable environment for aggressive pathogenic agents near the wound site. This infection can be caused by colonies of microorganisms, including aerobic and anaerobic bacteria, as well as fungal organisms. It can be challenging to resolve when dealing with drug-resistant organisms. Clinical manifestations of infected PUs may include symptoms such as erythema, purulent discharge, foul odour, and other adverse clinical outcomes. The composition of the cutaneous microbiome and the specific location of the PU contribute to the characteristics of the infection. A consortium was established, bringing together academia (Nursing School of Coimbra and University of Minho), International Iberian Nanotechnology Laboratory (INL), and the textile industry (Impetus), aiming to develop intelligent garments for the prevention of pressure injuries and associated infection. Thus, a garment with a suitable design for bedridden individuals with reduced mobility was enhanced by using a breathable textile that promotes thermophysiological control of the skin's microclimate and incorporating microparticles with antimicrobial properties and the potential for integrating pressure, relative humidity, and temperature sensing systems. The pajamas under development have been evaluated by different end users in the development process, having been recognized as a medical device that will be an asset in preventing the occurrence of pressure injuries and associated complications, namely infections. Thus, the application of smart clothing is expected to result in a decrease in the bacterial load, effectively mitigating the challenges associated with this clinical condition for the individuals who wear them. This innovative product will also make it possible to fill in the gaps in the health market.

Audience Take Away Notes

- With the presentation of this work, it is possible to demonstrate the importance of technological advancements in the field and their connection to the care and therapeutic areas, as well as the importance of creating multidisciplinary teams in science for the development of a product. This research can serve as a foundation for other faculty members to expand their own research or teaching activities
- Given the versatility of the developed product, it will facilitate task performance in providing care, whether it is by formal or informal caregivers. This device will not be specifically limited to healthcare units but will also be suitable for home environment. Therefore, it will be extremely useful for individuals who are bedridden and/or have reduced mobility, thanks to its adapted design for activities such as dressing/undressing, personal hygiene, and easy access to medical devices
- This research would be of utmost importance in monitoring infections associated with pressure

ulcers. According to the literature, it is known that pressure ulcers, being multifactorial, are typically associated with polymicrobial infections. Depending on the anatomical area, the establishment of research networks for mapping microbial species by anatomical regions would be crucial. Additionally, therapeutic strategies should also encompass drug-resistant species

Biography

Anderson da Silva Rego is a nurse with a strong academic background, including a bachelor's, masters and doctoral degree in Nursing. He is currently conducting postdoctoral research at the Nursing School of Coimbra in Portugal, where he is working on a project developing smart clothing to prevent pressure ulcers. He has published over 46 scientific articles, with 410 citations, and has served on evaluation committees for academic work. His research interests include public policies, adult health, non- communicable diseases, and home care. He has experience as a lecturer and volunteered as a nursing assistant in hospital units.

magnus Group

21-22 JUNE

DAY 02

IN-PERSON KEYNOTE FORUM

4th Edition of World Congress on

INFECTIOUS DISEASES

Phage therapy in clinical practice: Experience in chronic bone infections

Difficult-to-treat infections have led to a renewed interest in phage therapy as adjunct to conventional surgical and antimicrobials treatments. Chronic bone infections are biofilm-related infections difficult to eradicate; in vitro data indicate that phages are active against biofilms. Clinical phage treatment experiences with prosthetic joint infections, spinal hardware infection, trauma-related infections and craniectomy-related infection have been published with high successful clinical outcomes. We present our experience with phage therapy in three chronic bone infection cases who have failed multiple surgical interventions and prolonged antibiotic therapy. All the patients received phage products from Eliava Phage Therapy Center Tbilisi, Georgia.

Case presentations

Case 1: A 47 years old man with right tibia chronic osteomyelitis after bone fracture; a *Pseudomonas aeruginosa* isolate grew from infected bone fragments with no resistance to all anti-pseudomonas antibiotics; a long antibiotic therapy before with ev ceftazidime and after with oral ciprofloxacin was started. After several debridement interventions a tibia pseudarthrosis was resected and external fixators were applied; again *Pseudomonas aeruginosa* was isolated and a fistula persisted on the leg. After phagogram, phage treatment was applied by os and by fistula. The phage cocktail was integrated with a preparation against *Staphylococcus aureus* after isolation from fistula. After 4 weeks of phage therapy the fistula closed and after 4 years there isn't signs of infection.

Case 2: A 21 years old man with chronic right femur osteomyelitis after bone fracture by car accident. Initially it was treated with an intramedullary nail, that was removed after 1 year. After other 3 years he had a surgical curettage of right femur for *Pseudomonas aeruginosa* osteomyelitis. Despite antibiotic treatment there wasn't improvement and a new surgical curettage with complete old cement removal was done; *Staphylococcus epidermidis* was isolated in 5 specimens and fragments. He completed oral phage treatment for both microorganisms (*Pseudomonas aeruginosa* and *Staphylococcus epidermidis*) according to the phagograms, in association with targeted antibiotic therapy. After 18 months from phage and antibiotic treatment there isn't signs of infection and the patient resumed bycicle agonist activity. He suffered a stress fracture of the femor during exercise and underwent ostheosynthesis with plaque. All intraoperative swabs were negative for infections, and he fully recovered without any medical treatment.

Case 3: A 25 years old woman with chronic operculum craniectomy-related infection by *Pseudomonas aeruginosa.* At 1year old an hypothalamus-chiasma astrocytoma was removed and she was impaired

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Biography

Dr. Alfonso Recordare graduated in Bologna University in 1989. He's Specialist in General Surgery with a special interest in Hepatobiliary and Pancreatic (HPB) surgery, and liver transplantation. In 2015 he was the Chief of the HPB and transplant Unit in Batumi, Georgia, to start the Liver transplant program in the country. From that time he started a close cooperation with The Eliava Phage Therapy Institute in Tbilisi, and is involved in the clinical applications

with panhypopituityrasm, bilateral blindness and left hemiparesis. Soon after the bone operculum was removed for *Pseudomonas aeruginosa* infection; despite prolonged antibiotic therapy and numerous curettage interventions (almost 20 until now) the craniectomy-related infection persisted. She had a ceramic operculum with a persistent fistula when a targeted phage treatment for *Pseudomonas aeruginosa* was started by topical way (through the fistula) and os. After 4 weeks the fistula was dry and after 1 year there isn't signs of infection; in addition she is employed as a secretary.

Audience Take Away Notes

- Chronic bone infections are difficult-to-treat infections because are biofilm-related infections and antibiotic therapy alone my be not enough to cure
- Phage therapy may be a reliable therapeutic option for these difficult-to-treat infections
- It's necessary to increase the research on phage therapy and to know where to place phage therapy on the treatment management of infections until now phage therapy is possible only as compassionate use or off-label indications

of Bacteriophages in Italy. He's actually Director of the Oncological and Emergency Surgery Division at Dell'angelo Hospital in Venice Mestre. He has published more than 100 articles in SCI (E) journals.

BOOK OF ABSTRACTS

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21-22 JUNE

DAY 02

IN-PERSON SPEAKERS

4th Edition of World Congress on

INFECTIOUS DISEASES

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The impact of immunocompromise on outcomes of COVID-19 in children and young people

Background: Despite Children and Young People (CYP) having a low risk for severe COVID-19 outcomes, there is still a degree of uncertainty related to their risk in the context of immunodeficiency or immunosuppression, primarily due to significant reporting bias in most studies, as CYP characteristically experience milder or asymptomatic COVID-19 infection and the severe outcomes tend to be overestimated.

Methods: A comprehensive systematic review to identify globally relevant studies in immunosuppressed CYP and CYP in general population (defined as younger than 25 years of age) up to 31st October 2021 (to exclude vaccinated populations), was performed. Studies were included if they reported the two primary outcomes of our study, admission to Intensive Therapy Unit (ITU) and mortality, while data on other outcomes, such as hospitalization and need for mechanical ventilation were also collected. A meta-analysis estimated the pooled proportion for each severe COVID-19 outcome, using the inverse variance method. Random effects models were used to account for interstudy heterogeneity.

Findings: The systematic review identified 30 eligible studies for each of the two populations investigated: immunosuppressed CYP (n=793) and CYP in general population (n=102,022). Our meta-analysis found higher estimated prevalence for hospitalization (46% vs. 16%), ITU admission (12% vs. 2%), mechanical ventilation (8% vs. 1%) and increased mortality due to severe COVID-19 infection (6.5% vs. 0.2%) in immunocompromised CYP compared to CYP in general population. This shows an overall trend for more severe outcomes of COVID-19 infection in immunocompromised CYP, similar to adult studies.

Interpretation: This is the only up to date meta-analysis in immunocompromised CYP with high global relevance, which excluded reports from hospitalized cohorts alone and included 35% studies from low- and medium-income countries. Future research is required to characterise individual subgroups of immunocompromised patients, as well as impact of vaccination on severe COVID-19 outcomes.

Audience Take Away Notes

- This presentation will demonstrate to clinicians and policy makers that, similarly to in adults, immunocompromise increases the risk of severe COVID-19 infection in children and young people, which may support strategies for patient education, COVID-19 vaccination and treatment in this population
- This presentation will be beneficial to researchers with an interest in respiratory viruses as it will describe the first meta-analysis investigating the impact of immunosuppression in COVID-19 infection in cohorts of non-hospitalized children, which may direct future research in investigating other respiratory viruses or investigating the risk of severe COVID-19 infection in sub-groups of immunosuppressed children
- This presentation will be relevant to the entire audience as the study population of over 100,000 patients was diverse and multinational, with over 1/3 from low-and-middle-income countries

Biography

James Greenan-Barrett studied medicine at the University of Cambridge and University College London, graduating with distinction in his medical degree and intercalating in a bachelor's degree in virology, microbiology and parasitology. During his undergraduate studies he joined the research group of Dr Coziana Ciurtin at the Centre for Adolescent Rheumatology Versus Arthritis at UCL where he carried out research with a focus on the role of immunosuppression on COVID-19. He carried out Internal Medical Training at University College London Hospital where he obtained his MRCP (Membership of the Royal College of Physician) qualification.

Andrzej Zaleski[1], Ernest Kuchar[2], Mariusz Panczyk[3], Malgorzata Kloc[4, 5, 6], Robert Zdanowski[7], Jacek Z. Kubiak[7, 8*]

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Higher proportion of SARS-CoV-2-positive children vs. adults detected as early as four mounts after the outbreak of 2020 COVID-19 pandemic in Warsaw, Poland

Early during 2020 COVID-19 pandemics the proportion of children vs. adults positive for SARS-CoV-2 in a RT-PCR test was shown to be lower in different countries. This suggested that children are more resistant to the novel infection than adults. Here we show that in Warsaw, Poland this proportion was also lower during the first three months of the COVID-19 pandemics (March-May 2020) and was as follows: 3.26% (15/459) positive cases among the symptomatic pediatric patients, 5.58% (99/1774) among the symptomatic adults, none in the asymptomatic children (0/445), and 0.83% (2/239) in the asymptomatic adults. However, already in June 2020, i.e. four months after the first case of COVID-19 was reported in this country, more symptomatic children were tested positive (28.44%) for SARS-CoV-2 than symptomatic adults (16.39%). This proportion returned to the advantage of adults (14.41%) vs. children (5.35%) in July 2020, and was inverted again in August and remained so during September 2020: children – 28.01% and 32.77% vs. adults – 21.33% and 27.15% respectively for August and September, respectively. These proportions, when calculated cumulatively for the four mounts period (June-September 2020) were as follows: children 26, 17% vs. adults 20, 24%. These data show important fluctuations in proportions of symptomatic SARS-CoV-2-positive children to adults at the beginning of the pandemics in Warsaw, Poland. It suggests that the initial lower proportion of contaminated/infected children vs. adults could be rather due to the restrictions introduced very soon after pandemics declaration in Poland, and possibly due to the hyper-protection of children by their parents at the very beginning of this period and not because of their higher resistance to the infection.

Audience Take Away Notes

- We present here historical data concerning the beginning of the COVID-19 pandemics
- We show that the tendency of lower SARS-CoV-2 infection in children vs. adults observed in many countries was characteristic only to the very early stages of pandemics, and then fluctuated to invert the proportions
- These data show that the initial observations concerning unknown disease may rapidly change during the evolution of the pandemics
- It can provide a practical solution in case of future pandemics of a similar nature

Biography

Dr. Kubiak studied Biology at the Warsaw University, Poland and graduated as MS in 1983. He then joined the research group of Prof. Andrzej K. Tarkowski at the Institute of Zoology, Dept. Biology, Warsaw University. He received his PhD degree in 1988 at the same institution. After three years postdoctoral fellowship supervised by Dr Bernard Maro at the Institute Jacques Monod, Paris, France he obtained the position at the CNRS in France. He is now in the CNRS, France and in WIM-PIB in Poland. He has published more than 140 research articles in SCI (E) journals.

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Characteristics of healthcare workers infected with COVID-19: A retrospective descriptive study in a university hospital, Jeddah, Saudi Arabia

Introduction: Coronavirus disease 2019 (COVID-19) has become the most devastating public health issue in the entire world. The disease has been spreading internationally and has swept the world in a short period. It stated as a pandemic by the World Health Organization on March 11, 2020. Healthcare Workers (HCW's) are considered a high-risk group for getting infected by COVID-19. There were not sufficient studies in the Kingdom of Saudi Arabia on this title. Furthermore, studies did not focus on the healthcare workers. Our aim in this study is to determine the prevalence of COVID-19 infection and the high-risk group among HCW's at King Abdulaziz University Hospital, Jeddah, Saudi Arabia.

Methods: This is a single-centre retrospective record review of HCW's from 2020-2021. 746 of healthcare workers who infected with COVID-19 and tested positive at King Abdulaziz University Hospital were included in our study. All other healthcare workers who work at King Abdulaziz University Hospital who tested positive outside the hospital laboratory were excluded. Characteristics of the healthcare workers, presenting symptoms, and the source of infection were compared with different job titles.

Results: There were 503 out of 746 who females are while 243 out of 746 were males. Most of them were between 26-35 years old. 53.6% among healthcare workers were nurses while 17.2% only were physicians. Around 16% have a history of Diabetes and Hypertension. 99.5% had a complete recovery while 0.5% died. 86.7% of them were treated in an outpatient setting whereas 15% had a hospital stay that ranged from 1-5 days, 6-10 days, and > 10 days. The most common presenting symptom was fever, cough, and sore throat.

Conclusion: COVID-19 had huge impact in our healthcare system due to large numbers of infected healthcare workers at our hospital. Nurses are the most vulnerable group due to close contact with COVID-19 patients. Most of the healthcare workers had a complete recovery.

Audience Take Away Notes

- Healthcare workers are thought to be high-risk population for acquiring COVID-19 infection
- The COVID-19 emergence has had a profound effect on healthcare system
- We sought to investigate the COVID-19 infections among healthcare workers and their effects on the healthcare system
- Learn from our experience on how we dealt with the outbreaks of COVID-19

Biography

My name is Saleh Binmahfooz, a sixth-year medical student at King Abdulaziz University. I am interested in Internal Medicine and I have worked on many research activities in that field. My future plan is to pursue my residency program in Canada and to do a fellowship in Adult Congenital Heart Disease.

Mónika Madai[1*], F. Foldes[1], A. Kuczmog[1, 2], Zs. Lanszki[1, 2], H. Papp[1, 2], B. Zana[1], B.A. Somogyi[1, 2], F. Jakab[1, 2], X. Jia[3], O. Farago-Sipos[4], V. Palya[4], Cs. Nemes[4], P. Bajnoczi[4]

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Specific IgY antibodies protect Syrian hamsters against SARS-CoV-2 infection

The COVID-19 pandemic has led to an increased interest in the study of IgY (Immunoglobulin Y) as a potential inhibitor of SARS-CoV-2, the causative agent of COVID-19. IgY is a type of antibody found in birds, and reptiles, and it is similar in structure and function to the mammalian Immunoglobulin G (IgG) antibody. Therefore IgY would be a possible passive immunotherapeutic against SARS-CoV-2. In this study specific IgY antibodies were produced against the SARS-CoV-2 virus by vaccination of SPF laying hens. Babcock SPF laying hens were injected with a vaccine containing 10 µg SARS-CoV-2 S antigen mixed with water-in-oil type adjuvant. The first vaccination of the hens was accomplished at 18 weeks of age, then it was repeated three times. Subsequently an HCl-NH_3SO_4 precipitation technique was used to extract the IgY from egg yolk, and the purity was examined by SDS-PAGE. The SARS-CoV-2 inhibitory activity was tested using a virus neutralization assay. Syrian hamsters are considered a good model for studying SARS-CoV-2 as they are susceptible to the virus infection and develop symptoms that are similar to those seen in humans. Syrian hamsters received IgY or PBS (control) one hour before the virus infection, then every 8 hours in the first three days. Then from the fourth to the fifth day treatment was done twice a day. Oropharyngeal sampling was done every day once. Viral replication was analyzed with droplet-digital PCR. The majority of the samples in the IgY-treated group proved to be negative for SARS-CoV-2, while in the control group strong viral replication were measured. Furthermore, the control group developed severe pneumonia than the IgY-treated group. However, the virus was detected in some lung samples of the IgY-treated groups as well. Overall, our results indicate the potential use of IgY as a treatment for SARS-CoV-2, but further studies are needed to fully understand and confirm its efficacy.

Audience Take Away Notes

- Possible information on the protective effect of IgY against SARS 2 infection
- What is IgY antibodies (special knowledge)
- The audience could use the information for teaching or researching
- Pharmaceutical/industrial usability?

Biography

Dr. Monika Madai studied Biology at University of Pecs, Hungary and graduated as MS in 2010. She joined the Virology Research group of Prof. Ferenc Jakab at Szentagothai Research Centre, University of Pecs. She received her PhD degree in 2022. Until now she is a postdoctoral researcher at National Laboratory of Virology, University of Pecs, Hungary. She has published more than 20 research articles in SCI (E) journals.

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Level of vaccination against COVID-19 and post vaccination breakthrough infection among a cohort of healthcare workers in a tertiary teaching hospital in Ethiopia

Background: Coronavirus disease 19 (COVID-19) pandemic has posed a challenge to the health sector, and frontline Healthcare Workers (HCWs) are at higher risk of getting the infection. However, there is a scarcity of data on vaccination and post-vaccine breakthrough infections in Ethiopian HCWs. This study aimed at assessing vaccination levels, breakthrough infections, and associated factors among HCWs at a tertiary teaching hospital in Ethiopia.

Methods: A prospective observational cohort study was conducted among 469 HCWs at St. Paul's Hospital Millennium Medical College from February to July 2022. We used a standard questionnaire for enrollment, sociodemographic and clinical data collection, and biweekly follow-up using the Secure Data Kit, as well as real-time reverse transcription polymerase chain reaction for the COVID-19 test. SPSS v. 25.0 was used for data analysis, chi-square test to determine the association between vaccination and breakthrough infections, and bivariable and multivariable analyses to assess factors associated with vaccine uptake. A p-value of <0.05 was considered statistically significant.

Results: A total of 469 HCWs were enrolled, with a response rate of 98%. The majority of the participants were females (58.4%), and the mean age was 29.2 ± 6.5 years. Physicians have the highest proportion of ever COVID-19-testing status (86.6%), followed by midwives (74.9%), and nurses (71.9%), with patient transporters having the lowest (34.5%). Overall, 64.4% of HCWs were vaccinated against COVID-19, of whom 85.1% were fully vaccinated. Physicians (AOR = 7.94; 95% CI: 3.27–19.26) and having ever been tested for COVID-19 (AOR = 2.34; 95% CI: 1.46-3.75) were determinant factors for vaccine uptake. SARS-CoV-2 infection occurred in 34 (11.3%) of 302 vaccinated HCWs post vaccination, with 32 infections in fully vaccinated HCWs, implying a 10.6% incidence of breakthrough infection. There was no significant difference in the risk of infection between vaccinated and unvaccinated HCWs (p = 0.969).

Conclusion: COVID-19 vaccine uptake among HCWs was low and showed a significant occupational difference, with physicians having the highest level of vaccination. The high incidence of breakthrough infection in the study underscores the benefit of vaccination to reduce but not eliminate transmission.

Audience Take Away Notes

- COVID-19 pandemic is a global health challenge and frontline healthcare workers are at higher risk of getting the infection
- Vaccine uptake among HCWs has a significant occupational difference and implies a need of raising awareness
- Vaccine breakthrough infection is a common phenomenon but with mild and asymptomatic outcomes

Biography

Dr. Gadissa studied microbiology at Addis Ababa University, Ethiopia, and graduated as an MSc in 2007. He then joined the University of Gondar, Ethiopia, as a lecturer. Further, he received his MSc in infection and immunity in 2014 and his PhD in virology in 2018 from Erasmus University Rotterdam, the Netherlands. After a one-year postdoctoral fellowship at the same institution, he obtained the position of Assistant Professor of Molecular Virology at St. Paul's Hospital Millennium Medical College, Ethiopia.

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Co-infection of severe leptospirosis and Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) with multiple organ involvement in Indonesia

Leptospirosis co-infection and the pathogenesis of SARS-CoV-2 (Severe Acute Respiratory Syndrome Coronavirus 2) play a significant part in the emergence and progression of SARS-CoV-2 infection by enhancing the difficulty of identification, management, and outcome of COVID-19 well as worsening disease severity and death. We presented a 53-year-old man with severe Leptospirosis and diagnosed with severe SARS COV-2 Delta variant during the pandemic. He was admitted to the Hospital with moderate ARDS (Acute Respiratory Distress Syndrome), hypovolemic shock, bleeding manifestation, thrombocytopenia, multiple organ involvement such as acute kidney injury and liver failure. The Covid-19 antigen rapid test and Rapid Lateral Flow were negative in the first treatment day. Reverse-Transcription Polymerase Chain Reaction (RTPCR) finally was used to establish COVID-19, and Microscopic Agglutination Test (MAT) was carried out and repeated with interval 7 days to confirm the diagnosis of Leptospirosis. The patient was treated with functional, supportive care for COVID-19 such as Plasma Convalescent and antibiotic therapy for leptospirosis. The patient was given medication and guidance for 15 days before being discharged from the hospital with clinical and laboratory improvements. To highlight the importance of microbial co-infection in COVID-19, we outline the co-infection of bacteria with SARS-CoV-2, their effects on COVID-19, the grounds for co- infection, and their identification. Leptospirosis is one of the diagnoses that should be considered in especially developing countries in patients presenting with findings that may be confused with COVID-19 during the pandemic period.

Keywords: COVID-19, Co-infection, Leptospirosis, SARS-CoV-2 Delta Variant

Audience Take Away Notes

- To highlight the importance of microbial co-infection in COVID-19 during pandemic in the tropic area
- This case report will help the medical doctor especially in the developing countries to consider that there might be co-infection of bacteria such as Leptospirosis with SARS-CoV-2. Their co-infection can cause one of them to be misdiagnosed; medical doctors in tropical areas should be knowledgeable of the commonalities between these two diseases, particularly the early diagnostic presentation and pathogenesis. It is also necessary to highlight how critical it is to distinguish between these two disorders during the condition's early stages
- This case report will help the audience to improve their knowledge in management co-infection of Leptospirosis and COVID-19 with multiple organ involvement

Biography

Elfian Rachmawati studied in Faculty of Medicine Diponegoro University and graduated as MD in 2014. After one year of Internship in remote area, she then studied in Department of Internal Medicine at the same institution and graduated in 2022. She has published 1 research articles and 2 case reports.

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Barriers to antiretroviral medication adherence in People Living with HIV (PLHIV) at the time of COVID-19 pandemic in the Philippines

Background: Adherence to antiretroviral therapy (ART) reduces morbidity and mortality among People Living with HIV (PLHIV) by suppression of viral replication, restoration and preservation of immune function. However, poor adherence with ART may lead to treatment failure and death. PLHIV have a high probability of experiencing treatment interruptions due to lockdowns related to social distancing COVID-19 protocol. Moreover, mortality rate among the COVID-19 patients with HIV infection is higher than those COVID-19 patients without HIV infection.

Objectives: To determine the barriers to antiretroviral medication adherence in PLHIV at the time of COVID-19 pandemic in the Philippines and determine any significant association between the identified HIV treatment barriers and socio-demographic characteristics.

Methods: A cross-sectional study using online survey questionnaire was distributed via social media. Sample size was computed using Open Epi software. Data was analyzed using Stata software. Categorical variables were summarized using frequencies and percentages, quantitative data was summarized using mean and standard deviation. Chi-square test or Fisher's exact test, whichever is more appropriate, was used to determine association between socio-demographic characteristics and HIV treatment barriers.

Results: There is a total of 116 respondents, 115 were males, homosexual (59.5%), with mean age of 30.25 years old (SD = 6.22) and majority (53.4%) were from NCR. The most common HIV treatment barriers reported by people living with HIV in accessing treatment and care were unavailability of transportation and cost of courier services for ARV delivery (62.1%), location of treatment hubs (52.6%) and financial assistance (37.9%).

Conclusion: As the country continues to contain and delay the spread of COVID-19 virus, healthcare systems may miss out on patients with chronic diseases whose management may be worsened by this pandemic. There is significant association between the following treatment barriers and sociodemographic characteristics: location of treatment hubs and respondents who finished college/graduate studies; checkpoints and crossing borders and: 1. respondents from Northern Luzon Region, 2. unemployed respondents; financial assistance and: 1. Respondents 18 to 25 years old, 2. Unemployed respondents, 3. Respondents who finished elementary/high school; psychosocial support and: 1. Respondents from NCR, 2. Respondents 26 to 30 years old; stocks of ARVs and other medicines and employed respondents.

Audience Take Away Notes

- Medication adherence and medical related problems have arisen due to restrictions put in place to reduce the spread of COVID-19, along with the fear of exposure to COVID-19. Understanding the consequences of the COVID-19 pandemic in people with HIV is crucial to improve health care, provide safer accessibility to outpatient medical services and resources for this population during this and future pandemics

- It is important to recognize that all pandemics have biological, psychological, and social implications of which health care professionals play a crucial role. Acknowledging these implications give a deeper understanding and provide better approach to people living with HIV
- This research can be used as a guide in conducting investigation involving medication adherence of a different population (eg. Chronic Kidney Disease Patients on Hemodialysis)

Biography

Dr. Joves studied Biology at University of Santo Tomas in 2011 and earned his Doctor of Medicine degree at De La Salle Health Sciences Institute in 2015, Philippines. He finished his residency training in Internal Medicine at Adventist Medical Center Manila where he was supervised by Dr Matulac and Dr Pagcatipunan.

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Are your nasopharyngeal swabs stored in good condition

Background: Every year, Influenza A (FluA), Influenza B (FluB) and Respiratory Syncytial Virus (RSV) affect our communities and increase the number of patients in our health systems. Symptoms are similar to those of SARS-CoV-2, so diagnosis is essential to initiate an appropriate treatment and surveillance. Also, epidemiological studies can help to understand the progress of the infection. To achieve this, molecular techniques, such as real-time PCR, have become essential. High amounts of samples or retrospective studies may need the use of samples stored at different conditions and inadequate storage conditions may have a negative impact. This work provides information about the stability of Nasopharyngeal Swabs (NP) in Viral Transport Medium (VTM) for FluA, FluB and RSV stored at different conditions.

Methods: Twenty-eight negative FluA, FluB and RSV NP samples in VTM (Vircell, Spain) were used in this study. All samples were mixed into one pool and divided into 7 aliquots. One of them served as a negative control. The others were enriched (each) with different concentrations of viral cultures from ATCC (Table 1) to obtain two positive samples for each pathogen.

Table 1. Positive samples and virus concentration used in the study

Target virus	ATCC culture	Copies/µL
Influenza A (FluA)	VR-95PQ™ A/Puerto Rico/8/34	Low Positive: 1.25 Positive: 5
Influenza B (FluB)	VR1804PQ™ B/Florida/4/2006	Low Positive: 6 Positive: 20
Human Respiratory Syncytial Virus (RSV)	VR26PQ™	Low Positive: 3 Positive: 10

Samples were stored under specific conditions of time and temperature (Table 2) before being processed.

Table 2. Time and temperature conditions used for storage conditions

Temperature	Time
25°C	1 day
	2 days
4°C	3 days
	6 days
-20°C	8 days
	30 days
	6 months

Each condition was extracted in triplicate with the MagDEA Dx SV kit, using the magLEAD® 12gC instrument (Precision System Science Co.) and analysed with VIASURE SARS-CoV-2, Flu & RSV Real Time PCR Detection Kit (Certest Biotec S.L) in triplicate on CFX96™ Real-Time PCR Detection System (Bio-Rad). The results were compared with the data obtained on the first day (0 hours).

Results: All positive samples were detected in all conditions and matrices. No amplifications were observed in negative samples. There were no major differences compared with the data obtained on the first day. However, a Cq delay of around 1 unit was observed in all pathogens when samples were stored 2 days at 25ºC. For this reason, this storage condition would not be recommended.

Conclusions: Positive FluA, FluB and RSV nasopharyngeal swabs collected in VTM can be stored at 25°C for up to 1 day, 4°C for up to 6 days, or frozen at -20°C for up to 6 months, without impacting on their detection by real-time PCR. Samples stored at 25ºC for longer than one day could get degraded.

Audience Take Away Notes

- Audience will know about the impact of different storage conditions for nasopharyngeal swabs to detect respiratory virus such us Influenza, RSV and SARS-CoV-2
- Biological samples storage should be a matter of concern. Inadequate storage conditions can impact on the results of later analysis
- This study can help the audience to improve their storage conditions for biological samples. This can help to optimize the storage space, allowing to adopt a systematic work routine according to the laboratory needs
- Samples stored in good conditions will provide more reliable results in later analysis

Biography

Esperanza studied Biochemistry at the Faculty of Science from University of Zaragoza, Spain. She graduated as MS in 2009 and as MS master in 2010. Then she joined the Functional Genetics and Functional Genomics group at the Faculty of Medicine from University of Zaragoza, Spain, where she received the PhD degree in 2015. During her PhD, she performed internships at the International University of Catalunya (Spain), and the University of Lübeck (Germany). In 2017, she received a postdoctoral fellowship at Certest Biotec, where she has been working to the present day.

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Characterisation of the proteomic response of *Candida parapsilosis* to the silver (I) compound SBC3

The antimicrobial activity of silver has long been established and is widely used clinically. The low toxicity and broad-spectrum activity of silver make it a promising candidate in the fight against resistant pathogens. N-heterocyclic carbenes (NHCs) constitute a versatile range of organic compounds that readily bind transition metals. The NHC silver (I) acetate complex SBC3, derived from 1,3-dibenzyl-4,5-diphenylimidazol-2-ylidene (NHC*) has previously demonstrated antibacterial and antifungal properties however, the mode(s) of action of SBC3 remain unclear. To this end, quantitative label free proteomics was employed to assess protein abundance changes in the pathogenic yeast *Candida parapsilosis*. Exposure of the yeast to SBC3 induced an increase in proteins associated with cellular stress and detoxification (encoded by Candida Drug Resistance 1 (CDR1) gene; thioredoxin domain-containing protein) and decreased abundances in protein synthesis proteins (ribosomal protein L37), respiration (NADH dehydrogenase [ubiquinone] flavoprotein 1) and cell adhesion (Candida_ALS_N domain-containing protein).

The success of *C. parapsilosis* infection is largely attributed to biofilm formation. The identification of adherence and biofilm-associated proteins within the proteomics data guided subsequent studies revealing that pre-treatment of *C. parapsilosis* with SBC3 reduced the cell's capacity to bind epithelial cells by approximately 90% and reduced biofilm formation on an abiotic surface by 76%. This may be explained by the altered morphology and reduced presence of extracellular matrix in SBC3-treated *C. parapsilosis* visualized by scanning electron microscopy.

Audience Take Away Notes

- *C. parapsilosis* is an opportunistic pathogen that has rapidly emerged in the past two decades. Prolific biofilm production and the development of antifungal drug resistance have hindered treatment of infection. Thus, it is imperative to develop novel and/or repurposed therapies
- This work sheds light on promising novel silver therapeutic that has demonstrated broad-spectrum activity against bacterial and fungal pathogens. Quantitative label-free proteomics is a novel approach to better understand the antimicrobial mode(s) of action of SBC3
- Proteomics is a power tool that offers insight into drug efficacy and protein-drug interactions which can guide/compliment further phenotypic studies. Gel-free mass spectrometry techniques (coupled with liquid chromatography and analytical software tools) offer high-throughput analysis of entire microbial proteomes with enhanced sensitivity and reduced Labour and costs, often replacing dated and constrained gel-based methods
- Presentation of this work shares proteomic expertise with regards to methodology and data analysis and novel strategies to combat antimicrobial drug resistance. It is also an opportunity to meet experts in similar fields to gain invaluable knowledge and enhance future studies

Biography

Magdalena Piatek studied Biological and Biomedical Sciences in Maynooth University, graduating with a BSc in 2019. She worked with Prof. Kevin Kavanagh in the Medical Mycology Laboratory as part of her undergraduate research project: 'Analysis of the effects of Aspergillus fumigatus supernatant on the growth of Pseudomonas aeruginosa'. Her PhD on the 'Evaluation of novel antimicrobial agents for use in treating drug resistant bacterial and fungal pathogens' commenced in 2019. She has conducted numerous collaborations with Chemistry research groups in various institutions analyzing novel antimicrobials, with a focus on metal-based drugs. She has presented at several microbiology and inorganic chemistry conferences and has eight publications to date.

Klemen Bohinc
Faculty of Health Sciences, University of Ljubljana, Ljubljana, Slovenia

Microbial adhesion capacity on orthopedic implants

The application of orthopedic implants in our body is associated with the possibility of infection. To have the infections under control interactions between microorganisms and implant surfaces needs to be understood. Therefore, in this presentation we consider the microbial adhesion capacity of S. *aureus* on the implant surfaces modified by coatings. The surfaces are characterized by roughness, hydrophobicity, morphology, texture and electric potential measurements. Finally, the influence of different implant surface coatings on bacterial adhesion extent will be discussed.

Biography

Klemen Bohinc Assoc. Prof., graduated in the field of Physics at the Faculty of Natural Sciences, University of Ljubljana. In 2001 he received his Ph.D. in Electrical Engineering from the Faculty of Electrical Engineering, University of Ljubljana and in 2012 Ph.D. in Physics from the Faculty of Natural sciences and Mathematics, University of Maribor. Currently he teaches Biomechanics and Biophysics at the Faculty of Health Sciences, University of Ljubljana. His research interests are electrostatics and statistical physics of biological macromolecules/membranes, characterization of nanoparticles as well as microbial adhesion to material surfaces.

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To develop an overall diagnosis and treatment strategy to the epidemic situation of infectious diseases and establish an innovative medical model for precise diagnosis and treatment of cytokine storm

In recent years, the frequent outbreaks of infectious diseases such as SARS and COVID-19 infection have seriously threatened human life and health and socio-economic development. Since there is no specific medicine for virus infection in medicine so far, the medical community and governments of all countries face major challenges in scientific response to the epidemic decision-making. It is urgent to develop a set of overall diagnosis and treatment strategies for scientific response to the epidemic situation of infectious diseases and create an innovative medical model for accurate diagnosis and treatment of cytokine storm. Because infectious diseases damage the human body through cytokine storm, but because of the extreme complexity of the cytokine network, the current modern medicine cannot identify and grasp the characteristics of cytokine storm in different diseases and/or different patients, and cannot achieve precision diagnosis and treatment, making the current cytokine therapy with great blindness, unable to achieve the desired effect. The author has independently studied comparative medicine of Chinese and Western medicine for 28 years, revealing the scientific essence of traditional Chinese medicine and the scientific principles of traditional Chinese medicine treatment using modern medical theory. And we have integrated traditional Chinese medicine and modern medicine to establish a new medical theory of integrating traditional Chinese and Western medicine. Based on this, we have cracked the abnormal changes and overall patterns of cytokine networks (cytokine storm) in the process of human diseases. According to the new medical theory established by the author, the article has formulated a set of overall diagnosis and treatment strategies for scientific response to the epidemic situation of infectious diseases that can be understood and applied in modern medicine and have clear medical diagnosis and treatment principles, and has established a precise diagnosis and treatment model of infectious diseases that judge and recognize the characteristics of cytokine storm based on clinical manifestations, which can accurately diagnose and treat the characteristics of cytokine storm of infectious diseases and improve the efficacy. The authors believe that this overall diagnosis and treatment strategy and precise diagnosis and treatment model are of great significance for medicine and governments to scientifically respond to various major disease outbreaks in the future. No matter what major disease outbreaks may occur worldwide in the future, this achievement can be used for scientific response and precise diagnosis and treatment.

Key words: Infectious diseases, Cytokine storm, Virus infection, Precise diagnosis and treatment

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Leptospirosis in rural Colombia: Moniquira's case series in 2022

Introduction: Moniquira is a small town in Colombia, with 20,800 inhabitants. The main economic activity is agriculture. Leptospirosis is a zoonotic disease related with contaminated water, animals, and poverty. The aim of this paper is to describe the clinical course of the disease and identify possible sources of the infection in this series of cases.

Methods: A descriptive analysis was performed using data of Leptospirosis cases reported to the National Institute of Health in Colombia.

Results: Seven leptospirosis cases were reported in Moniquira during 2022 confirmed by microagglutination testing. All cases were male adults, between 23 and 64 years old with jobs in agriculture. On average, they consulted on day 7 of symptom onset. 7 patients presented with fever, 6 with headache, 5 with myalgias and two with jaundice. One case was an outpatient. Two patients were in the intensive care unit due to septic shock and kidney failure. No deaths were reported. Possible sources of contamination are described in Table 1. Some possible reported sources were animals within the household, rats around or inside the household, and drinking water from the town's aqueduct.

Conclusions: Out of 7 cases reported, 6 required inpatient care and two patients had critical illness but recovered fully. Main symptoms were fever, myalgias and headache, as generally reported. Jaundice was reported in only two cases, and the severe cases were related with septic shock and kidney failure. All cases were related with frequently described risk factors for Leptospirosis: agriculture jobs, coexistence with animals, and rats within households. Most patients reported consuming water from the city's aqueduct system and considering the number of cases reported and Moniquira's population it is unlikely that was a source of contamination.

Table 1: Possible sources of contamination

Age	Animals within household	Rats around or within household	House's water sources
27	Dogs, cows	No	River
38	Mouses	Yes	City's aqueduct
30	Cows, pigs	No	City's aqueduct
23	Chickens	No	City's aqueduct
64	Dogs	No	City's aqueduct
62	Dogs	Yes	House pond
46	Cats	No	City's aqueduct

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Tuberculosis meningoencephalitis and drug side effects: The important role of early diagnosis and therapy modification for better outcome in Indonesia

Background: Tuberculous (TB) meningoencephalitis is a major global health problem and the most severe form of extrapulmonary TB with high mortality rate. In case *Mycobacterium Tuberculosis* (MTB) is suspected as the etiology, early diagnosis and treatment with Anti-Tuberculosis Drugs (ATD) should be given as soon as possible. This procedure will save lives and reduce neurological deficits.

Clinical Case: We presented a 37-year-old man diagnosed with tuberculosis meningoencephalitis, pulmonary TB relapse case, sepsis, drug liver injury, toxic optic neuropathy, and ototoxicity. He was full awareness when admitted to the hospital with fever and severe headache complaint, but his consciousness gradually decreased into delirium. We established the TB meningoencephalitis from the clinical sign, contrast head CT-scan showed gyral enhancement of the right occipital lobe, lakuner infarction on right semiovale sentrum, right capsula crus, and hydrocephalus communicans, *Liquour Cerebrospinal* is (LCS) analysis obtained clear, protein 155 mg/dl, glucose 64 mg/dl, *mononuclear>polimononuclear* cells. MTB Rapid molecular diagnostic (Xpert MTB/RIF) were medium detected from LCS, and sputum. Patients were treated by rifampicin, isoniazid, ethambutol, moxifloxacin, streptomycin, ceftriaxone, dexametason, acetylsalicylic acid, B complex vitamin, and supportive care. Consciousness, and physical condition gradually recovered, then patient was discharged on 21st day of treatment with full awareness, verbal, motoric and laboratory improvements. But, on the 2nd months of the treatment, complaints of icterous appeared, so rifampicin, isoniazid, and pirazinamid were stop. Rechallenge drug administration was started about 1 week later, clinical and laboratory gradually improved. Following other complaints such as decreased bilateral visual acuity that was diagnosed toxic optic neuropathy appeared, so ethambutol was also stopped. The last, on the 3rd months, patient complained hearing impairment was diagnosed with ototoxicity from streptomycin usage, and it was stopped too. Brain clinic examinations showed the cognitive impairment, language function, verbal memory and executive function impairment. He got physiotherapy and transcranial magnetic stimulation twice a week for 1 month, patients gradually improved, currently he can do daily activities well independently.

Keywords: Tuberculous meningoencephalitis, Drug liver injury, Toxic optic neuropathy, Ototoxicity, Rechallenge drug administration

Audience Take Away Notes

- To highlight the important role of early diagnosis of TB Meningoencphalitis for saving life, and also reducing the neurological deficits
- To explain ATD medication rechallenges administration in patient with severe case extrapulmonary TB with multiple drug side effects

- This case report will help the medical doctor to consider drug modification of ATD in patient with critically ill with extrapulmonary and pulmonary TB in order to get better outcomes
- To improve the audience's knowledge in comprehensive and simultaneous of management TB meningoencephalitis

Biography

Ratna Ayu Cahaya Kusuma Dewi studied in Faculty of Medicine Diponegoro University and graduated as MD in 2015. After two year of internship in Kajen, Pekalongan District, Central Java and worked as GP in Semarang city, Central Java, she then studied in Department of Internal Medicine at the Diponegoro University and graduated in 2022. She has published 1 research in Nephrology and 2 case reports in Cardiology and Tropic Infection Department.

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Clinico-epidemiological presentation of acute encephalitis syndrome in patients visiting a tertiary hospital in Kathmandu, Nepal: A descriptive cross-sectional study

Acute Encephalitis Syndrome (AES) is defined as acute onset of fever and a change in mental status (including symptoms such as confusion, disorientation, coma or inability to talk) and/or new onset of seizures (excluding simple febrile seizures) in a person of any age at any time of year. It is a complex, severe, neurological syndrome that is associated with significant morbidity and mortality and often it is associated with meningitis. Etiologies include viral, bacterial, rickettsial, fungal, parasitic, para or post infectious and antibody associated or those associated with paraneoplastic syndrome. In most cases, the cause of encephalitis is unknown. Specific etiologies are identified in less than 50% of cases. It usually presents with fever and altered sensorium (confusion and behavioral abnormalities) or depressed level of consciousness ranging from mild lethargy to coma. It may also present with seizures (focal or generalized), focal findings like aphasia, ataxia, weakness of extremities and cranial nerve deficits (ocular palsies, facial weakness). Meningism can be seen if there is associated meningitis. Diagnosis is made by the clinical picture, laboratory investigations (blood and CSF samples) and radiological imaging. Acute encephalitis syndrome (meningitis, meningoencephalitis, encephalitis) is a cause of significant morbidity and mortality in Nepal. Not only Nepal, it is a burden worldwide with annual incidence estimated to be 0.07 to 12.60 cases per 100,000 population. Encephalitis represents a challenging condition for physicians to evaluate and to treat given the variability of its presentations and etiologies and low diagnostic yield. In limited resources setup, especially like that of Nepal, initiation of empirical treatment post suspicion is of great importance than treatment post definitive diagnosis. My research would be of great aid in suspicion of AES. The true incidence of these infections is difficult to determine because the diagnosis may not be considered, many cases are unreported, or a specific viral etiology is never confirmed. Thus, my research would help in categorising the possible cases of AES. As observed in my study, AES often results in an increased number of cases with unknown etiology due to its poor diagnostic yield. We, thus, can conclude that diagnostics for acute encephalitis syndrome require a significant amount of resources; however, standard protocols can be incorporated to identify AES. To standardise such protocols, studies like mine will prove to be of great value. Future studies should include participants from multiple centres worldwide and analyze the clinical spectrum. Periodic hospital-based epidemiological investigations essential to determine the spectrum of agents that cause AES, similar to what my research offers; the information can be used to develop preventive measures against specific etiologic agents.

Biography

Dr. Bidhi Dhital completed her MBBS from Manipal College of Medical Sciences, Kathmandu University, Nepal in 2014. She attended Maharajgunj Medical Campus, Tribhuvan University, Nepal for Master's in Internal Medicine as a full scholar and finished post-graduation in 2019. She then served for two years as a Lecturer at Pokhara Academy of Health Sciences, which is, one of the largest tertiary care center in Nepal. Since then she has been practising medicine as Physician in private sectors. Currently, she has been working as consultant Physician at Charak Memorial Hospital Pvt. Ltd. Pokhara, Nepal.

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Antibiotic-resistant strains of klebsiella pneumoniae harbouring novel virulence proteins with rising temperature

Antimicrobial resistance is a serious issue since, by 2050, it's predicted to cause up to 10 million deaths globally. The emergence of fatal bacterial strains that are drug-resistant has been attributed to a number of factors, including the overuse of antibiotics, the sluggish development of new medicines, a lack of healthcare resources, and an increase in the average global temperature. One of those very virulent types that cause serious human illnesses is Klebsiella pneumoniae. Recently, the increased incidence of K. pneumoniae and novel virulent characteristics brought on by temperature-dependent genetic transfer and pathogenic alteration of drug resistance genes have drawn attention. The relationship between temperature increase, pathogenicity, and antibiotic resistance in clinical isolates of K. pneumoniae is examined in a number of recent researches. For instance, Weibin Li et al. observed that a 1.14-fold increase in carbapenem-resistant K. pneumoniae was connected to a 1o C rise in average ambient temperature. Another research by MacFadden et al. found that antibiotic resistance in K. pneumoniae increased by 2.2% for every 10°C rise in temperature across areas. In addition, warmer temperatures made it easier for bacteria with resistance to antibiotics to spread among people, animals, and the environment . As a result, temperature rise is a significant factor in the development of antibiotic resistance in K. pneumoniae, which is linked to the expression of a variety of distinctive and potentially virulent factors, including aminoglycoside O-phosphotransferase, lipopolysaccharide proteins, tyrosine-protein kinase, peroxidase proteins, and ELaB protein. Yet, it is still unclear how K. pneumoniae develops resistance more quickly than other bacteria and produces more pathogenic proteins when the temperature rises. With this perspective, the goal of this study is to investigate the mechanisms underlying this rapid resistance, to comprehend the genomic variations, mutations, gene-regulated pathogenic expression, pattern formation, and functional changes of K. pneumoniae as a result of global warming, as well as to pinpoint the virulence factors that contribute to severity.

Biography

Mohammad AL Mamun is a Research Fellow in nutritional and clinical biochemistry areas and also works as a Biochemist in clinical pathology. He has over eight years of research experience and more than six in clinical pathology. He has a good foundation in medical science and is well-equipped to engage in cutting-edge biomedical research. Six of his research articles have already been published in international peer-reviewed journals, and according to Google Scholar, he has an h-index of 3 with over 100 citations. He recently concentrated on sourcing the potential linkages between antibiotic resistance and climate change. From this point on, he plans to devote his professional life to the study and advancement of pharmaceutical technology and pharmacology. He is presently looking for a PhD program at one of the world's best institutions.

Musa Corr[1], Peter Adewuyi[1], Ousman Badjie[2], Lamin Badjie[2], Bah Sadou[2], Mustapha Bittaye[3], Yaya Dambelleh*, Karafa Jarju*, Essa Joof*, Abdoulie Senghore*

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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

Tafaani Khan

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Progression of pneumococcal nasopharynx colonization in relation to the pneumococcal conjugate vaccines in children between the ages of 2 months to 5 years at Boston medical center

The Nasopharyngeal Surveillance Study clinically investigates the progression of Streptococcus Pneumoniae (SP) Naso Pharynx (NP) colonization in relation to the Pneumococcal Conjugate Vaccines, specifically 7-Valent Pneumococcal Conjugate Vaccine, 13-Valent Pneumococcal Conjugate Vaccine and 20-Valent Pneumococcal Conjugate Vaccine (20vPnc) over the course of 5 years (2021-2026). This study aims to examine pneumococcal colonization 2 years prior to and 3 years after 20vPnC introduction, to understand how nasopharyngeal colonization of this bacteria has evolved in the patient population of 2-month-to-5-year-old children at Boston Medical Center. Pneumococcal nasopharynx colonization, detected through nasopharyngeal calcium alginate swabs, has been identified as a major source of pneumococcal transmission between the pediatric and adult populations. Scrutiny of pneumococcal colonization has led to a deeper understanding of Pneumococcal Conjugate Vaccine (PCV) effectiveness on various serotypes, the invasive capability of each serotype and the advancement or regression of antimicrobial action, such as PCV and antibiotics, on *Streptococcus Pneumoniae* over time in the aforementioned patient population. In this 5-year-study, researchers in the Pelton Lab at Boston Medical Center set out to understand SP NP prevalence for 13vPnC serotypes, 20vPnC serotypes, and individually discovered serotypes across the pediatric population. It is expected that increased prevalence of the 19F serotype with 13vPnc introduction many years ago foreshadows the pattern of increased prevalence of 13vPnC serotypes amidst 20vPnC introduction this year.

Audience Take Away Notes

- Understand the extent of vaccination required in the pediatric community to establish herd immunity among adults
- Understand how serotypes and mutations of a microbe, not accounted for in a vaccine, create future medical implications
- Understand the immunological mechanisms that control microbial persistence in the human body
- Allows vaccine developers and current researchers to consider newer, more effective ways of creating vaccines that account for plausible microbial mutations and alterations
- Allows researchers to improve methods of microbial surveillance linked to pediatric infectious diseases through creative research methods and procedures

Biography

Tafaani Khan studied Neural Science at New York University with a double-minor in Chemistry and Public Health, graduating with a B.S. Degree in May 2021. She is currently enrolled in a Medical Sciences Program at Boston University Chobanian & Avedisian School of Medicine, graduating with a M.S. Degree in May 2023. Tafaani has over 4 years of clinical research experience in Multiple Sclerosis Treatments, as well as Pediatric Infectious Diseases. She has received the Reporter Acknowledgement Award for the COViMS Registry Study in October 2021. Tafaani will continue her career as a newly accepted medical student and future medical doctor.

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IN-PERSON POSTERS

4th Edition of World Congress on

INFECTIOUS DISEASES

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A strong sominance in the spread of influenza viruses over that of the SARS-CoV-2 during the 2022/2023 season in Bulgaria

After a period of two seasons of absence (2020/2021) or low prevalence (2021/2022) of influenza viruses, the 2022-2023 seasons was characterized by high influenza activity in Bulgaria. The objectives of this study were to analyze the pattern of influenza virus circulation with respect to that of SARS-CoV-2 during the 2022-2023 seasons. Influenza type A/B viruses and SARS-CoV-2 were tested simultaneously using a Multiplex real-time RT-PCR kit (FluSC2, USA). The spread of influenza viruses began earlier – in mid-November 2022 and peaked in the 3rd week of January 2023 amid a low spread of the SARS-CoV-2. Seasonal influenza viruses A(H1N1)pdm09, A(H3N2), and B/Victoria- lineage were detected in 256 (13.4%), 189 (9.9%), and 22 (1.2%) out of 1913 patient samples studied, respectively, and SARS-CoV-2 was identified in 78 (4.1%) samples. Six cases of co-infections between the influenza virus and SARS-CoV-2 were identified. The proportions of influenza detection in outpatients and inpatients were similar (25.7% and 23.2%, respectively). In SARS-CoV-2-infected patients, these proportions were 4.2% and 4%, respectively. Influenza viruses were detected in 6, 5% (11/168), 21.6% (69/319), and 22.2% (8/36) of the studied patients with bronchitis/bronchiolitis, pneumonia, and CNS involvement, respectively. SARS-CoV-2 was identified in 2.5% of patients with pneumonia. Clinical features of the infections were analyzed. In conclusion, a strong dominance in the spread of influenza viruses over that of the SARS-CoV-2 was found during the 2022/2023 season in Bulgaria, which is related to the dropping of non-pharmaceutical anti- COVID-19 measures and low coverage with influenza vaccine in the country. Influenza A viruses predominated with a larger proportion of A (H1N1) pdm09 viruses.

Audience Take Away Notes

- Influenza has great clinical and epidemiological significance. Influenza viruses affect millions of people worldwide there are 600 million cases of influenza worldwide each year, with 3 million having severe disease. Awareness of the prevalence of influenza and its clinical significance is an important part of our health and disease education
- The threat of new influenza pandemics is a hot topic today, and therefore there is a need to track the spread of influenza viruses and facilitate the development of seasonal vaccines that would help reduce hospital admissions worldwide. Such information is important for developing optimal strategies for influenza prevention and control
- The results of this study confirm the diversity of circulating influenza viruses and the presence of co-infections with SARS-CoV-2, which would pose a risk of worsening patients' conditions
- The emergence of such co-infections at a higher rate since the beginning of the pandemic indicates the need to develop vaccines that include both pathogens

Biography

Ivelina Trifonova is an assistant at the National Center for Infectious and Parasitic Diseases, National Laboratory of Influenza and SARS, Sofia, Bulgaria since July 2020. She obtained a Ph.D. in virology at the National Center for Infectious and Parasitic Diseases (NCCPD), Department of Virology, 2020. She is the head of a project on Molecular-genetic and clinical characteristics of the human coronavirus. Study of the role of SARS-CoV-2 in co-infections with other respiratory viruses. She has published 13 articles with an impact factor, has a total of 22 publications, and has a personal H index of 4.

Michael Ansah
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The potential of guanidino and amidopropyl dimethylamine compounds as topical treatments for diabetic foot ulcer infections

Diabetic Foot Ulcer (DFU) infections caused by Multidrug Resistant (MDR) organisms cost approximately 1% of the annual NHS budget, mainly through pre/post op management of complications/amputations. The aim of this study is to investigate the potential of guanidino based compounds and amidopropyl dimethylamines as repurposed topical treatments for DFU infections. Compounds from these groups have demonstrated a wide range of uses including antiseptics, antimalarial, antidiabetic and anticancer compounds. These compounds also demonstrate antimicrobial activity through disruption of the cellular membrane. The study investigated the activity of guanidino based and amidopropyl dimethylamine compounds against a broad range of MDR organisms including *Staphylococcus aureus* (S. aureus), *Pseudomonas aeruginosa* (*P. aeruginosa*) and *Candida albicans* (*C. albicans*). This study has demonstrated that of the guanidino based compounds, Polyhexamethylene Guanidine (PHMG), Polyaminopropyl Biguanide (PAPB) and Polyhexamethylene Biguanide (PHMB) demonstrated significant activity against all the test organisms. PHMG, PHMB and PAPB demonstrated complete kill within 24 hours against S. aureus at 0.05 µg/ml and complete kill within 2 hours at 0.1 µg/ml against P. aeruginosa. PHMG demonstrated complete kill of C. albicans within 6 hours at 0.05 µg/ml. This study has also demonstrated that several amidopropyl dimethylamines demonstrate significant activity against the test organisms. Palmatamidopropyl Dimethylamine (PAPD) at 7.8 µg/ml demonstrated complete kill within 1 hour against S. aureus and within 24 hours against *C. albicans*. PAPD and N,N-dimethylhexadecylamine demonstrated complete kill against P. aeruginosa within 4 hours and 2 hours respectively at 1 µg/ml. This study has demonstrated that guanidino based and amidopropyl dimethylamine compounds warrant further investigation for inclusion in the topical treatment of DFU infections.

Audience Take Away Notes

- The audience will learn that gaunidino and amidopropyl dimethylamine compounds demonstrate activity against several MDR organisms including S. *aureus*, P. *aeruginosa* and C. *albicans*
- Although this is framed in the setting of diabetic foot ulcer infection, these organisms are capable causing several other types of infection
- Therefore, this study highlights such compounds for the potential use against a number of bacterial and fungal infections.
- The study also highlights that the length of the carbon chain attached to the functional group influences the antimicrobial activity of the compound
- This information will be useful for those synthesizing similar compounds for potential treatment of bacterial and fungal infections

Biography

Michael Ansah studied biochemistry at Keele University, England and graduated in 2019. He then went on to complete his MPhil in Parasitology at Keele University, supervised by Prof. Helen Price, with the thesis title of Screening of an open-source compound library against the livestock parasite *Trypanosoma evansi* He is currently a third year PhD student at the University of Wolverhampton, supervised by Dr. Wayne Heaselgrave, with the proposed thesis title of Investigating current treatments and untested compounds for the topical treatment of leishmaniasis and MDR bacterial and fungal diseases.

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Prevalence and characteristics of *Neisseria meningitidis* carriage among high school students from the Vilnius region, Lithuania

Neisseria meningitidis causes Invasive Meningococcal Disease (IMD), which is associated with significant mortality and long-term consequences, especially among young children. The incidence of IMD in Lithuania was among the highest in European countries during the past two decades reaching 2.9 cases/105 population in 2017. The worst disease-affected region was the Vilnius region, accounting for the majority of disease cases across all age groups. In 2020-2022, the incidence of IMD decreased in Lithuania accounting for approx. 0.36 cases/105 population. The drop is presumably related to COVID-19 restriction measures and vaccination against serogroup B meningococci. Oropharyngeal carriage of N. meningitidis is thought to be a prerequisite for the development of IMD. In industrialized countries, meningococcal carriage reaches a peak in young adults, however no data exist on N.meningitidis carriage among Lithuanians of 18-25-years-old. For the current study, oropharyngeal swabs were collected in 2022 from 300 students. N.meningitidis was detected and identified by culture and quantitative real-time PCR by targeting ctrA and porA genes. The genogroup and the MLST profile of isolates were determined by conventional PCR. Carriage prevalence was 4.33% (13/300). Most carriage isolates were genogroup B (30%) and capsule null (53.8%). Two isolates possessed the ctrA gene, however they were non-genogroupable in genotypic assays. The dominant genogroup B was compatible with that implicated in IMD in Lithuania, however the majority of clonal complexes (cc) of carriage isolates were not similar to invasive ones: the most common clonal complex was cnl cc198, cc269, and cnl cc1136. Noticeably, cnl cc198 was also dominant among Swedish, Dutch and Italian young adults. One isolate of ST-213 (cc213) has the same genotype as that causing IMD in Lithuania. Circulating isolates of genogroup B cc269 have invasive potential as cc269 is among the IMD-causing isolates in many countries.

Audience Take Away Notes

- Oropharyngeal carriage of N. *meningitidis* is thought to be a prerequisite for the development of invasive meningococcal disease (IMD)
- This study provides new data on the meningococcal carriage in Lithuania, a country with high IMD incidence
- The epidemiology of carriage revealed N. *meningitidis* isolates having an invasive potential
- The understanding of meningococcal epidemiology in countries with high IMD incidence is crucial for the development of future public health and vaccination policy
- The faculty could use the results of the current study to expand their research or teaching to address public health interventions

Biography

Dr. Aurelija Zvirblienė is Research Professor at the Institute of Biotechnology of Life Science Center of Vilnius University (Lithuania), president of the Lithuanian Society of Immunology. She studied Biochemistry at Vilnius University and received her PhD degree in the field of Immunology. After the habilitation procedure in 2008, she obtained the position of Research Professor and head of Department of Immunology at the Institute of Biotechnology. The interests of her research team are focused to the development of immunodiagnostic tools for infectious diseases, prevalence studies of viral and bacterial infections, studies on the innate immune responses to pathogens.

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Profile of beta-lactamases in multidrug-resistant (MDR) *Acinetobacter baumannii* strains in Lithuania 2016-2017 and 2021-2022 years

Introduction: *Acinetobacter baumannii* (A. *baumannii*) is an important nosocomial pathogen that possesses not only intrinsic resistance to many classes of antibiotics, but also has a propensity for rapid development of antimicrobial resistance during treatment.

Aims & Objectives: Aim of our study was to investigate A. *baumannii* strains producing different beta-lactamases. A total of 223 A. *baumannii* were isolated from different clinical samples of patients treated in 2016-2017 and 2021-2022 years in Hospital of Lithuanian University of Health Sciences.

Methods: ESBL plus AmpC screen disc kit (Abtek Biologicals, UK) was used to determine the production of the Extended Spectrum β-Lactamase (ESBL) and AmpC β-lactamase. Combination meropenem disc test was used to determine the co-production of KPC and MBL carbapenem ases. For the statistical analysis were used Chi-square test and multivariate analysis; $p < 0.05$ was considered statistically significant.

Results: All isolates had a multidrug resistant profile, and all were resistant to the carbapenems but remained susceptible to colistin. Phenotypic method showed that 60.9% (n=142) of A. *baumannii* strains were AmpC β lactamase, 11.6% (n=27) ESBL and 76.8% (n=179) KPC β lactamase producers. 46.3% (n=108) of A. *baumannii* strains had AmpC plus KPC β lactamases, 2.6 % (n=6) AmpC plus ESBL, 2.6 % (n=6) ESBL plus KPC and 3.8% (n=9) AmpC plus KPC plus ESBL.

All tested strains were divided into fourth groups: non-producing β - lactamase (9.9%, n=23), producing only AmpC, KPC or ESBL (34.8%, n=81), producing two different β - lactamases: AmpC plus KPC, AmpC plus ESBL or ESBL plus KPC (51.5%, n=120) and the last group: producing all β - lactamases (3.9%, n=9). We have found that all A. *baumannii* strains were β - lactamase producers in 2021/2022 while 17.7% (n=23) strains didn't produce any β - lactamase in 2016/2017. In 2016-2017 only one β - lactamase producing stains were detected in 62.3% of tested strains while in 2021-2022 no one only one β - lactamase producing strains were detected. A. *baumannii* strains producing two different β - lactamases were more frequently identified in 2021/2022 compared to 2016-2017 (94.2% (n=97) compared to (17.7% (n=23), $p<0.001$). ESBL, AmpC and KPC β - lactamase producing strains were identified 5.8 % (n=6) in 2021-2022 and only 1.3 % (n=3) in 2016-2017 ($p<0,001$).

Conclusions: Increased synthesis of β - lactamases in 2021-2022 compared to 2016-2017 years is a serious warning because β - lactamases are a major threat to the effectiveness of antibiotics that are currently available for medical uses.

Audience Take Away Notes

- Phenotypic methods for the detection of β - lactamases are easy and simple and can be implemented in routine diagnostic laboratories along with susceptibility testing. These data will assist the clinicians in the management and control of infections

Biography

K. Cerniauskiene studied at Kaunas Medical University, Lithuania and graduated as MS in 2010. She then studied in residency, obtained the qualification of laboratory medicine phisition at the Lithuanian University of Health Science in 2016. In the same year, she started to work as a laboratory medicine phisition in the Departament of Laboratory Medicine in Laboratory of Microbiology. In 2017, she entered the Phd studies program at the Lithuanian University of Health Sciences, the topic of her dissertation is the microbiological and molecular characteristics of *Acinetobacter baumannii* and its importance in clinical practice. Head Department of Laboratory Medicine prof. Astra Vitkauskiene is responsible for development of a new methods and technologies in laboratory medicine. Her research interests are to examine pathogenicity factors and resistance mechanisms to antibiotics of clinically important pathogens. She has great experience in molecular genetics techniques, serology, immunochemistry, culturing methods and etc., participated in more than 10 clinical trials, led 5 clinical trials and more than 22-year experience in laboratory medicine overall. Astra Vitkauskiene is author and co-author of more than 100 of research publications, member of board of Lithuanian Society of Laboratory Medicine, head of board of Kaunas branch.

Zsaklin Varga[1,2,3*], Rebeka Csiba[1,2,3], Agota Abraham[1,2,3], Gabor Kemenesi[1,2,3], Kornelia Kurucz[1,2,3]

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The role of aedes koreicus in the circulation of Dirofilaria repens and dirofilaria immitis filarial nematodes in a middle-sized European city, in Hungary

The mosquito-borne pathogens are present worldwide, notable among these are *Dirofilaria immitis*, which causes heartworm disease, and *Dirofilaria repens*, known as the causative agent of subcutaneous dirofilariasis. These two species are unfortunately endemic throughout Europe and are well known pathogens in animal health.

In addition, the emergence, more efficient and faster spread of invasive mosquito species may further increase this risk. Invasive species can compete with native species for limited resources, alter habitats, reduce biodiversity, introduce new diseases into an area and can also be a potential vector of an already present pathogen. One of Hungary's invasive mosquito species is Aedes koreicus, which has been present in one of the southwestern cities (Pécs) for years, has been under continuous monitoring since its emergence, and more data on its spatio-temporal dynamics and ecological requirements are available every year. Our aim in this study was to monitor the population of Aedes invasive and other common mosquito species in the area identified as a focus of infection, including an animal shelter, and in several locations within the city of Pécs, and to test the collected mosquitoes for Dirofilaria species. In addition, we aimed to investigate the dependence of mosquito infestation on weather, location and species with particular attention to *Ae. koreicus.*

In terms of our results, we processed more than 300 pools of mosquito samples collected in the 2022 season by qRT-PCR, including common species and invasive *Ae. koreicus*, as well as blood fed individuals. Our positive samples for filarial parasites include both *Ae. koreicus* and common species as well (*Aedes vexans*, *Culex pipiens* and *Ochlerotatus sticticus* etc.) collected from different trap sites, and the pathogen was also detected in the head-thorax part of blood fed *Ae. vexans.* In the light of our preliminary results we have not found a clear correlation between the spread of *Ae. koreicus* and Dirofilaria infestation of mosquitoes. However *D. repens* is rarely but capable of infecting humans, and recently several human cases have been described in Pécs from close proximity to each other and coinciding with the most favourable urban areas for *Ae. koreicus.* Thus, we plan to extend our work by processing further samples and to investigate the circumstances of the human cases.

The exploration of this phenomenon is also of paramount importance from a practical point of view, as understanding the underlying determinants of human disease provides an opportunity for preventive interventions, and this research design aims to provide a basis for this.

Biography

Zsaklin Varga graduated with a Bachelor's degree in Biology in 2019 and a Master's diploma in 2021 at the Faculty of Sciences of the University of Pécs, Hungary. During her Master's studies, she joined the National Laboratory of Virology, at the University of Pécs, and currently she is a member of the group as a PhD student. Her research activities and interests are zoonoses, the virological, genetic and ecological background of vector-borne diseases, mosquito surveillance, invasive mosquito species in the light of the One Health concept.

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CD11c+ dendritic cells are required for survival in murine LPS induced ALI

Purpose: Dendritic Cells (DCs) are always known as professional APCs which play a crucial role in the link between innate and adaptive immunity. DCs can initiate both immunity and immunological tolerance, which means efficacy either in amelioration or exaggeration of inflammation response. LPS induced Acute Lung Injury (ALI) is resulted in dysregulated inflammation and sequential pulmonary endothelial and epithelial injury. DCs are known increased in LPS in tracheal instilled lung but it is still unclear about their role in outcome and their priority of either immunity or immunological tolerance.

Method: Transgenic mice (B6.FVB-Tg.Itgax-DTR/EGFP.57Lan/J) expressing the Diphtheria Toxin (DTX) receptor on the CD11c promoter(Itgax),which can be used as DCKO mice after receiving i.t injection of 50 ng DTX 24h prior to LPS i.t instillation. Lungs are harvested after 24h and Wet Weight and Body Weight ratio (WW/BW) is measured to illustrate the degree of permeability. Lungs were fixed overnight at room temperature in neutral buffered formalin and then are embedded. Five micrometers sections were deparaffinised, rehydrated, and stained with H&E and then were scored for deflation, hemorrhage, thickness and infiltrating cells. DCs are identified by CD11c+ MHCII+F4/80- cells by Flow cytometry after preparation of single cell suspension while macrophages are identified by CD11c+ F4/80+ cells. Pulmonary cytokines expression are evaluated by quantitative PCR performed with the SYBR Green Master Mix after total RNA extraction from smeared lung tissue and cDNA synthesis according to the manufacturers' protocol. Survival was measured following DTX treatment and LPS instillation in DCKO mice and wide-type littermates (eight individuals per group). Statistical analysis was performed using Graph Pad Prism, version 9.1.1 (Graph Pad Software Inc., San Diego, CA).Values of P less than 0.05 were considered as significantly different.

Result: DCKO mice received 50ng DTX, which resulted in significant reduction of CD11c+MHCII+ cells compared to wide-type littermates. After pretreatment of DTX, WW/BW of DCKO mice is increased in LPS induced ALI (4.90 vs 6.36mg/g; $p < 0.05$). Meanwhile, lung HE stain shows deflation and infiltration and lung injury scored of DCKO mice is significantly increased (5.06 vs 7.83;$p < 0.05$). Pretreatment of DCKO mice with DT resulted in reduced survival in LPS induced ALI compared with DT-treated wild-type littermates (12.5% vs 62.5%; $p < 0.05$) This increased mortality was not associated with plasma cytokine concentrations.

Conclusion: These data confirm that DCs are essential in the LPS induced ALI and maintain DC numbers or immunological tolerance function may improve outcome.

Audience Take Away Notes

- Explain the efficacy of dendritic cell in acute lung injury
- Help understand the dendritic cell in innate immunity when ALI
- Help expand the research of DCs in ALI

Biography

Mrs. Tang studied Clinical Medicine at the Southeast University, China, and graduated as Bachelor in 2017. She the join the post-graduate Programme in Critical medicine department supervised by Prof. Haibo Qiu and graduated as MS in 2019. Then she joined the research group of Prof. Fengmei Guo atat the Southeast University and is applying the PhD degree.

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Identification of novel *P. falciparum Kelch13* (PfK13) interacting partners via co- Immunoprecipitation (co-IP)

Malaria remains a global health issue affecting half of the world's population. The current treatment regimen which includes artemisinin and other combination therapies is being threatened with the rapid emergence of resistance. *P. falciparum* under drug pressure has revealed insights into mechanisms of resistance most commonly used antimalarial, such as Chloroquine, Amodiaquine, Piperaquine, DHFR inhibitors etc. There are currently no alternative drugs available to replace Artemisinin should render it obsolete. ART resistance has been shown to be mediated by the *Plasmodium* Kelch13 (PfK13) protein. Pf kelch 13 gene is situated in chromosome 13 and associated with ART resistance, owing to the association of majority of mutations at the kelch BTB/POZ & propeller domain. The present study recombinant expressed the PfK13-p (BTB/POZ & propeller domain) and generated anti-PfK13-p antibodies for cellular localization and co-immunoprecipitation (co-I P) assays and mass spectroscopy was performed to identify the PfK13 interacting partners. Unique coimmunoprecipitated proteins were identified barring few proteins overlapping with previous studies- Protein disulfide isomerase, heat shock proteins, Merozoite Surface Protein n 1 (MSP1), L-lactate dehydrogenase, elongation factor 1-alpha. The unique hits of the study were- falcilysin, enolase, phosphoethanolamine N-methyltransferase, glide some-associated protein 50, fructose-bisphosphate aldolase, adenylate kinase, peptidyl-prolyl cis-trans isomerase, thioredoxin-related protein, putative, 20 kDa chaperonin, ornithine aminotransferase, rhoptry-associated protein 1. The identified proteins were categorized into protein folding, protein binding/invasion, cellular metabolism and mobility functions. Further, bioinformatics proteins identified by the STRING database represent the PfK13 protein and the respective potential interactors or performing shared functions are shown in network. The minimum interaction score was set to medium confidence level (0.400) and no more than 10 interactors were selected. PGK (Phosphoglycerate Kinase) and Q7KQL9 (Fructose- biphosphate aldolase) are the two predicted proteins, which have been identified via co-IP assays. In other experiment, strong binding affinities of PfK13-p and two coimmunoprecipitated proteins- Heat Shock Protein 70 and PfFBAP (6.6 and 7.6 μM, respectively) were observed using surface plasmon resonance (SPR). Using anti-PfK13-p antibodies, the endogenous PfK13 protein was observed to localization with a cytosolic marker-PfAspRS (aspartyl transfer-RNA synthetase). Together, this work identified unique interacting partners of endogenous PfK13 protein, which might have crucial implications in the PfK13 protein network and its role in mediating ART resistance.

Keywords: Malaria, Artemisinin, *P. falciparum*, Kelch 13 protein, Protein-protein interactions

Audience Take Away Notes

- A fuller understanding of the resistance mechanism will underpin the efforts to develop alternative antimalarial strategies
- A better understanding of the mechanisms of the action, and resistance to artemisinins is now emerging; this may help us to understand why resistance is currently limited in geographic spread and results in only partial loss of efficacy

- These insights should also support efforts to prolong the lifespan of this class of drugs and to discover new drugs with related mechanisms of action
- Systematic identification of interacting proteins partners of pfK13 could help us to understanding the networking with other protein partners

Biography

Preeti Chaudhary studied biotechnology at the Manav Rachna International University, India graduated in 2015 and then joined as lab assistant in clinical laboratory for 1 year at Asian Institute of Medical Sciences and joined lab as PhD scholar at the Host-Parasite Interaction Biology Group, ICMR-National Institute of Malaria Research, New Delhi, India under the supervision of Dr. Kailash C. Pandey (Scientist-F).

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Evaluation of the national immunization program by estimating immunoglobulin G antibody prevalence of measles and rubella in Lao people's Democratic Republic

Objective: To eliminate measles and rubella, it is critical to develop strategic and efficient immunization programs. This study aimed to evaluate the population immunity and the measles-rubella program's effectiveness by estimating anti-measles and anti-rubella IgG prevalence in the general population of the Lao People's Democratic Republic (PDR).

Methods: A nationwide seroprevalence survey was conducted in Lao PDR between May and June 2019, using the multi-stage cluster sampling method. In the first and second stages, 26 districts and two villages from each province were selected using probability proportional to size sampling. In the third stage, 42 people were randomly selected from the residents' list in each village. Dried blood spot samples were collected onto WhatmanTM 903 filter paper by finger prick. IgG titers were measured by Enzygnost® enzyme-linked immunosorbent assay, and the results were considered positive at ≥120 mIU/ml for measles and ≥ 10 IU/ml for rubella.

Results: We approached one thousand nine hundred people and enrolled ninety-three subjects (females: 53.0%, mean age: 23.1 years (1-89 years), excluding those with inappropriate specimens, were included in the analysis. IgG prevalence was estimated to be 98.3% [95% CI: 97.7-98.8] for measles and 87.8% [86.4-89.2] for rubella. Measles IgG prevalence was estimated to be greater than 95% except for those aged 1-2 years, and rubella was estimated to be greater than 80% except for those aged 1-2 years and 25-34 years.

Conclusions: Overall, IgG prevalence of measles and rubella was higher than those herd immunity thresholds required to eliminate both viruses. However, the prevalence for antibodies for both pathogens in people aged 1-2 years was lower than herd immunity, indicating a need for a more robust immunization program. Special attention should be paid to the rubella vaccinations in 25-34 year olds to minimize the potential risk of creating congenital rubella syndrome.

Yuefeng Song*, Wenmei Wang

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Analysis of oral clinical manifestations and serological test results of secondary syphilis

Objective: To analyze the correlation between serological test results and oral clinical manifestations of patients with secondary syphilis, and to provide reference for clinical diagnosis and treatment.

Methods: From January 2016 to December 2020, 30 patients with secondary syphilis were treated in Nanjing Stomatological Hospital and Nanjing Stomatological Hospital, School of Medicine, Nanjing University, and they were retrospectively analyzed to investigate the correlation between oral clinical manifestations (including the number and grade of lesions) and serological test results [Rapid Plasma Reactin ring card test (RPR) titers].

Results: Among the 30 patients included in the study, 14 were male and 16 were female. There were 11 young people (≤44 years old), 10 middle-aged people (45-59 years old) and 9 elderly people (≥60 years old). There was no significant difference in gender distribution among different age groups (P>0.05). The oral mucosal lesions of the patients were characterized by mucosal plaques and mucositis, and the most frequent sites were lips, tongue, pharynx, palate and buccal division. Patients with high RPR titer (≥1:128) had more oral mucosal lesions and higher clinical lesion grade compared with patients with low RPR titer (<1:128), with statistical significance (P<0.05).

Conclusion: RPR titer of secondary syphilis patients with oral mucosal lesions is closely related to the number of oral mucosal lesions and clinical lesions grade.

Audience Take Away Notes

- Introduce our research about the correlation between serological test results and oral clinical manifestations of patients with secondary syphilis
- Provide ideas and suggestions to further study the significance of serological test in the diagnosis of syphilis

Biography

Dr. Yuefeng Song graduated from the Medical School of Nanjing University in 2017 with a master's degree in stomatology. She is now an attending physician in the Department of Oral Medicine of the Nanjing Stomatological Hospital and is good at the diagnosis and treatment of common diseases of oral mucosa. She has published 4 papers as the first author/co-first author and participated in the compilation of 2 monographs.

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Effect of a novel anti-splash mask on preventing aerosol in dental practice

Objective: To evaluate the effect of a new anti-splash mask on preventing aerosol pollution in dental clinics.

Methods: The aerosol distribution characteristics in different types of splash operations were analyzed in dental clinics at first. Different splash operations were composed of cavity preparation, tooth preparation, interproximal enamel reduction, and supragingival scaling. Then tooth preparation on isolated teeth was simulated in dental phantom head. According to whether to use the anti-splash mask, experiments were divided into the experimental group and the control group. The droplets of aerosol at multiple time points were sampled before, during, and after dental procedures. The effectiveness of preventing aerosol pollution by the novel anti-splash mask was analyzed.

Results: The aerosol concentrations caused by diverse splash operations in the clinics increased respectively ($P<0.05$). The aerosol concentration resulting from tooth preparation was the highest ($P<0.05$). To simulate dental treatment, tooth preparation was performed on isolated teeth in dental phantom head. It was found that the aerosol concentration was significantly decreased when using anti-splash masks ($P<0.05$).

Conclusion: Diverse dental splash procedures initiated a large amount of aerosol respectively. The use of novel anti- splash mask in the process of dental diagnosis and treatment can reduce the aerosol concentration in dental clinics, which have a positive effect on preventing the spread of COVID-19.

Audience Take Away Notes

- Introduce a new anti-splash mask on preventing aerosol pollution in dental clinics developed by our research group, which has been authorized the national invention patent
- Analyse the effectiveness of preventing aerosol pollution by the novel anti-splash mask
- Provide ideas and suggestions to further improve the performance of the anti-splash mask according to the requirement on the field of vision

Biography

Dr. Wenmei Wang was admitted to Hubei Medical College (now the School of Stomatology of Wuhan University) to study for a master's degree in 1987, and graduated in 1990 with a master's degree in stomatology. She is now a professor, master tutor at the Medical School of Nanjing University and medical supervisor at the Nanjing Stomatological Hospital. She is mainly engaged in the diagnosis and treatment of oral mucosal diseases, scientific research and teaching, and has rich experience in the diagnosis and treatment of rare diseases related to oral mucosa. Combined with clinical research work, she presided over and completed more than 10 projects at various levels, published more than 200 papers, translations and reviews in SCI and core journals, and participated in the editing of 8 books.

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Development of novel vaccine adjuvant formulation against IBV for the poultry industry

Adjuvants were described as substances used in combination with a specific antigen that produced a more robust immune response than the antigen alone. There is an urgent need for the development of new and improved vaccine adjuvants. Infectious Bronchitis (IB) is one of the most relevant infectious diseases of poultry, and it is caused by the Infectious Bronchitis Virus (IBV). Most commercially available IB vaccines are inactivated whole-virus preparations that do not induce long-term protection. This can be overcome by the administration of an effective immune adjuvant that generates a strong enough immune response to provide long-term protection against infection. Within the scope of the project, new adjuvant candidates were developed containing glycoside molecules in oil-based (W/O) and examined for the first time against IBV in poultry and commercialized. For this purpose, the IBV H120 strain was produced in Specific Pathogen-Free (SPF) Embryonic Chicken Eggs (ECE) and 50% Embryo Infectious Dose (EID50) values were determined. Subsequently, formalin-inactivated virus and new candidate vaccine adjuvants were used in the vaccine formulation. After quality control and stability tests, vaccine formulas were administered to chickens subcutaneously. Vaccination efficiency was evaluated for serum antibody (IgY), mucosal antibody (IgA) responses, and changes in cytokine levels by ELISA. The cellular response was measured as a ratio analysis of the T lymphocyte subset (CD4+/ CD8+) in peripheral blood by flow cytometry. Evaluation of the protective efficacy of vaccine formulations was determined using the virus challenge test in Specific Pathogen-Free (SPF) challenge ocular-nasal route with M41 virus strain and their protection was assessed in trachea and kidney post-challenge to determine the virus shedding using RT-qPCR. The physical and chemical analysis values of the newly developed adjuvants (CORALVAC) within the scope of the project are among the limit values. When the stability, which is one of the critical parameters in the use of adjuvants, is evaluated, the product maintains its stability for a long time at 4˚C. The low emulsion viscosities of CORALVAC adjuvants facilitate their injectability. When the responses of anti-IBV antibodies were examined, faster and higher antibody responses were obtained compared to commercial adjuvants. When the protection of the vaccine was examined after the challenge test, higher IgA antibody responses were obtained compared to commercial adjuvants. The cytokine levels of IL-1β, IL-2, IL-4, and IFN-γ at Days 14 and 28 after vaccination were examined. On day 28, splenocyte T lymphocyte subsets (CD4+ and CD8+) were examined by flow cytometry analysis. Considering the findings obtained, it was determined that the CD4+ and CD8+ responses of CORALVAC adjuvants were balanced. Tissue samples taken from the

trachea, cecal tonsil, lung, and kidney were examined by RT-qPCR to evaluate the protective efficacy of vaccine formulations and to determine the protection of the vaccine and virus spread after challenge, and positive results were obtained compared to commercial adjuvants. When the results obtained within the scope of the study were examined, the CORALVAC adjuvants developed within the scope of the project were found suitable for use in commercial vaccines.

Audience Take Away Notes

- Within the scope of the project, the training of new young academics was supported
- The efficacy of alternative adjuvant systems for commercially developed vaccines is presented
- The efficacy of oil-based adjuvants in poultry vaccines was investigated
- For the prevention of infectious bronchitis in poultry industry, which causes great economic losses, a local adjuvant system has been developed

Biography

Dr. Akın studied Chemistry at the Kocaeli University, Turkiye, and graduated with a PhD. in 2020 from the same institution. He then joined Petro Yag ve Kimyasallar San. ve Tic. A.Ş the Research and Development Center as manager. His specialist area is biochemistry. He has published more than 20 research articles in SCI (E) journals.

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Culture-proven bloodstream infection in children managed at a tertiary hospital in Oman

Objective: Bloodstream Infection (BSI) in children causes significant morbidity and mortality and is associated with longer hospital stays and higher healthcare costs. Our objective is to study the incidence and risk factors and identify causative organisms and outcomes of BSI among Omani children in a tertiary hospital.

Methods: A retrospective study of laboratory-confirmed BSI was conducted among children managed at Sultan Qaboos University Hospital, Oman, between 2014 and 2018. Patients' demographic, clinical, and laboratory data were extracted from the hospital's electronic records. Univariate and multivariate logistic regression analysis was used to explore the relationship between death within 30 days in children with confirmed BSI and the other studied factors.

Results: A total of 1253 positive blood cultures were identified during the study period. Among these, 592 were probable contaminants, representing 47.2% of positive blood cultures. Overall, 404 (32.2%) clinically significant episodes of BSI were identified in 272 patients. Two-thirds of the patients (346; 85.6%) were ≤ 5 years old. Overall, 5 years incidence of BSI was 13 per 1000 admission. Three-hundred thirty-three (82.4%) episodes were either hospital-onset or healthcare-associated. Comorbidities were present in 366 (90.6%) of these children including prematurity (106; 26.2%), hematological malignancies (90; 22.3%), gut-related pathologies (71; 17.6%), and metabolic/genetic syndromes (47; 11.6%). Of the significant isolates, 211 (52.2%) were gram-negative bacteria, 168 (41.6%) were gram-positive bacteria, and 25 (6.2%) were Candida species. *Enterobacteriaceae* (152; 37.6%) was the most common organism identified followed by Coagulase-negative *staphylococci* (63; 15.5%) and *Staphylococcus* aureus (47; 11.6%). Of the *Klebsiella spp* and *Escherichia coli* isolates, only 60% were susceptible to 3rd generation cephalosporins. Among the potential factors predisposing to BSI, the central venous catheter was the most frequent (182; 45%). The crude mortality at 30 days was 9.2%. Moreover, both Pediatric Intensive Care Units admission (COR = 2.24, 95% CI: 0.98-4.78) and the presence of Graft-Versus-Host Disease during bacteremia (COR = 7.99, 95% CI: 1.52-37.76) were associated with increasing death within 30 days.

Conclusions: We reported a high percentage of contaminants among our positive blood culture isolates, which highlighted an urgent need to follow aseptic precautions during blood culture collection. Since a large proportion of BSI was hospital related, there was an urge to optimize infection control strategies and Central Vein Access Device care. Adding gentamicin to the BSI empiric antimicrobial cover is highly recommended given the high rates of gram-negative organisms to third-generation cephalosporins.

Audience Take Away Notes

- A comprehensive understanding of the impact of BSI on the childhood population
- Implementation of guidelines to improve the recognition and management of bacteremia
- Providing insights about antimicrobial therapy and outcomes of BSI

Biography

Dr. Marwah AL Thuhli, M.D., Sultan Qaboos University, 2018. Pediatric Residency Training Program, 4th year, Oman Medical specialty Board (OMSB), Muscat, Oman. This research got 1st place in our annual research day at OMSB.

Asmma Doudin[1], Nagendra Babu[2], Theeb Sulaiman[3], Omar Jamil[4], Rida Arif[5], Fatima Al Saada[2], Hadi Yassine[6], Mohammad Elrayees[6], Mohamed M. Emara[2], Ibn Mohammed Masud Danjuma[2,3], Abdul Latif Al Khal[2,3], Abdel-Naser Elzouki[2,3], Farhan S. Cyprian[2], Abdallah Musa Abdallah[2*]

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Metabolic predictors of COVID-19 mortality and severity: A Survival Analysis Study

Metabolomics has been increasingly utilized in studying the host response to viral infections and for understanding the progression of multi-system disorders such as COVID-19. The analysis of metabolites in response to SARS-CoV-2 infection provides a snapshot of the endogenous host metabolism and its role in shaping the interaction with SARS-CoV-2. In this study, using a targeted metabolomics approach, the metabolic signatures of mortality and severity were studied in COVID-19 patients. Blood plasma concentrations were quantified through LC-MS using MxP Quant 500 kit, which has a coverage of 630 metabolites from 26 biochemical classes including different classes of lipids and small organic molecules. We utilized Kaplan-Meier survival analysis to investigate the correlation between various metabolic markers and patient outcomes. A comparison of survival rates between individuals with high levels of various metabolites (amino acids, tryptophan, kynurenine, serotonin, creatine, SDMA, ADMA, 1-MH, and indicators of carnitine palmitoyltransferase 1 and 2 enzymes) and those with low levels showed statistically significant differences in survival outcomes. We further used four metabolic markers (tryptophan, kynurenine, asymmetric dimethylarginine, and 1-Methylhistidine) to develop a COVID-19 mortality risk model through the application of multiple machine learning methods. These metabolic predictors can be further validated as potential biomarkers to identify patients at risk of poor outcomes. Finally, integrating machine learning models in metabolome analysis of COVID-19 patients can improve our understanding of disease mortality by providing insight into the relationship between metabolites and survival probability, which can lead to the development of potential therapeutics and clinical risk models.

BOOK OF ABSTRACTS

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INFECTIOUS DISEASES

Essential functions of RNA virus genome beyond the storage of protein-coding information

RNA viruses are a major threat to the human health. They are responsible for infections with high morbidity and mortality rates and an extraordinary socioeconomic burden. In the last decades, different RNA viruses have produced major outbreaks against which there were no efficient therapeutic strategies. Some recent examples are HCV, HIV, influenza A virus (H5N1), SARS, ZIKV, Ebola and SARS-CoV-2 being the most recent one, which in fact has demonstrated the great vulnerability of humanity as a whole and has managed to shake the most powerful economic structures. Many data indicate that the probability of new pandemic is high. The question is whether human beings are prepared for it. Viruses have to make use of the cellular machinery and interfere with the cellular defense strategies, using them to their advantage. The viral RNA genomes are compact entities, which carry all the information that the virus requires to successfully complete the infectious cycle. In addition, to the protein coding information RNA viruses store an important amount of their genetic information in highly conserved structural elements. These structural elements perform essential functions on their own, without being translated into proteins. Deciphering the mechanisms that underlie each of the functions they perform would provide information of enormous importance to understand the molecular mechanisms that govern the virus infection and replication cycles, and to address the control of infections caused by RNA viruses. The genomic functional RNA elements constitute a large repertoire of potential targets against which to direct RNA-binding molecules. Numerous studies have reported the function of genomic structural elements of different RNA viruses. In this talk, I will summarize the work carried out by our research group to identify and characterize the functional role of RNA elements of the HCV and WNV genomes primarily. The results provide clear evidences of the existence of a genomic network of RNA/RNA interactions that govern the regulation of the essential viral processes. Our work has also demonstrated the potential of interfering with the functioning of specific structural RNA elements of viral genomes to develop antiviral strategies.

Audience Take Away Notes

- Protein coding information only represents a small portion of the viral genetic load
- RNA viruses store essential information in the form of RNA structural elements
- RNA genomes can be considered as a sequence of cis-acting ncRNAs
- Potential therapeutic application of Interference with structural elements of viral RNA genomes

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Biography

Alfredo Berzal-Herranz Graduated in Biology in 1986 at the Complutense University of Madrid, Spain. Received his Ph.D in 1990, his work was supervised by Prof. Ramon Diaz-Orejas at the CIB-CSIC, Madrid. He spent three years as Postdoctoral fellow at Prof. John Burke, University of Vermont, USA. He joined the IPBLN-CSIC, Granada, Spain in December 1993, where he established his own research group. His main research interest is the Biological activity of the RNA. He has published near 100 research articles and is editor In-Chief of Biopharmaceuticals section of Pharmaceuticals. He has been Director of the IPBLN since 2005 to 2014.

- To think beyond the viral proteins
- To deepen in the molecular biology of RNA viruses
- To understand biological virus-cell interaction
- Yes, it is this research that other faculty could use to expand their research or teaching
- This is essential information that has not been considered so far when trying to understand the molecular mechanisms of viruses
- Provides new knowledge for the design antiviral strategies
- Information for alternative solutions
- Information to assist in the alternative design of potential solutions to address a problem

Comparisons of the molnupiravir, sotrovimab, and remdesivir use for COVID-19 patients in a tertiary hospital of Japan

Background: New antiviral agents for COVID-19, including molnupiravir for the oral treatment and sotrovimab as the monoclonal antibody for the intravenous treatment are currently authorized and available in addition to remdesivir for the intravenous treatment in Japan.

Methods: We investigate the clinical use of molnupiravir, sotrovimab, and remdesivir for COVID-19 patients in our tertiary hospital from January to May 2022, which was the omicron strains dominant term.

Results: 35 COVID-19 patients received the molnupiravir administration orally. Among the 35 patients, 32 patients were used combined with intravenous administration of sotrovimab. The patients were 67.3 years old (26-90 y.o) and all survived. In the same term, the patients treated by either sotrovimab alone or sotrovimab plus remdesivir were either 14 cases of 79.0 (63-92) y.o. or 26 cases of 59.3 (36-97) y.o., respectively. Furthermore, the mild/moderate patients treated by molnupiravir were 15/20 cases although all patients with sotrovimab alone were mild, and the patients treated by sotrovimab plus remdesivir were 19 mild and 7 moderate, respectively. All patients treated by sotrovimab plus remdesivir were survived similar to the patients treated by molnupiravir; however, one patient treated by sotrovimab alone was died.

Conclusions: Most of the molnupiravir were used in the combination with sotrovimab. Molnupiravir may be useful for the COVID-19 patients who could accept oral administration of antiviral agents in the clinical setting.

Seki Masafumi MD

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Biography

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

Quality control of infectious disease testing

Historically, testing for antibodies to infectious diseases was performed using biological assays such as haemagglutination inhibition or complement fixation. In recent times, this testing has moved to binding assays, firstly microtitre plate enzyme immunoassays and then to high throughput instruments. These instruments perform a range of testing for clinical chemistry, immunoassay as well as infectious diseases, and are commonly managed by the clinical chemistry laboratorians. It is not surprising therefore that approaches used to monitor the performance of clinical chemistry assays have been applied to infectious disease testing. However, infectious disease testing, in particular the detection of disease specific antibodies is quite different to the quantification of inert chemicals such as glucose and potassium. This session will comprise of three main presentations. The initial presentation will review the differences between testing for infectious diseases and inert chemicals. It will highlight the heterogeneity of antibodies compared with chemistry analytes, discussing the changes in antibodies throughout the maturation process, the differences in responses to different strains of organisms and review the concepts of antibody avidity and affinity. The presentation will also review the regulatory environment applied to the manufacture and registration of *In-Vitro* Diagnostics Devices (IVDs) used for infectious disease testing. The second presentation will discuss the complications experienced when applying traditional Quality Control (QC) rules to infectious disease serology and explain the deficiencies of traditional rules in this setting. The presentation will introduce the concept of QConnect, a QC monitoring approach designed for infectious disease testing that uses historical data to estimate QC acceptance limits. A comparison of Connect and other traditional QC approaches will be provided. The final presentation will be interactive QC case studies. Using true QC data, several real-world cases will be presented and discussed. This will emphasise the information presented in the first two presentations and give the participant a deeper understanding of the principles of QC especially where qualitative data that use numbers are concerned. It is expected the participant will better understand the nature of QC for infectious diseases and make informed decisions when implementing QC programs in their laboratory.

Audience Take Away Notes

- Better understanding of the differences between infectious disease serology and clinical chemistry testing
- Identify the reasons why using traditional QC methods are inappropriate for infectious disease serology, even when tested on automated platforms
- Offer a different approach to QC monitoring
- Provide options for introducing a more fit-for-purpose and efficient, cost-effective approach to QC of infectious disease testing

Wayne Dimech*, Giuseppe Joe Vincini*

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Biography

Wayne Dimech is Executive Manager, Scientific and Business Relation of the NRL, a WHO Collaborating Centre. Mr. Dimech obtained a B.App. Sci; an MBA and has two professional Fellowships. He specialised in serology. His research interests include the control and standardization of infectious disease testing. Mr. Dimech is an advisor for several working groups, including European Commission expert panels in the field of medical devices; ISO TC/212 WG5 Biosafety; Joint Committee for Traceability in Laboratory Medicine (JCTLM) – Nucleic Acid Testing and consultancies under the auspice of WHO. He has authored or co-authored about 50 peer-reviewed articles and three book chapters.

Applications and prospects of metagenomics in fish gut microbiota research

Diseases of microbial aetiology of economic significance have surfaced in the aquaculture sector leading to high mortality and economic losses for farmers. Various environment- friendly remedial measures have been taken up as an alternative to antibiotics to control microbial diseases. But before using any therapeutic product against bacterial diseases it is important to understand the degree of damage caused to gut microbiota as well as host- microbes interactions in relation to a particular pathological condition. The applications of metagenomics in aquaculture are an emerging tool to investigate the alterations of gut microbial communities during stress conditions. It also provides an opportunity to reveal microbial genetic diversity as well as their functional attributes in a comprehensive manner along with their contribution to health and disease. A study on the composition of gut microbiome of freshwater striped phantasies catfish and catla fish in healthy and during disease condition was carried out. The gut samples from healthy and *Aeromonas hydrophilic* infected fish were collected and pooled for metagenomic analysis. To understand the gut microbiota composition of healthy and disease affected fish, the community analysis was performed by targeting the 16s rRNA gene. The OTUs consisted of four major phyla, Proteobacteria, Bacteroidetes, Actinobacteria and Firmicutes. Taxonomic abundance of the microbiota at phylum, class, order, family, genus and species levels showed Bacteroides as the most dominant phylum in healthy phantasies fish whereas Firmicutes was dominant in diseased fish. Proteobacteria was dominant in healthy catla fish and Bacteroidetes was observed in abundance in infected fish. The paper further discusses various metagenomic approaches and future prospects in fish gut microbiota research.

Keywords: Metagenomics, Fish gut, Microbiome, Taxonomic abundance, Health and Disease

Audience Take Away Notes

- Complete profile on the gut microbiome and its responses during pathogenesis will generate substantial report on bacterial diversity that will provide important insights into the microbial ecology and adaptability of gut microbiome during different stages of disease progression. A better understanding of the intricate microbial players will help in finding the best possible solution
- Such studies will help to understand the utilization of gut microbes that exhibits a positive effect on the animal health and thus lead to the usage of potential microbes as probiotics

Gayatri Tripathi*, R. Bharathi Rathinam

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Biography

An accomplished scientist and experienced professional, armed with a Ph.D. degree in Life Sciences. She is working as Principal Scientist in the Aquatic Environment and Health Management Division of ICAR-Central Institute of Fisheries Education, Mumbai. She possesses comprehensive experience in aquatic animal diseases & their diagnostic research encompassing embryonic stem cell biology, Nano toxicology, and immunotoxicology. A recognized researcher with an enviable track record of scientific achievements through publications as well as researching and implementing new scientific concepts and procedures. More than 60 publications in international journals and national journals, having 1635 citations, i10 index-31 and h-index of 20.

The role of novel cold atmospheric plasma technology in preventing infectious diseases

Infectious diseases are becoming a health burden, causing numerous hospitalisation cases and deaths and leading to global economic losses. The prevention and control of infectious diseases have become more important as a result of the COVID-19 pandemic. Traditional disinfection methods are inadequate nowadays due to their numerous drawbacks. Therefore, novel, innovative solutions are needed to disinfect infectious disease-causing microorganisms. Thus, cold atmospheric plasma is the most contemporary no thermal technique being explored in the field of medicine and food science at present. The cold atmospheric plasma operates at sub-lethal or room temperature driven by high voltage field electric, and the plasma is generated between electrodes with dielectric barriers preventing spark formation. Moreover, it is an environmentally friendly technique that is easy to operate and cost-effective. The cold atmospheric plasma has been employed to disinfect or inactivate viruses such as the SARS-CoV-2 virus, wounds such as skin diseases and cancers, medical instruments, heat-sensitive medical materials and irregular geometric medical surfaces. The plasma-generated reactive species have been revealed to be responsible for the pathogens' disinfection or inactivation by acting on the virus's capsid proteins and/or nucleic acids. Consequently, cold atmospheric plasma is powerful in disinfecting and inactivating bacterial, fungal and viral infections, enabling wound healing, preventing cancer spread, and improving psoriatic or vitiligous wounds. Hence, utilising the novel cold atmospheric plasma in preventing infectious diseases could be a revolutionary approach that can increase clinical success in the field of infectious diseases.

Audience Take Away Notes

- They will learn about cold atmospheric plasma technology
- They will learn the various applications of cold atmospheric plasma
- They will learn the mechanisms of the cold atmospheric plasma
- They will learn the future research trends on cold atmospheric plasma
- The audience can utilise the cold atmospheric plasma in almost all aspects of their job
- It will make the audience work faster and more effectively.
- This research can help other faculty to expand their research or teaching knowledge.
- Indeed, this presentation will provide a practical solution to problems that could simplify or make a designer's job more efficient
- It will improve the design accuracy and provide new information to assist in a design solution for a problem

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Biography

Prof Chunyang Li attended Heilongjiang College of Commerce and obtained a Master's degree (Food Engineering) in 1992. He obtained his PhD (Food Science) degree in 2006 from Jiangnan University. He joined the Institute of Agricultural Products Processing, Jiangsu Academy of Agricultural Sciences, in 2006. He served as a visiting scholar in Alberta University and University of Manitoba, Canada from 2008 – 2009 and 2015 – 2016, respectively. He has published over 120 papers in highly reputed journals, presided over 40 national and provincial projects, and had 15 national-authorised invention patents. Also, he has trained 5 doctoral students and more than 40 master's students.

Potential of *Lactobacillus plantarum* in amelioration of LPS-induced infertility in mouse model

Bacterial infections in the genital tract are one of the causes of female infertility worldwide with a prevalence rate of 30–40 %. Infertility in these cases is generally recognized as a consequence of inflammation. Bacteria may lead to inflammation due to the presence of LPS, as it is the foremost and an abundant component of the outer membrane of the cell wall of Gram-negative bacteria. Being one of the primary modulators of the inflammatory response in the host, LPS is widely used to stimulate in vivo inflammation. Recently, advancements in probiotic research and their effect on disease and host immune systems, such as alleviation of allergic symptoms and of inflammatory bowel disease, have been reported. It appears that probiotic lactobacilli may produce a potential anti-inflammatory response, and hence it can be speculated that they might play a therapeutic role in inflammation-induced infertility. Therefore, in the present study, LPS from *Escherichia coli* was used to induce inflammation in the mouse vagina in order to study its effect on fertility outcome to assess the role of the probiotic *Lactobacillus plantarum* in amelioration of LPS-induced inflammation and infertility. For this, BALB/c mice were infused intravaginally with a single dose of 20 ul sterile normal saline containing 5, 10 or 20 ug LPS and divided into two groups for evaluation of tissue histology and pregnancy outcome. In the first group, aimed at observing changes in tissue histology, inflammation was observed in vaginal sections of mice instilled with a single dose of 20 ug LPS, which were sacrificed on days 2, 5 and 8. In the second group, aimed at evaluating pregnancy outcome, female mice were administered 20 ug LPS, which rendered them infertile upon mating on days 2, 5 and 8. In another experiment, normal histology of vaginal sections was observed in mice administered a single dose of 20 ug LPS, followed by 10^8 cfu. *L. plantarum* in 20 ul at 24 h intervals, until the mice were sacrificed on days 2, 5 and 8. Following similar treatment, female mice, when mated with proven male breeder mice on days 2, 5 and 8, retained their fertility and delivered pups. These results were further confirmed by the downregulation of pro-inflammatory cytokines and an increase in anti-inflammatory cytokines on treatment with *L. plantarum*, revealing the role of probiotics in ameliorating inflammation-induced infertility.

Audience Take Away Notes

- The audience will get deeper insights into how probiotics can lead to amelioration of infertility induced by microorganisms
- This research can be used further to understand the mechanisms of amelioration by *Lactobacillus plantarum*
- Alternative measures can be exploited to ameliorate the infertility caused by various microorganisms

Praveen Bhandari, Praveen Rishi, Vijay Prabha*

Department of Microbiology, Panjab University, Chandigarh, India

Biography

Dr. (Mrs.) Vijay Prabha is working as Professor in the Department of Microbiology, Panjab University, Chandigarh, India. She has 30 years of teaching and 40 years of research experience. Her area of expertise is Role of microorganisms in male and female infertility and exploitation of microbial factors as male and female contraceptive agents. She has guided number of M.Sc. and Ph.D students. She has about 97 publications in national and international journals. She has also presented her work in various national and international conferences as an invited speaker. She is life member of Association of Microbiologists of India and Panjab University Research Journal of Science. She is editorial board member of various international and national journals.

The monogenic conception of disease: How to avoid some pitfalls in understanding it in the context of sars-cov-2/ COVID-19

Louis Pasteur (1822-1895) and Robert Koch (1843-1910) are the intellectual giants who pioneered the Age of Bacteriology in the nineteenth century. Pasteur developed a vaccine against anthrax while Koch discovered the cause of tuberculosis to be the tubercle bacillus in 1882, for which he received the first Nobel Prize in Physiology (and Medicine) in 1905. This discovery is an instantiation of what has come to be called the Monogenic Conception of Disease. Simplistically put, this is: one cause (the pathogenic micro-organism), one effect (the disease in terms of its signs and symptoms in the patient infected by the pathogenic micro-organism). This model of disease causation has been extended to cover not only pathogenic bacteria but also viruses as well as other factors including defective genes. Hence, SARS-CoV-2, the pathogenic virus is said to be the cause of COVID-19 (the disease).

Unfortunately, owing to some ambiguity with which Koch had formulated his postulates, some confusion has crept into the understanding of the Monogenic Conception of Disease. I contend that the confusion is due to a failure to distinguish between what I call the Classical Version on the one hand, and (following Stewart 1968) when it is held as a dogma, on the other. The Classical Version refers to a profound change in the paradigm of scientificity in Medical Thinking which constitutes a demarcation line between what is pre-Modern (Western) Medical Thinking and Modern (Western) Medical Thinking. Pre-Modern (Western) Medical Thinking rested on the Humoral Theory (based on the work of Galen, the ancient Greek physician) which held that good health depended on a balance of four fundamental fluids in the human body: blood, yellow bile (choler), phlegm and black bile. Besides the Humoral Theory, other theoretical approaches included the Miasma Theory which held that diseases were caused by unhealthy vapours rising from the ground or from decomposed material – a kind of environmental model of disease causation. However, since Pasteur and Koch, from the standpoint of authoritative Modern Science-Medicine, pathogenic micro-organisms are held be the cause of infectious diseases. The other context involves understanding the Monogenic Conception of Disease in an over-simplistic fashion by failing to distinguish clearly between necessary and sufficient conditions, overlooking the understanding of the cause of a phenomenon in terms of both its necessary and sufficient conditions. Being exposed to and infected by SARS-CoV-2 is only a necessary condition but unless the infected person also happens to satisfy other sufficient conditions, the person would not succumb to the disease in spite of being infected by the pathogen. One needs to grapple with the notion of inter-connected complexities in disease infection and expression or manifestation.

Keekok Lee

Honorary Research Fellow
Faculty of Humanities University of Manchester, UK

Biography

Keekok Lee is a graduate in philosophy of the University of Singapore, the University of Oxford, and the University of Manchester. She taught briefly at the University of Singapore before joining the University of Manchester where she remained until she took early retirement in 1999. Since then, she has continued to be active in research and publication, affiliated initially to the University of Lancaster, and latterly to the University of Manchester as Honorary Research Fellow.

Audience Take Away Notes

- The audience will understand illness and disease in their inter-connected complexities
- It will help the audience to arrive at a proper diagnosis of the patient's condition which in turn will lead to appropriate treatment or appropriate treatments
- Yes, this research that other faculty could expand their research
- Yes this provide a practical solution to a problem that could simplify or make a designer's job
- Yes it improve the accuracy of a design, or provide new information to assist in a design
- Understanding and grasping the concept of inter-connected complexities should help not simply in the context of infected diseases but all forms of disease, including even mental health condition. The concept is intended as an analytic tool – it is up to each researcher to adapt the tool for their own research purposes

Selection underlying evolution and spread of SARS-CoV-2 variants

The Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) is a highly infectious RNA virus that was first identified in December 2019 in Wuhan, China. It is the pathogen responsible for the present coronavirus disease 2019 (COVID-19) pandemic. A large number of genetic variants of the original Wuhan-Hu-1 strain of the virus have rapidly evolved and spread throughout the world. Selective forces driving genetic changes in SARS-CoV-2 differed between the early stages of the pandemic and later after widespread COVID-19 infection and vaccination. The different immunological and virological causes for the evolution of SARS-CoV-2 variants and their rapid spread will be summarized, and its evolution compared with that of the Influenza a RNA virus.

Audience Take Away Notes

- Appreciate molecular biology of RNA viruses, virus evolution and immunity to viruses
- Assist teaching of public health, epidemiology, immunology and virology
- Help develop research ideas to advance knowledge on SARS-CoV-2 virus and COVID-19
- Establish and promote collaborative research links in the field
- Improve knowledge of the current pandemic and help develop measures to mitigate its effects

Ranjan Ramasamy

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Biography

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

Novel nasal formulations containing ec16 to combat long COVID

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. By Dec 1, 2022, over 643 million cases have been reported worldwide, with 6.63 million people lost their lives. 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 hypothesize that EGCG-palmitate (EC16), a compound with a broad spectrum of antiviral activities, has potential to become a new drug agent against SARS-CoV-2 replication in nasal epithelial cells, thereby minimizing post COVID neurologic symptoms.

Method: Formulations suitable for intranasal applications were developed and tested in vitro against human α coronavirus 229E (CoV-229E) and β 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 (#18) suitable for animal and human tests was selected and tested in comparison of Remdesivir in cell culture infection systems following two test protocols (with or without direct contact with the virus).

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 #18 was able to inhibit viral infectivity by >99.99%, exceeding the efficacy of Remdesivir. To the best of our knowledge, this result represents the first approach using EC16-containing nasal formulations to inhibit human coronavirus. Future studies are planned to investigate the *in vitro* and *in vivo* efficacy against SARS-CoV-2 variants (on going) and suitability for clinical trials toward new drug application.

Conclusion: With its, antiviral, antioxidant, anti-inflammatory, and neuroprotective properties, EC16 in nasal formulations could be further developed for clinical applications to COVID-19 patients for minimizing Long COVID neurologic symptoms.

Stephen Hsu

Dental College of Georgia, Augusta University, Augusta, GA, United States

Biography

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

Audience Take Away Notes

- Understand the neurologic symptoms caused by SARS-CoV-2 infection
- Understand how natural and non-toxic compounds could be applied in antiviral nasal formulations
- Understand the advantages of nasal drug delivery to combat respiratory virus infection and protect the brain from virus-induced damages
- Gain knowledge of new technologies and novel formulations developed to prevent neurologic symptoms

Novel functions of IRF3 in viral infection and inflammation

Virus infection causes various types of diseases in humans, and the innate immune responses serve as the first line of defense against viruses. Virus infection causes rapid induction of antiviral and inflammatory genes in the infected cells, leading to the establishment of an antiviral state in the host. Virus infection is recognized by the pattern-recognition receptors, which activate the transcription factors IRF3 and NF-κB, to induce antiviral genes, e.g., Interferons (IFNs). IFNs further amplify the response by inducing IFN-Stimulated Genes (ISGs), which specifically inhibit the steps of the viral life cycle. Recently we performed a high throughput screen to isolate novel ISGs against virus replication. Our screen revealed TDRD7, a novel ISG that inhibits virus-induced autophagy to suppress virus replication. It has become increasingly clear that in addition to viral load, virus-induced inflammation is a major determinant of viral pathogenesis. Our studies revealed that IRF3 inhibits viral inflammation by inhibiting NF-¤B, the major transcription factor responsible for inflammatory gene induction. We used various cell types to show that IRF3 deficiency caused enhanced NF-kB activation and inflammatory responses. IRF3 deficiency causes susceptibility to viral diseases, and both ISG-inducing and anti-inflammatory functions contribute to the protection. Targeting these pathways may help reveal new therapeutics that can be applied to treat viral infection.

Audience Take Away Notes

- Audience will learn how innate immune response provides antiviral protection
- The audience can use the knowledge to enrich their teaching and research
- Novel therapeutics can be developed in the future

Saurabh Chattopadhyay[1*], Sukanya Chakravarty[1], Shumin Fan[1], Amol Koli[1], Nathan Pan[1],

Suneha Shelke[1], Amal Kachour[1], and Ritu Chakravarti[2]

[1]Department of Microbiology and Immunology, University of Toledo College of Medicine and Life Sciences, Toledo, OH, USA

[2]Department of Physiology and Pharmacology, University of Toledo College of Medicine and Life Sciences, Toledo, OH, USA

Biography

Saurabh Chattopadhyay, Ph.D., is an Associate Professor in the Department of Medical Microbiology and Immunology at the University of Toledo College of Medicine and Life Sciences, Toledo, Ohio, USA. He is a virologist studying respiratory virus infection and its interaction with host immune responses. His laboratory has been involved in the state and university-wide COVID-19 surveillance program using wastewater testing. Research in his laboratory is funded by the National Institutes of Health, Ohio Department of Health, Center for Disease Control, American Heart Association, Medical Research Society, and UT-COMLS. He graduated from the Indian Institute of Technology Delhi in Biotechnology and did a postdoctoral fellowship in Virology at the Cleveland Clinic. He moved to the University of Toledo as an Assistant Professor in 2016.

21-22 JUNE

DAY 02

VIRTUAL SPEAKERS

4th Edition of World Congress on INFECTIOUS DISEASES

Nai An Lai
Intensive Care Services, Mater Health, Brisbane, Queensland, Australia
School of Medicine, Griffith University, Brisbane, Queensland, Australia

Molecular diagnostics in critically ill patients with severe pneumonia

Severe pneumonia is one of the most common causes of sepsis and respiratory failure requiring intensive care. Despite advances in diagnostic techniques, antimicrobial therapy, respiratory support and organ support modalities; mortality and morbidity of severe pneumonia remain significantly high. In this session, epidemiology of severe community acquired pneumonia and hospital acquired pneumonia will be discussed. Current challenges in management of severe pneumonia will be highlighted. A broad overview of current and emergency molecular and syndrome testing for severe pneumonia will be provided including a discussion of advantages and limitations of such technique. A summary of current research into molecular diagnostics in severe pneumonia will be provided and future research directions will be explored.

Audience Take Away Notes

- Epidemiology of severe community acquired and hospital acquired pneumonia requiring intensive care
- Current challenges in the management of severe pneumonia in the ICU
- Benefits and limitations of molecular diagnostics in the management of severe pneumonia
- Current and future research directions

Biography

Dr Lai is the Director of Intensive Care Services at Mater Health and an Associate Professor at Griffith University. He graduated from Monash University Medical School holds the Fellowship of the Royal College of Physicians of Edinburgh, Royal College of Surgeons of Edinburgh, College of Intensive Care Medicine of Australia and New Zealand and the Royal Society of Medicine. He attained the European Diploma in Intensive Care Medicine and has a Postgraduate Diploma in Echocardiography and Clinical Ultrasound from the University of Melbourne. Dr Lai is the founder, convener and faculty member of a number of courses and symposia including the Basic Intensive Care Medicine (BICMed) course, A-B-C Critical Skills for ICU, the Australian Short Course in Intensive Care, Basic Assessment and Support in Intensive Care (BASIC), Antimicrobial Master class (AIM) for Acute Care Practitioners, Short Course in Critical Infections and the Advanced Diagnostic and Physiological Monitoring in Critical Care (ADP-MoCC) Symposium. Dr Lai is a reviewer for the Respiratory Care journal and an expert consultant on mechanical ventilators for the Therapeutics Goods Administration (TGA) of Australia.

Jing Wan, Shuyun Liu*

Science and education department of Wenjiang district People's Hospital of Chengdu City, Sichuan Province, P. R. China

Research on the mental health of medical interns in clinical teaching base in the post-pandemic era - data from China

Background: During the COVID-19 epidemic, depression of medical staff showed a worsening trend year by year. Interns in clinical teaching bases who are also in the front line of the fight against the epidemic are more likely to have mental health problems due to the unfamiliar environment and lack of experience in epidemic prevention and control. It is necessary to investigate their mental health status and explore the corresponding countermeasures.

Methods: Symptom Checklist 90 (SCL-90) and Simple Coping Style Questionnaire (SCSQ) were used to investigate the somatization symptoms and coping styles of 312 medical interns in December 2022, and their symptom self-test scores were compared with the Chinese youth group norm results.

Results: The average scores of somatization, compulsion, interpersonal sensitivity, depression, anxiety, phobia, paranoia and psychosis of the interns in the base were higher than those of the Chinese youth group norm, and the differences were statistically significant ($P < 0.05$). There were significant differences in somatization and phobic factor scores between male and female interns ($P < 0.05$). There were significant differences in the scores of nine factors among interns with different educational levels ($P < 0.05$), and the scores of each factor of interns with bachelor's degree or above were higher than those of interns with college degree. The score of negative coping style was positively correlated with the total score of negative factors of mental health (somatization, compulsion, depression, anxiety) ($\beta=-0.569$, $P < 0.05$). Positive coping style was negatively correlated ($\beta=0.899$, $P < 0.01$).

Conclusion: The mental health level of interns in the base in the post-pandemic era is lower than that of the national youth norm, and there are statistically significant differences in the mental health level of interns with different genders and educational levels. Negative coping style can significantly affect their mental health status. Bases, schools, families and the society should pay attention to the mental health problems of medical interns, carry out effective psychological intervention in time, and adopt positive coping methods to ensure the physical and mental health of interns during the epidemic.

Diana Gonzaga Ramos MD[1*], Arthur Dessi E. Roman MD[2]

[1]Fellow-in-training, Medical Department – Research Institute for Tropical Medicine, Muntinlupa City, Philippines

[2]Medical Specialist, Medical Department – Research Institute for Tropical Medicine, Muntinlupa City, Philippines

Determinants of early virologic failure among HIV patients on first-line anti-retroviral therapy

Background: The initiation of Anti-Retroviral Therapy (ART) effectively restores immune function and reduces HIV-related morbidity and mortality. However, virologic failure while on ART may lead to increased morbidity and compromised quality of life. The aim of this study was to determine the prevalence and determinants of early Virologic Failure (VF) among HIV patients on first-line ART enrolled at the Research Institute for Tropical Medicine, Philippines.

Patients and methods: A retrospective cohort study was conducted involving treatment-naïve HIV patients who were started on ART during the period of January 2004 – December 2018. Early virologic failure was defined as HIV-1 viral load of > 1,000 copies ml of plasma blood taken within 6 months or more of first-line ART. Data regarding patients' sociodemographic profile, baseline clinical characteristics, and treatment-related information were collected through database review. Data were analyzed using STATA 15.0. Descriptive statistics, cross-tabulations, and univariate and multivariate logistic regressions were utilized. P<0.05 was used to determine clinical significance.

Results: Among the 1900 subjects included in this study, 1839 were males (96.79 %). The mean age at ART initiation was 30.36 years (SD 6.89) with a baseline CD4 count of 232.30 cells / mm3 (SD 204.19). The average time from ART initiation to the first VL determination was 4 years (SD 28.62). A total of 72 (3.79 %) subjects were found to have virologic failure. Younger age (15-20 years), baseline CD4 count <50 cells/ mm3, and TB co-infection were found to be significant predictors of early virologic failure in the univariate logistic regression analysis. Multivariate logistic regression showed that patients with age 15-20 years were 5-6 times more likely to have VF (1 / adjusted OR 0.18 = 5.55, p-value of 0.024) while patients with baseline CD4 count of <50 cells/mm3 were 3 times (1 / adjusted OR 0.35 = 2.86, p-value <0.01) more likely to have virologic failure.

Conclusion: The prevalence of early virologic failure among HIV patients on first-line anti-retroviral therapy is 3.79 %, relatively lower compared to other published data. Early virologic failure was most likely to occur among patients 15-20 years old and/or those with baseline CD4 count below 50 cells/mm3. Presence of these factors should be used as a marker for intensified adherence counselling especially in the absence of reliable or readily available viral load monitoring.

Keywords: HIV, Early virologic failure, Risk factor, Anti-retroviral drugs, First-line anti-retroviral therapy

Audience Take Away Notes

- To the knowledge of the principal investigator, this study provides the first local data for early HIV virologic failure in the Philippines
- This study highlights the need for intensified adherence counselling in the presence of risk factors for early virologic failure
- This study also emphasized special attention to early tuberculosis diagnosis during ART enrollment being a possible risk factor in early virologic failure which can also be used in future studies

Biography

Dr. Diana Gonzaga Ramos is a practicing internist and infectious disease specialist in Las Pinas City and Muntinlupa City, Philippines. She completed her Medical Degree at Pamantasan ng Lungsod ng Maynila in 2007. She finished her residency training in Internal Medicine at Ospital ng Makati in 2013 and completed her subspecialty training in Infectious Diseases at Research Institute for Tropical Medicine in 2019. She is also a Fellow of the Philippine College of Physicians and a Diplomate of the Philippine Society for Microbiology and Infectious Diseases.

Maria Yvez Erika P. Ugale*, M.D,FPCP, Rontgene M. Solante, MD, FPCP, FPSMID, Edna M. Edrada, MD, FPCP, FPSMID, Ruel O. Teano, MD, MGM, FPAMS, FPSV

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Bacterial co-infection and secondary infection in SARS-CoV-2 (COVID-19) adult patients in a national tertiary infectious disease hospital

Introduction: The SARS-CoV-2 virus, the main causative agent of COVID 19 infection was first detected in the province of Hubei in Wuhan China in December of 2019 and has overwhelmed the capacity of the government and hospitals to provide healthcare services to cater to the growing number of COVID-19 confirmed cases. In relation with the exponential growth of COVID-19 confirmed cases in the Philippines, there is need to fill the gap in knowledge regarding the use of antibiotics for the treatment of COVID-19. An understanding of bacterial co-infections and secondary infections, the causative pathogen and antimicrobial use is vital for treating patients with COVID-19. This information will help in optimizing empirical antimicrobial management strategies, ensure responsible use of antibiotics hence minimizing misuse and overuse. Furthermore, this knowledge will have a significant impact in antimicrobial stewardship.

General Objective: To describe microbiologically confirmed co-infections (upon admission) and secondary infections (during admission), and antimicrobial use, in patients admitted to a tertiary hospital with COVID 19.

Methodology: Retrospective research design was used in the study. Demographic data pertinent to this study were the following: age, past medical history, recent antibiotics use and pertinent physical examination. Any positive cultures from blood, sputum, or deep respiratory samples were considered COVID-19 related infections, while growths from other sample types were considered unrelated. Cultures that showed as mixed growth, colonizer or contaminant were excluded from all sample types.

Result: The most common clinical symptoms of COVID 19 patients with bacterial co-infection and secondary infection were cough (79.7%), fever (77%) and dyspnea (68.9%). Out of 74 patients 31.1% were given high flow nasal cannula oxygen support. Most of these patients had severe and critical COVID 19 infection in 32.4% and 47.3% respectively. Among the admitted patients the most common bacterial co-infection isolates were *Klebsiella pneumoniae* (26.9%), *Acinetobacter baumannii*, *Staphylococcus aureus* and ***Haemophilus parainfluenzae*** (11.5%) while for secondary infection *Klebsiella pneumoniae* (33.3%), *Stenotrophomonas maltophilia* (18.7%) and *Pseudomonas aeruginosa* (16.6%). The most common antibiotics administered upon admission were Ceftriaxone (51.4%) and Azithromycin (41.9%). Antibiotics prescribed 48 hours after admission were Meropenem (31.1%), Levofloxacin (28.4 %) and Piperacillin tazobactam (20.3%). Among patients included in this study 62.2 % were discharged improved.

Conclusion: The overall incidence of patients who tested positive with COVID-19 patients with bacterial co-infection and secondary infection from February 1, 2020 to December 31, 2021 is 3.35%. Out of 2210 patients who tested positive with COVID-19 from February 1, 2020 to December 31, 2021 only 74 (3.35 %) patients had bacterial co-infection and secondary infections.The most common bacterial isolates among COVID 19 patients with bacterial co-infection were *Klebsiella pneumoniae* (26.9%), *Acinetobacter baumannii*, *Staphylococcus aureus* and *Haemophilus parainfluenzae* (11.5%) while for secondary infection *Klebsiella pneumoniae* (33.3%), *Stenotrophomonas maltophilia* (18.7%) and *Pseudomonas aeruginosa* (16.6%). Antibiotic use in admitted COVID-19 patients was high regardless of low incidence of bacterial pneumonia during the first pandemic wave.

Audience Take Away Notes

- An understanding of bacterial co-infections and secondary infections, the causative pathogen and antimicrobial use is vital for treating patients with COVID-19
- This information will help in optimizing empirical antimicrobial management strategies, ensure responsible use of antibiotics hence minimizing misuse and overuse
- Furthermore, this knowledge will have a significant impact in antimicrobial stewardship

Biography

Dr. Maria Yvez Erika P. Ugale graduated at Far Eastern University Dr. Nicanor Reyes Medical Foundation. She finished her residency in Internal Medicine at Mariano Marcos Memorial Hospital and Medical Center. She recently finished her fellowship training program in San Lazaro Hospital, Manila, Philippines.

Rajaa Sulaiman Al Aamri[1*], Badriya Al Adawi[2], Laila Al Yzidi[3], Hilal Al Hashami[4], Amal Al Jabri[5]

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Burden of invasive group b *Streptococcus* infection among infants less than 90-day old in Oman: A multicentre study

Aim of study: Group B Streptococcus (GBS) is a leading cause of invasive infection among neonates and infants worldwide, with two described syndromes, Early Onset GBS (EOGBS) disease and Late Onset GBS (LOGBS) disease. In our study, we investigated the incidence of invasive GBS disease among infants less than 90-day-old in three tertiary hospitals in Oman and described their risk factors, clinical presentations, and clinical outcome.

Methods: We retrospectively collected data of less than 90-day-old Omani infants with culture-positive GBS from sterile samples from three tertiary hospitals in Oman (RH, SQUH and KH) from 2009 to 2018. Their clinical data was reviewed to identify risk factors, clinical presentations, and complications during admission, neurodevelopmental sequelae, and clinical outcome. The data was analysed using SPSS version 23.0 and P-value of less than 0.05 was taken as significant. The incidence was calculated per 1000 live births.

Results: Over 10 years, we identified 92 cases of culture-confirmed invasive GBS infection from 178,285 live births in the study-hospitals, giving the overall incidence of 0.53 per 1000 live births (95% CI 0.4 to 0.7). Of those, 64.1% (n=59) had EOGBS disease and 35.9% (n=33) had LOGBS disease. The annual incidence of invasive GBS disease was significantly higher in the last five years from 2009 to 2013 (0.69 per 1000 live births, 95% CI 0.5-0.9) compared to the previous years from 2014 to 2018 (0.69 per 1000 live births, 95% CI 0.5-0.9), (P=0.004). A significant increase in annual incidence of invasive GBS disease was observed over the study period. Infants in the LOGBS disease group had a higher risk of meningitis compared to EOGBS disease group (30.3% vs 10.2%, P=0.021). The mortality rate was 13.5% and of the remaining survived infants, only 43 infants were followed up. About 12% of them developed neurodevelopmental impairment following invasive GBS disease.

Conclusion: The incidence of invasive GBS disease in Oman is similar to what was reported worldwide, however the burden of the disease in terms of complications and mortality is high. In addition to that, a significant increase in annual incidence of invasive GBS disease in Omani infants was found over the study period. Therefore, measures to prevent perinatal transmission need to be emphasized and implemented. Further studies considering the potential benefit of universal culture-based screening of pregnant women on the burden of invasive GBS disease in Oman is needed, and studies considering serotypes and maternal vaccination needs are recommended.

Audience Take Away Notes

- The burden of neonatal invasive GBS disease
- Measures to prevent perinatal transmission of GBS

Biography

Dr. Rajaa Al Aamri Studies Medicine in Sultan Qaboos University and graduated on 2013. She completed Medical Microbiology Residency program on 2022.

Georgios D. Theodorakopoulos
Queen Margaret University, Greece

Facial pressure ulcers incidence within pandemic in critical care depts are there feasible strategies to prevent this complication?

The last 2 years after breakout of Covid pandemic there have been reported and published skin integrity complications mostly in critical care department's covid infected patients. International literature highlights the spread per 57% of facial pressure ulcer development, as consequence of critical care patient prone position, basic therapeutic element which minimize respiratory distress and reduce possible atelectasis presence. Increased number of hospitalized covid patients entering ICU on the onset of pandemic led to prolong hospital stay and cohort measures. On the other hand, mechanical force (mostly because of pressure >32mmHg and shear) in face (cheek), ears and chest area maximized magnitude of skin complication and put extra stress to intensivists and critical care dept. staff of how they could avoid skin damage without discounting lung therapy and patient discharge. Aim of presentation is to sum up worldwide literature around FPU's incidence and impact, explaining critical care environment limitation for prevention of skin complications and feasible treatment options. Moreover, taking into consideration covid generated issues such as quality of health services within critical care, staff need for minimal contacts to avoid cross-contamination, possible lack of medical consumables and low skin integrity protocol compliance due to understaffing and difficulty in inspection of patient skin status. It is suggested from clinicians that tackling FPU's in critical care to be a special focus prior to prone positioning including increase of skin protocol compliance, improved preventative measures, assess patients with fragile skin or malnourished, ensure offloading and redistribution of pressure. Finally, active involvement of more medical professions in critical care dept with expertise around skin complications to those areas such as ENT, Dermatologists and Wound Specialists would help dept. to report lower FPU's incidence rate.

Audience Take Away Notes

- Audience will be able to implement take away messages around strategic prevention of FPU's in critical care by following a specific bundle of care around skin integrity during prone position
- Presentation will provide insights and condensed knowledge on how to protect skin at risk covid patients without jeopardizing respiratory therapy. Audience will be able to review robust up-to-date evidence and clarify available and feasible solutions by classifying initial and final steps of their future prevention FPUs strategy
- Audience will have the opportunity to hear a wound expert with over of 13 years' experience in acute and chronic/ hard-to-heal wounds, former ICU Nurse well established in regional level among peers

Biography

Mr. Theodorakopoulos studied RN at Technological Institute of Patras and graduated in 2009. He worked for 4 years in neonate and adult ICU of Univ. Hospital of Patras and Olympion Clinic. In 2013 enter medical device market and worked for leading multinational companies as Clinical & Education Specialist. His passion around wound care and socioeconomic impact led him to receive an MSc in Wounds Care and an MBA in Health Economics. Currently he is a student of Podiatric Medicine (Queen Margaret Univ). He holds a certification in IC. Lecturer in national and international conferences around wound treatment-skin integrity and IC.

Jaime David Acosta-España*, Rida Al, Dolly E. Montaño, Hea-Reung Park, Mohamed A. Hassan, Hans-Martin Dahse, Susann Hartung, Marie von Lilienfeld-Toal, Axel A. Brakhage, Kerstin Voigt

University of Jena, Germany

In vitro whole leukocyte infection model and detection of Hydrophobic surface-Binding Protein A (HsbA) in L. *Corymbidera*

Mucormycosis is a fungal infection caused by members of the order Mucorales, the most prominent group among zygosporic fungi (formerly ascribed to Zygomycetes). A total of 26 mucoralean species can infect humans. Among these, the highest proportions of infections are caused by *Rhizopus arrhizus* (ex: *R. oryzae*), *Mucor circinelloides*, and *Lichtheimia corymbifera*. In this study, we present the interaction between *L. corymbifera* with professional phagocytes which represents the first line of defense after infection. We demonstrate an *in vitro* whole leukocyte infection model and detection of Hydrophobic surface-Binding Protein A (HsbA) by Liquid Chromatography-Mass Spectrometry analysis (LC-MS /MS). Initially, our analysis revealed the presence of the predominant spore coat protein (CotH) and HsbA on the surface of *L. corymbifera* sporangiospores. Interestingly, it was possible to detect the secretion of HsbA by *L. corymbifera* spores. Subsequently, coinfection (MOI 1:2) of leukocytes (1) with *L. corymbifera* spores (2) allowed detection of HsbA in the supernatant after 72 hours by LC-MS / MS. Finally, HsbA was shown to bind predominantly to monocytes and macrophages. In addition, this work established the antiproliferative and apoptosis-inducing effects of HsbA on MH -S cells. Altogether, our results suggested that HsbA plays a key role in interaction with the host immune system and helps to unravel the pathogenicity mechanism during mucormycosis.

Biography

Jaime David Acosta España graduated with a medical doctorate from the Central University of Ecuador in 2014. In Brazil, he completed postgraduate studies in medical microbiology at the Federal University of Ceará with a scholarship from the Organisation of American States.In Spain, he completed a Master's degree in Infectious Diseases and another Master's degree in Human Immunodeficiency Viruses. At Harvard,he completed the Training to Teach in Medicine certificate. He was the head of medical microbiology in 4 public and private hospitals in Quito. He worked as an infectious disease consultant for Padre Carollo Hospital in Quito. In 2020 he was invited to be part of the Emergency Response Committee in Ecuador for COVID -19. in 2021, he received a research award from the National Institute for Research and Public Health (INSPI). He is currently working as a research associate at the University of Jena, Germany, in association with the Leibniz Institute for Natural Product Research and Infection Biology e. V. Hans Knoell Institute. And he is a professor of the Postgraduate Programme in Infectious Diseases at the Pontificia Universidad Católica del Ecuador. He is also doing his Ph.D. in Microbiology and Infection Biology at the University of Jena, Germany.

Waqar Ahmad[1*], Bushra Gull[1], Jasmin Baby[1], Erum Rehman[3], Asif M. Salim[3], Rubina Lone[4], Hamda H. Khansaheb[5], Maya M.H.D. Zahri Habou[3], Laila Mohamed Jasim Ali AlDabal[3], Saif S. Alqassim[6], Alawi Alsheikh-Ali7, Tahir A. Rizvi[2], Farah Mustafa[1]

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Identification of microRNAs dysregulated in SARS-CoV-2 infected patients in the ethnically-diverse population of the United Arab Emirates (UAE)

The Severe Acute Respiratory Syndrome Coronavirus-2 (SARS-CoV-2) has infected more than 760 million people globally with over 6.8 million deaths to date due to COVID-19. Alteration of the host immune system upon infection can lead to multi-organ failure followed by critical pathological consequences at both clinical as well as molecular levels. Our study aimed to identify differentially-regulated microRNAs (miRNAs) in SARS- CoV-2-infected (COVID-19-positive), ethnically-mixed population in the United Arab Emirates. miRNAs was used to identify the dysregulated miRNAs in nasal swab samples collected from COVID-19 patients in the Emirate of Dubai. This was accomplished by recruiting 25 healthy controls and 132 infected patients diagnosed with mild, moderate, or severe COVID-19 or those who had recovered from the disease. Several bioinformatics tools were used to predict the target genes followed by network analysis. Out of 1818 detected miRNAs, 85 were detected as differentially regulated miRNAs with FC≥1 and 48 with FC≥2. GO and pathway analysis of the possible target genes regulated by these miRNAs revealed changes in various pathways, including MAPK signaling, endocytosis, endocrine resistance, Ras signaling, Wnt signaling, EGFR signaling and prolactin signaling. Most of the target genes belonged to biological process like neurogenesis, transcription, transcriptional regulation and host-virus interaction. Activation of these processes could be linked to various disorders like cancer, aging, immune response and dysregulated nervous system. Expression profile of at least 22 differentially-regulated miRNAs was identified from our study which agreed with previously-published reports despite the diversity of our patient population, differences in their disease severity, and differences in the viral strain dominant at the time of sample collection. Thus, these miRNAs may reflect those associated with viral infection, while others may correlate better with disease severity. Due to the diversity of ethnicities in the UAE representing people from 196 countries, we believe that our results may reflect a more significant correlation of miRNAs with SARS-CoV-2 infected patients than those from regions with more homogeneous populations.

Audience Take Away Notes

- The audience will learn about virus-host interactions and how miRNAs control cellular and viral gene expression as well as pathogenesis
- In particular, they will learn about how miRNAs are differentially-expressed in SARS-CoV-2 infection of humans during different disease stages and upon recovery

- Other researchers can study similar interactions in their systems to see how their virus replication is affected by host and viral miRNAs and disease profile
- miRNAs can be used as biomarkers for disease diagnosis, disease stage, or disease severity
- Furthermore, miRNA-based anti-sense can be developed as therapeutics to inhibit infection and reduce disease severity

Biography

Waqar Ahmad has established skills in the life-science research with emphasis on the mechanistic studies of the human diseases. After completing his PhD from the University of Queensland, Australia, he joined Prof. Farah Mustafa's Lab at College of Medicine and Health Sciences, United Arab Emirates University, UAE and is currently working as a Medical Research Specialist. One of the research priorities of Prof. Mustafa is deciphering the molecular basis of SARS-CoV-2 replication and pathogenesis by focusing on the role of miRNAs during infection and pathogenesis. The lab is interested in the detection of possible miRNA-based biomarkers to distinguish infected patients from healthy ones and those that predict disease severity.

Mohammad Alshomrani

Microbiology Department, Riyadh Regional Laboratory and Blood Bank, Riyadh, Riyadh Region, Saudi Arabia

Updates in COVID 19 laboratory diagnosis

Coronavirus disease 2019 (COVID-19) is caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) and has wreaked havoc on healthcare and economic systems worldwide. Despite extensive scientific research and efforts, there are still knowledge gaps regarding pathophysiology, clinical severity, and diagnosis in the COVID-19 patient population. In this presentation, I will discuss various diagnostic approaches for SARS-CoV-2; the most common methods, the gold standard method. I will compare between the commonly used methods in terms of sensitivity, specificity, turnaround time, feasibility, type of specimens used. I will elaborate some of clinical and epidemiological purposes, advantages and disadvantages of each test. I will present some of the recent advances in diagnostic methods, and the most updated guidelines in the laboratory diagnosis. Briefly, I will discuss how to interpret the results of COVID 19 in context with clinical presentation. In addition, I will explain how to initiate COVID 19 testing in your lab and how to select the appropriate methods based on your setting and requirements.

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 Bacteriology Unit in Riyadh Regional Laboratory. He published one study about ''Immunoglobulin Rapid Test Sensitivity in PCR-Positive COVID-19 Patients". In addition, he is conducting other study projects in different fields of microbiology.

Tharanika Ahillan[1*], Matthew Emmerson[2*], Bethan Swift [3, 4], Hadiya Golamgouse[5], Kaiyang Song[2], Angela Roxas[6], Sakina Bano Mendha[7], Elena Avramovic[6], Jatin Rastogi[6], Binta Sultan[8]

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Covid-19 in the homeless population: A scoping review and meta-analysis examining differences in prevalence, presentation, vaccine hesitancy and government response in the first year of the pandemic

Aims: People Experiencing Homelessness (PEH) have been identified as being increasingly susceptible to Coronavirus Disease (COVID-19), with policies enacted to test, isolate, increase hygiene practices and prioritise vaccines among this population. Here, we conduct a scoping review of the current evidence-base pertaining to the prevalence and presentation of COVID-19 in PEH, COVID-vaccine hesitancy rates and government interventions enacted within the first year of the pandemic for PEH.

Materials and methods: A systematic search was conducted on Pubmed, Cochrane, Embase and MedRxiv databases for studies reporting primary data on COVID-19 prevalence and clinical characteristics in PEH, vaccine uptake for PEH and policies enacted targeting PEH. Study qualities were assessed with The National Heart, Lung and Blood Institute's set of Study Quality.

Results: Eighty-three studies were included in our final analysis. The overall prevalence of symptomatic COVID-19 infection in PEH is estimated at 35%. The most common symptoms found were cough and shortness of breath, followed by fever. Concerns regarding vaccine hesitancy amongst PEH related to thoroughness of COVID-19 vaccine clinical trials, side effects and mistrust of the government. The main strategies implemented by governments were mass testing, adaption of healthcare service provision, provision of alternative housing, encouraging personal hygiene (hand sanitation and mask wearing), and inter-organisational communication.

Discussion: In our meta-analysis, 35% of PEH with a COVID-19 infection presented symptomatically; the low prevalence of symptomatic COVID-19 infection suggests widespread testing following outbreaks would be beneficial for this group of individuals. Temporary recuperation units and measures for housing stability in the pandemic, namely provision of alternative housing and stopping evictions, were found to be highly effective. High rates of vaccine hesitancy means that education and encouragement towards vaccination would be beneficial for this vulnerable population, where comorbidities are common. Finally increased focus in research should be placed on the mental health burden of COVID-19 and the pandemic on PEH moving forwards.

Keywords: COVID-19, Homeless, Homelessness, Policies, Prevalence, SARS-COV-2, Scoping review, Symptoms

Biography

Tharanika Ahillan is a junior doctor working in London. She completed her medical degree and her intercalated BSc in Global Health at University College London medical school, with which she graduated with a Merit in her final year and a 2:1. She is passionate about infectious diseases and health equity and has published numerous articles in these fields, one of which was highlighted in the British Medical Journal's anti-racism resources in 2020. She was awarded the John Yudkin Prize for global advocacy in 2018 for her work at students for global health UCL. She will be presenting an oral presentation based on a recently published paper on COVID and homelessness, inspired by her elective placement at the Hospital of Tropical Diseases in London.

Biography

Matthew Emmerson is a 5th year medical student at the University of Oxford. He achieved a 2.1 in his intercalated BA in molecular pathology and systems neuroscience as well as receiving a Merit in his 4th year. He has an eclectic range of interests and is active on a number of regional and national committees, for example as a research team member with Suture UK, Oxford Regional representative for Student and Foundation Doctors of Otolaryngology and an Editor with Polygeia, a global health student think-tank. He is excited to give an oral presentation based on his first co-first authored publication on COVID-19 and homelessness.

Kushal Kalvit
Tata Memorial Hospital, India

Measles sans rash - An atypical cause of New-Onset Refractory Status Epilepticus (NORSE)

Introduction: NORSE is an umbrella term with different aetiologies. The usual suspects are structural lesions, infections, toxins, metabolic causes, autoimmune or paraneoplastic encephalitis. Measles is a common infection that presents with a rash and is typically self-limiting. It may lead to encephalitis in rare instances and pose a diagnostic challenge without a history of fever with rash.

Case Presentation: A 10 years old female was admitted with a history of drowsiness, irrelevant talk, lip smacking and focal seizures in the right lower limb for 5 days. The patient had episodes of generalized tonic-clinic seizures 3 days prior for which she was treated in another hospital. She had history of a self-limiting acute febrile illness one month prior to the admission. The patient also had B-cell acute lymphoblastic leukaemia for which she was under chemotherapy. She was diagnosed to have refractory status epilepticus and was started on multiple antiepileptics in addition to midazolam, propofol and thiopentone infusion with EEG monitoring. Workup for the seizures revealed hyperintensities in MRI involving the cortex, thalamus and basal ganglia sequentially. CSF analysis revealed negative bacterial culture, viral multiplex PCR, autoimmune encephalitis and paraneoplastic encephalitis panel. The patient was started on high dose methylprednisolone, IVIg therapy and a ketogenic diet in view of NORSE and a provisional diagnosis of ADEM with unknown aetiology. The patient was then investigated for CSF measles antibody which came back positive along with a brain biopsy to look for viral inclusion bodies. The child was eventually diagnosed as Acute Post-Infectious Measles Encephalitis (APME) and was transferred out of the ICU with complete abolition of seizures and improved cognition.

Conclusion: APME is extremely uncommon and should be sought after in case of contact with an index case or a recent outbreak. NORSE is difficult to treat and needs intensive monitoring with use of multiple medications and continuous EEG.

Biography

Dr. Kushal Kalvit is practising intensives from India. He is currently working as an Assistant Professor at the Tata Memorial Hospital in Mumbai, India. He has completed his specialization in Internal Medicine and Critical Care Medicine. He has many publications in indexed national and international journals and has been a faculty in many regional critical care workshops. He has authored and co-authored numerous chapters in textbooks of critical care medicine. He is also a reviewer for the British Medical Journal and the Annals of Internal Medicine journal.

Brandon Lucke-Wold
Baylor University, United States

The neutrophil to lymphocyte ratio in post-stroke infection: A systematic review and meta-analysis

Ischemic and hemorrhagic strokes have multiple downstream consequences for patients. One of the most critical is post-stroke infection (PSI). The goal of this systematic review and meta-analysis was to critically evaluate the literature regarding the use of the neutrophil to lymphocyte ratio (NLR) as a reliable means to detect early PSI development, particularly post-stroke pneumonia (PSP) development. Web of Science, PubMed, and Scopus were searched and 25 studies were included in the qualitative review. The studies had to be from high quality journals using the Newcastle-Ottawa Scale and any language was acceptable. Among them, 15 studies were included in the meta-analysis. Standardized mean difference (SMD) was reported with a 95% confidence interval (CI) for the NLR levels. Patients with PSI had significantly higher NLR levels than stroke patients without infection (SMD=1.08; CI 95%=0.78-1.39, P-value<0.001). In addition, the NLR levels of the stroke patients with pneumonia were significantly higher than those without pneumonia (SMD=0.98; CI 95%=0.81-1.14, P-value< 0.001). However, data extracted from the qualitative review suggested that NLR could not predict urinary tract infection, sepsis or ventriculitis in stroke patients. Our study indicated that NLR could be recommended as an inexpensive biomarker for predicting infection, particularly pneumonia, in stroke patients. It can help clinicians institute early interventions that can reduce PSI and improve outcomes.

Biography

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

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Anticoronavirus formulations based on chitosan

Our interdisciplinary working group was motivated by the challenge of proposing tools for the fight against the sudden pandemic caused by SARS-CoV-2 in 2020 and the present. We have obtained several formulations based on chitosan, a biodegradable, non-antigenic, non-toxic, and biocompatible natural polymer. These formulations have different characteristics and applications. We developed novel antiviral cotton fabrics impregnated with different formulations based on Chitosan, citric acid, and Cupper nanoparticles. The resulting impregnated textiles exhibited integrated properties of good adhesion without substantially modifying their appearance and anti-herpes virus and betacoronavirus efficacy (~ 100%), which enabling to serve as a scalable biocidal layer in protective types of equipment by providing contact killing against pathogens. The antiviral activity of formulations based on chitosan with copper nanoparticles was described for the first time in our work. This proposal may be considered a potential tool to inhibit the propagation and dissemination of enveloped viruses, including SARS-CoV-2. Another of the main current challenges is to optimize the use of personal protection elements without the detriment of biosecurity. For this proposal, we obtained sprayable formulations based on chitosan. It is known that the combination of both metals (copper and silver) enhances the antibacterial activity of each one individually. We obtained the first antiviral spray based on chitosan and both (silver and copper) nanoparticles. The spray has simplified production, with potential use in industry, it´s easy to use and apply, for domestic use, is biodegradable, has immediate antiviral action, has antibacterial, and it is non-toxic, and does not produce skin irritation. The spray is applicable to any type of woven or non-woven fabric, and plastic surfaces. Implementing this kind of sprayable product would allow the face masks to be reused without the need sterilization or their elimination after use. Therefore, the two major advantages attributable to Chitosan formulations are the prevention of the spread of viruses, including SARS-CoV-2. Secondly, these technologies will contribute significantly to the reduction of waste production.

Audience Take Away Notes

- The present work contributes to expanding knowledge in the development of antivirals applicable in materials
- The audience will learn how certain antivirals can be applied on materials converting them into functionalized materials
- This work will provide tools to develop antivirals applicable to surfaces for different types of viruses, the constant emerging and re-emerging viruses worldwide needs to be stopped with products that not only act on the patient but also prevent viral spread

Biography

Dr. Victoria Ayala studied Biochemistry at the Universidad Nacional del Sur (UNS), Bahía Blanca, Argentina, and graduated in 2008. She then joined the research group of Dr. Scolaro Luis at the Facultad de Ciencias Exactas y Naturales, Universidad de Buenos Aires, Argentina and in the Dr. Graciela Santillan group at UNS. She received her PhD degree in 2014 at the same institution. She is Assistant Professor at the UNS. She founded two laboratories of virology and is chief of one of them. She was twice awarded for her achievements in virology. Together with his work group obtained the patenting of an antiviral product. She has published more than 10 research articles in SCI (E) journals.

S.N. Surendran[1], R. Nagulan[2], A. Tharsan[1], K. Sivabalakrishnan[1], Ranjan Ramasamy[1*]

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Dengue transmission and aedes vector dynamics before, during and after COVID-19 travel restrictions

Contrary to expectation, dengue incidence decreased in many countries during the period when stringent population movement restrictions were imposed to combat COVID-19. Using a Seasonal Autoregressive Integrated Moving Average model, we previously reported a 74% reduction in the predicted number of dengue cases from March 2020 to April 2021 in the whole of Sri Lanka, with reductions occurring in all 25 districts in the country. The fall in dengue incidence was accompanied by an 87% reduction in larval collections of *Aedes* vectors in the northern Jaffna city. It was proposed that movement restrictions led to reduced human contact and blood feeding by *Aedes* vectors accompanied by decreased oviposition and vector densities that were responsible for diminished dengue transmission. These findings are extended here by investigating the relationship between dengue incidence, people movement restrictions and vector larval collections, between May 2021 and July 2022 when movement restrictions began to be lifted, with their complete removal in November 2021. The new findings further support our previous proposal that population movement restrictions imposed during the COVID-19 pandemic reduced dengue transmission primarily by influencing human-*Aedes* vector interaction dynamics.

- **Audience Take Away Notes**
- Appreciation of dengue virus transmission in relation to Aedes mosquito vector dynamics
- Assist teaching of public health, epidemiology and virology
- Help further research to advance knowledge on dengue virus epidemiology
- Understand neglected aspects of population exposure to mosquito disease vectors
- Appreciate epidemiological aspects of dengue and other mosquito-borne diseases

Biography

Ranjan Ramasamy graduated from the University of Cambridge, UK and then obtained a PhD also from the University of Cambridge. He has since held academic appointments in the UK and abroad including Australia, Sri Lanka and the USA. He was the Chairman of the National Science Foundation of Sri Lanka, Professor of Life Sciences at the Institute of Fundamental Studies in Kandy in Sri Lanka, Professor of Biochemistry in the University of Jaffna in Jaffna Sri Lanka, Professor of Immunology in the University Brunei Darussalam Medical School and held institute appointments at the Babraham Institute in Cambridge in the UK & Scripps Clinic and Research Foundation in La Jolla in the USA. He has more 250 publications in fields pertaining to Medical Sciences.

Agnes Nagy[1, 3*], Gabor Endre Toth[2], Balazs Antal Somogyi[2], Csaba Istvan Pereszlenyi[1], Gergely Csaba Babinszky[1], Ferenc Jakab[2]

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Amplicon-sequencing method for strain-level subtyping of *Bacillus anthracis* in field laboratory

Bacillus anthracis is the first ranked on the list of potential bioweapon agents. In case of biothreat emergency accurate and timely data resulted from on-site strain-level subtyping of the agent help to determine the origin of the used strain and provide the first bio forensic information for confirmation of deliberate misuse of pathogen. The study aimed to develop an amplicon-based targeted sequencing method on Nanopore platform combined with in-silico multiple-locus variable number tandem repeat analysis (MLVA) of 31 loci for strain-level subtyping of *Bacillus anthracis* directly from environmental samples. We determined the genotype of 31 tandem repeat loci of 13 *Bacillus anthracis* strains with capillary electrophoresis and Sanger sequencing, and the results were used as reference. Performance and effectiveness of the newly developed method was evaluated by two approaches: (i) the number of correctly identified repeats and (ii) the number of consensus sequences identical to the reference. Performance evaluation included analysis of the 13 different MLVA genotype strains. Effectiveness was tested with Bacillus anthracis spore suspensions, and spiked environmental samples of three sample matrices (soil, surface, sludge) to determine the lowest spore concentration and DNA copy number that results in the correct identification of all 31 markers. Repeat numbers and sequences of the 31 loci were correctly determined and showed 100% agreement with the reference for all 13 strains. The concentration limit of correct identification of all 31 markers was 10^5 colony forming unit/sample in pure spore suspension, soil and surface samples. In sludge samples with this concentration 30 of 31 repeats were correctly typed. The lowest DNA copy number which resulted correct repeat typing was between 300 and 1000 copies depending on sample type. Our results demonstrated that PCR-based amplicon sequencing with portable MinION device is a suitable method for on-site pathogen genotyping directly from low pathogen containing environmental samples.

Biography

Agnes Nagy is the leader of the Scientific Research Department of Hungarian Defense Forces Medical Centre Epidemiological and Scientific Research Institute. Since graduating in biology at Eotvos LorAnd University of Sciences in 2001, she has been working as a scientist in a military officer position at the military medical research institute. Her primary field of interest is methodological development to identify bio warfare agents and epidemiologically significant pathogens and sub-type them at the strain level. She was the leader of an applied research project aimed at developing a prototype of a field-deployable biodefense laboratory for the Hungarian Defense Forces.

Fejiro Chinye-Nwoko*, Oyelola Makanjuola, Amenze Eguavoen
Nigeria Solidarity Support Fund (NSSF), Lagos, Nigeria

Mobilizing the private sector resources for a strengthened COVID-19response

Background: Nigeria attested to the Abuja Declaration to allocate 15% of the annual budget to health. However, current allocation is about 4.7%. This left the country extremely vulnerable to the COVID-19 pandemic. As of December 2020, Nigeria had over 87,000 confirmed cases of COVID-19 and over 1,000 deaths according to WHO. Although vaccines were rapidly developed, Nigeria's response was impeded by limited resources. Despite receiving 4,000,000 does of the COVID-19 vaccines and a target to vaccinate 70% of people, by December 2022 by March 2021 only 3% of the population had been vaccinated. This paper documents the role of NSSF in mobilizing resources in support of the governments COVID-19 response efforts.

Methodology: The Nigeria Solidarity Support Fund (NSSF) was birthed in 2020, from a partnership between the Global Citizen, and the Nigeria Sovereign Investment Authority (NSIA) as an innovative platform for resource mobilization to supplement diverse efforts to mitigate the adverse economic effects of the Covid-19 pandemic on Nigerians. The resource mobilization framework is outlined below.

Collaboration: NSSF promotes partnerships and collaboration to catalyze funding and scale impact. This includes combining the expertise of GC in advocacy and resource mobilization, with the expertise of NSIA in fund management, accountability and transparency.

Local Ownership: NSSF partnerships ensure local ownership of the fund and its programs through government buy- in and also through active engagement of the general public as co-funders through their donations, or as advocates and solution drivers.

Active board: NSSF relies on an active board to raise funds through their personal and professional networks. The sources of unrestricted funding enable the organization co-design appropriate interventions with relevant stakeholders at the state and national levels.

Transparency and accountability: Board members were selected from both NSIA and GC. Financial activities are audited (internally and externally) and published, grant administration and impact evaluations are conducted by reputable 3rd party organizations such as KPMG, PwC, Allen & Overy.

Additionality: Funding support is used to scale existing nationally approved interventions and strategies.

Inclusive Grants development: NSSF co-designs grants in collaboration with national and state-level stakeholders.

Results: NSSF raised over $2,000,000 in its 1st year of existence. NSSF leveraged on our board leadership to raise financial and technical support in the aim of building credibility, transparency, and accountability of the COVID-19 vaccinations.

With the National Primary Healthcare Development Agency, NSSF supported the scale-up of COVID-19 vaccination in 6 states across the country. Through the campaign 12,000 health workers were trained on safe immunization and 12 million people were reached with accurate communication. As of 2022, over 4.9 million people have been vaccinated.

In addition to this, NSSF launched the WeNaija contest to reskill and retool youth for the post COVID-era. 120 youth were given seed funds and tools to enhance their skills. NSSF held 4 Fireside Chats, a forum for engaging the public and stakeholders in conversations to advocate for change, and NSSF published a policy brief and other editorials on COVID-19.

Conclusion: The success of the COVID-19 vaccination campaign gives an insight into what can be achieved through effective collaboration, resource mobilization, and private sector mobilization for the health sector.

Audience Take Away Notes

- The importance of creating partnerships with private and government stakeholders in project implementation to achieve greater impact
- The paper presents our experience as a non-governmental, non-profit organization, working with the government to increase uptake of the COVID-19 vaccines in Nigeria. People will learn that through partnerships and collaboration, it is possible to scale vaccination efforts and reach many people in a short time
- The partnership between the National Primary Health Care Development Agency and the Nigeria Solidarity Support Fund shows that when organizations work together and provide financial and technical support, it is possible to achieve significant progress in vaccination efforts. Additionally, it highlights the importance leadership, management, and coordination in health service delivery and how this can be strengthened through effective communication and data management
- In this partnership, the NPHCDA and NSSF worked with information available from previous experiences and built on that to drive COVID-19 vaccination coverage. Nigeria and several LMICs still struggle with poor childhood immunization coverage and the information that will be provided through this presentation will help healthcare workers design more effective programs
- The grant was not implemented as a parallel project, rather it was implemented in the principle of additionality. This allowed the NPHCDA and NSSF to geometrically increase impact
- Electronic real-time data management was a key part of the success and a backbone for improving data quality, accountability, and transparency, which allowed gaps to be identified and bridged on time

Biography

Fejiro Chinye-Nwoko is a qualified medical doctor and an accomplished executive. She started her career with the Lagos State Health Service Commission and then moved into the development sector. Dr. Fejiro has over ten years of experience in program management and has overseen several multi-donor projects from inception to completion. She is passionate about quality healthcare delivery and is ideally placed to drive health systems strengthening in Nigeria. Fejiro has an MSc. in Global Health Policy from the London School of Hygiene and Tropical Medicine and is the General Manager of the Nigeria Solidarity Support Fund (NSSF).

Vladimir Zajac

Formerly scientist at the Cancer Research Institute, BMC, SAS, SAV, Dúbravska cesta 9, 84505, Bratislava, Slovakia

An evolutionary view of the CORONA virus epidemic process

Every virus is a parasite that cannot exist on its own and is fully dependent on its carrier. This is the basic condition of its existence. The parasite must have its host, and thus is a living cell. Based on our long-term study of BLV and HIV, we conclude that the carriers of these viruses are bacteria or yeast. Viruses can exist in these carriers for months or years. Carriers do not mind at all that the virus multiplies and mutates in them. The mutant can arise in one individual, under optimal conditions it can reproduce in it and pass on to other individuals. However, it is possible that a new mutant may have originated in several placess. It is only a matter of time before how many mutations can occur in one virus. In the case of Omicron, it is probably a longer period of time, perhaps years, until so many mutations have taken place. It can be assumed that the creation of more than 30 mutations in the spike protein could not take place in 2-3 years from an epidemiological point of view. In reality, this can take place between 10 and 20 years. This corresponds to the period after the first SARS-1 infection in 2004. According to our idea that the virus can survive for months or years in its carriers - bacteria or yeast - then the omicron ancestor may date back to the first SARS-1 epidemic. Let's not stubbornly look for the first patient of SARS-2, let's try to look at the epidemic process from an evolutionary point of view. We monitored the presence of novel coronavirus in the intestinal tract of infected individuals. Rectal swabs were taken from persons who overcame the infection with a new coronavirus. The results show that the vast majority of patients who have overcome the infection, the virus is still present in the stool and their intestinal tract and can induce a de novo infection in a patient and infect others.

The novel coronavirus in its carrier may persist in the intestinal tract and infections may therefore recur. If the virus carrier is not detected and removed, the infections will keep recurring and we will not get rid of the virus. By identifying the carrier or carriers of the virus and their subsequent elimination, we also destroy the virus.

Only then can we stop the epidemic. Vladimir Zajac has completed his PhD. in 1982 at the Cancer Research Institute of Slovak Academy of Sciences in Bratislava (Slovakia), where he worked as the Head of Department of Cancer Genetics from 1996 to 2010. He joined the Medical Faculty of the Comenius University as Associate Professor of Genetics in 2007. He has published 76 papers mostly in reputed journals and he was editor of the book Bacteria, viruses and parasites in AIDS process (In Tech, 2011).

Isra Mufadal Abdulkareem[1]*, Dr. Moumen Mukhtar[2], Dr Shahinaz Bedri[3]

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The prevalence of COVID-19 infection in patients presented with acute exacerbation of asthma, COPD and idiopathic pulmonary fibrosis at the emergency department of Al-Shaab teaching hospital from July 2021 to November 2021

Background: Even though respiratory viruses are one of the most common triggers for asthma exacerbations, not all of these viruses affect patients equally.

Objective: To assess the prevalence of covid19 infection in patients presented with acute exacerbation of asthma, COPD and idiopathic pulmonary fibrosis patients.

Method: This was a cross-sectional descriptive hospital based study. The study was conducted in Al-Shaab Teaching Hospital during the period from July 2021 to November 2021. The study sample was 345 patients presented with acute exacerbations fulfilled the inclusion criteria of the study. Data was collected using a questionnaire which filled with the patients after taking informed consent.

Results: The study included 175(50.7%) presented with asthma, 116(33.6%) with lung fibrosis and 54(15.7%) had chronic obstructive pulmonary disease. The prevalence of COVID 19 among the patients was 58(16.8%). Considering the three groups the higher prevalence of COVID was reported in 22(40.7%) of the patients with chronic obstructive pulmonary disease, followed by 16(13.8%) of the patients with idiopathic pulmonary fibrosis and 20(11.4%) of asthmatic patients (P value < 0.05). Among the positive COVID asthmatic patients the common age groups were 25 – 34 years and 35 – 44 years, while among COPD and IPF patients the prevalence was higher among patients aged 55 years and above (P value < 0.05). In the COPD and IPF patients, the prevalence of COVID 19 was significantly higher among males than in females (P value < 0.05).

Conclusion: The study concluded that among the patients presented with acute exacerbations was higher among patients of chronic obstructive pulmonary disease than patients with asthma and idiopathic pulmonary fibrosis.

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Treatment of old world cutaneous leishmaniasis with paromomycin cream, oral dapsone alone and in combination in Algabal Algarby Libya

Background: Cutaneous Leishmaniasis (CL) is endemic in many regions of the world, and has a significant economic and health impacts. Despite the numerous proposed therapies for this zoonotic parasitic disease. Currently, there is no definitive cure for CL. Meglumine antimony compounds are regarded as the typical treatment for leishmaniasis. However, they have a rather high incidence of adversative effects that always, are not successful. Alternatively, Paromomycin and dapsone were used in various studies, though, with conflict results.

Aim of study: This study aims to evaluate the clinical efficacy and safety of using of paromomycin cream, oral dapson and their combination in treatment of CL.

Patients and Methods: This study is a prospective randomized clinical trial was carried out at the private outpatient Al- Ahlam Center of Dermatology and Cosmetology in city of Gharyan, Libya. That started from 1st of January 2020 to end of Dec 2021. 42 patients were joining this study, and randomly were divided into three groups according to protocol of treatment to assess the clinical response of the treatment methods.

Results: Regarding the outcome of the three different treatment regimen and after exclusion of the patients stop their follow-up; we found that 50% of dapsone treated group cleared the lesions in 1-2 months versus only 40% in paromomycin & Dapsone treated group and 0% for the paromomycin group, only 8 patients had no improvement with received treatment; 4 (33.3%) from dapsone group, 2 (20%) from each other group (P=0.036).

Conclusion: Using of paromomycin & dapson combination in treatment of cutaneous leishmaniasis shows better result and early clearance LC lesions, whereas, using of topical paromomycin cream or oral dapsone alone were effective. Also, our result showed that, paromomycin is effective, safe and well tolerated in children.

Keywords: Cutaneous leishmaniasis, Paromomycin, Dapson Gharyan, Libya

Biography

Dr. Ahlam Ab Almabrouk MBs MSc - Dermatologist at Al- Ahlam Center of Dermatology and Cosmetology in city of Gharyan, Libya. She is lecturer at Faculty of pharmacology, University of Ghanyan/ Ghanyan-Libya.

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Use of tixagevimab/cilgavimab in omicron outbreak in China: Baseline characteristics and interim analysis of the clinical outcomes

Introduction: The prevalence rate of SARS-CoV-2 Omicron variant infection reached approximately 80% in late 2022 in China. Tixagevimab/cilgavimab, a combination of two neutralizing monoclonal antibodies, showed significant efficacy for preventing COVID-19 in previous clinical trials. This study aimed to investigate the utilization and clinical outcomes of tixagevimab/cilgavimab in a real-world setting in China.

Methods: This observational study used real-world data obtained during the Omicron outbreak in China. Subjects who received tixagevimab/cilgavimab from July to December 2022 were included. Data on COVID 19 diagnosis, outcomes, and adverse events were collected up to at least 6 months after administration. COVID-19 diagnosis was confirmed by RT-PCR or rapid antigen test and its severity was classified based on the WHO Clinical Progression Scale and Guideline on Diagnosis and Treatment of Novel Coronavirus Pneumonia (10th Interim Edition). Here we report the baseline subject characteristics and interim analysis results of the clinical outcomes based on the Modified Full Analysis Set (mFAS), including subjects who received at least one dose of tixagevimab/cilgavimab (300 mg) for pre-exposure prophylaxis.

Results: A total of 248 subjects received tixagevimab/cilgavimab, only one (0.4%) of whom received two doses of the drug and the remaining 247 (99.6%) had a single dose. In total, 229 subjects were included in the mFAS. As of the cut-off date for interim analysis (March 28, 2023), the median follow-up time was 95 (range, 19-263) days. The mean age of the subjects was 44.4±15.92 years, 11.8% of whom were ≥65 years old and 41.5% were males. The majority (88.2%) of the subjects were never smokers. Fifty-eight (25.3%) subjects had comorbidities, including diabetes (3.1%), obesity (3.9%), hypertension (14.8%), chronic obstructive pulmonary disease (0.4%), asthma (1.3%), and cardiovascular diseases (4.8%). Thirty-seven (16.2%) subjects had key immune compromised conditions, including hematologic malignancies (4.4%), solid organ transplantation (4.8%), autoimmune diseases (2.2%), solid tumors (3.5%), and chronic kidney diseases (1.7%). In total, 195 (78.6%) subjects had previously received one (4.8%), two (15.7%), three (55.5%), more than three (1.7%), or unkown (0.9%) dose(s) of COVID-19 vaccines. Further, 4.0% of the subjects had experienced a previous SARS-CoV-2 infection. In subjects with at least one post-baseline record in the mFAS (n=221), 72 (32.6%) had laboratory-confirmed and/or healthcare-attended SARS-CoV-2 infection up to 3 months after the first administration of tixagevimab/cilgavimab, including 71 (98.6%) mild and 1 (1.4%) moderate cases. Two (0.9%) patients had COVID-related hospitalization; one had prior renal transplantation and the other had haematological malignancy. No COVID-19-related ICU admissions or

deaths occurred. In patients with SARS-CoV-2 infection, the most common (>10%) signs or symptoms were fever (62 [86.1%]), cough (48 [66.7%]), muscle aches (17 [23.6%]), sore throat (14 [19.4%]), headache (10 [13.9%]), fatigue (9 [12.5%]), and new loss of taste (8 [11.1%]). Treatment-emergent adverse events were observed in 5 (2.2%) patients, and only one (0.4%) patient experienced a serious adverse event (upper respiratory tract infection) which was moderate in severity.

Conclusions: Prophylactic tixagevimab/cilgavimab administration led to a low risk of COVID-19-related hospitalization, ICU admission, or death. Tixagevimab/cilgavimab needs to be promoted among those with comorbidities and immunocompromised individuals.

Keywords: COVID-19, Tixagevimab, Cilgavimab, Neutralizing antibody, Real-world setting

Audience Take Away Notes

- This was the first study investigating the use and clinical outcomes of prophylactic tixagevimab/cilgavimab in a wide range of populations during the Omicron outbreak in a real-world setting in China
- Tixagevimab/cilgavimab could protect immunocompromised individuals and people with comorbidities from severe/critical COVID-19 or COVID-19-related death
- Tixagevimab/cilgavimab demonstrated a good safety profile in a real-world setting, with extremely low incidences of treatment-emergent adverse events and serious adverse events

Biography

Dr. Qu received his PhD degree and graduated from Fudan Medical College. He is now working in Ruijin Hospital Affiliated to Shanghai Jiao Tong University School of Medicine, specializing in the clinical diagnosis and treatment of difficult and critical diseases of respiratory system. His main research interests are etiology analysis and clinical diagnosis and treatment of respiratory tract infection, and mesenchymal stem cell treatment of refractory lung diseases and its mechanism research. He has published more than 130 research articles in SCI (E) journals.

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Jernell Robert D. Malixi*, MD, MPM and Rozelle Jade Javier MD, FPCP, FPISMD

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Three year retrospective study on the survival analysis of ventilator acquired pneumonia adult patients at batangas medical center, Philippines

Background: Hospital Acquired Pneumonia is an important public health concern. Even with the advent of new anti-bacterial, there is an increasing prevalence of anti-microbial resistance worldwide. In particular, Ventilator Acquired Pneumonia can increase mortality risk in patients admitted. Batangas Medical Center is a multi-specialty tertiary hospital located at Batangas City which caters different diseases. Due to increased number of patients, hospital acquired pneumonia can be acquired which can complicate existing diseases especially for intubated patients. However, there is no existing data on Ventilator Acquired Pneumonia Patient's survival analysis done in this institution.

Objectives: This study aims to determine the clinico-demographic profile and survival analysis of adult patients diagnosed with Ventilator Acquired Pneumonia at a tertiary government hospital.

Methodology: The study was a retrospective cohort study at Batangas Medical Center from January 2017 to December 31, 2019.

Results: The study included two hundred thirty-one patients diagnosed with ventilator acquired pneumonia. It concluded that majority of isolated bacteria were Acinetobacter baumannii (33%), Klebsiella pneumoniae (22%), and Pseudomonas aeruginosa (12.68%). Among Pandrug resistant organisms, Acinetobacter baumannii was frequently isolated followed by Klebsiella pneumoniae. There were no significant findings on the survival analysis of VAP patients based on age, sex, and co-morbidities. In this study, it showed that patients who underwent tracheostomy had significant decreased mortality as compared to patients without surgical intervention.

Conclusion: Ventilator acquired pneumonia was a risk factor on morbidity and mortality among adult patients admitted at a tertiary hospital. Among the different risk factors (age, sex, comorbidities and surgical intervention), tracheostomy decreased mortality and morbidity of patients diagnosed with ventilator acquired pneumonia.

Audience Take Away Notes

- Explain the prevalence of ventilator acquired pneumonia at a tertiary government hospital in the Philippines
- Determine clinico-demographic factors affecting the survival of ventilator acquired pneumonia patients
- For clinicians, it can help on determine on empiric treatment needed for patients based on clinico-demographic profile
- This research can help other clinician and researchers study on Ventilator Acquired Pneumonia especially on other intervention such as early or delayed tracheostomy

Biography

Dr. Jernell Robert D. Malixi finished his medicine degree at University of the City of Manila, Philippines in 2014. He joined the Doctors-to-the-Barrio program under the Department of Health wherein he provides clinical services in Geographically Isolated and Disadvantaged Areas. While providing health services in far flung areas, He finished his Masters in Public Management Major in Health Systems and Development at the Development Academy of the Philippines, Manila. In 2021, he finished his residency training on Internal Medicine at Batangas Medical Center, Philippines.

Houda Limam*, Sarra Dhraief, Lamia Thabet

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In vitro activity of colistin against *Pseudomonas aeruginosa* with difficult-to-treat resistance isolates from critically ill burn patients

Background: *Pseudomonas aeruginosa* is an opportunistic pathogen, commonly causing hospital-acquired infections in burn patients. P. *aeruginosa* with Difficult-To-Treat Resistance (DTR-PA) is resistant to all of the following: piperacillin-tazobactam, ceftazidime, cefepime, aztreonam, meropenem, imipenem-cilastatin, ciprofloxacin and levofloxacin and presents a significant clinical challenge. In low- to-middle-income countries, where costly novel antipseudomonal antibiotics are not available, colistin remains an important option against multidrug resistant gram-negative bacteria, particularly P. *aeruginosa*. The aim of this study was to investigate the in vitro susceptibility of DTR-PA to colistin and determine its Minimum Inhibitory Concentration (MIC).

Methods: We conducted a monocentric retrospective study of clinical P. *aeruginosa* isolates collected from critically ill burn patients over a period of 5 years (2018-2022). Isolates were identified using conventional methods. Antimicrobial susceptibilities to amikacin, piperacillin-tazobactam, ceftazidime, cefepime, aztreonam, meropenem, imipenem-cilastatin, ciprofloxacin and levofloxacin were determined by the disk diffusion method. Susceptibility was assessed according to European Committee on Antimicrobial Susceptibility Testing breakpoints. The MIC of colistin was determined using broth micro dilution. Isolates with a colistin MIC ≤2 mg/L were considered to be susceptible.

Results: During the study period, 150 non-repetitive strains of DTR-PA were isolated, accounting for 19, 1% of all P. *aeruginosa* isolates from burn patients. Most isolates were recovered from male patients (64%) of all ages. DTR-PA strains were obtained from pus/wound swabs (46%), followed by central catheter cultures (26%), blood (13%), respiratory samples (10, 3) and urine (4, 1%). Almost 98% of the isolates were resistant to amikacin. Only one isolate was found to be colistin resistant.

Conclusion: This study highlights the high prevalence of DTR-PA among critically ill burn patients. The majority of DTR-PA isolates remained susceptible to colistin. Effective antimicrobial stewardship is crucial to ensure the appropriate use of colistin in order to preserve this antibiotic of last resort.

Audience Take Away Notes

- The emergence and spread of *Pseudomonas aeruginosa* with difficult-to-treat resistance are challenging given the already limited therapeutic options
- Colistin has excellent activity against *Pseudomonas aeruginosa* with difficult-to-treat resistance
- Constant surveillance of antimicrobial resistance is important

Biography

Dr Houda Limam is a senior resident doctor (infectious diseases) in Tunisia.

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Integration of immunoinformatics and cheminformatics to design and evaluate a multitope vaccine against *Klebsiella pneumoniae* and *Pseudomonas aeruginosa* coinfection

Introduction: *Klebsiella pneumoniae* (*K. pneumoniae*) and *Pseudomonas aeruginosa* (*P. aeruginosa*) are the most common Gram-negative bacteria associated with pneumonia and coinfecting the same patient. Despite their high virulence, there is no effective vaccine against them.

Methods: In the current study, the screening of several proteins from both pathogens highlighted FepA and OmpK35 for K. pneumonia in addition to HasR and OprF from *P. aeruginosa* as promising candidates for epitope mapping. Those four proteins were linked to form a multitope vaccine, which was formulated with a suitable adjuvant, and PADRE peptides to finalize the multitope vaccine construct. The final vaccine's physicochemical features, antigenicity, toxicity, allergenicity, and solubility were evaluated for use in humans.

Results: The output of the computational analysis revealed that the designed multitope construct has passed these assessments with satisfactory scores where, as the last stage, we performed a molecular docking study between the potential vaccine construct and *K. pneumonia* associated immune receptors, TLR4 and TLR2, showing affinitive to both targets with preferentiality for the TLR4 receptor protein. Validation of the docking studies has proceeded through molecular dynamics simulation, which estimated a strong binding and supported the nomination of the designed vaccine as a putative solution for *K. pneumoniae* and *P. aeruginosa* coinfection. Here, we describe the approach for the design and assessment of our potential vaccine.

Biography

Khalid Abd-Elghany studied Pharmaceutical Science at Al Azha University, Egypt and graduated as MS of Microbial Biotechnology in 2014 from El Sadat city University, Egypt. Ph.D, of Microbial Biotechnology from El Sadat city University, Egypt 2018.

Armin Mehmedović[1*], K. Bodulic[2], M. Hrabak Paar[3], K. Viskovic[1]

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Use of modified brixia score in predicting mortality in hospitalized patients with COVID-19 pneumonia

Purpose: To evaluate the value of modified Brixia scoring system in predicting mortality in hospitalized COVID-19 patients.

Methods and materials: An observational retrospective pilot study included 292 patients (178 male and 114 female) with PCR-confirmed COVID-19 infection hospitalized at the University Hospital for Infectious Diseases Dr. Fran Mihaljevic from February 2, 2020, to December 31, 2021. Initial chest X-ray images performed at admission were analysed and scored according to the modified Brixia scoring system, having each lung divided in three zones – upper zone, middle zone, lower zone (aortic arch profile and lower profile of left pulmonary hilum being landmarks for dividing). A numerical value was added for each zone based on the morphology and extent of opacities (0 - normal lung parenchyma; 1 - interstitial involvement only; 2 - presence of radiopacity for less than 50% of the visible lung parenchyma; 3 - presence of radiopacity for 50% or more of the visible lung parenchyma, maximum value 18). Statistical analysis was done using R. Mann-Whitney U test was used to analyse differences in values of modified Brixia score in patients based on the outcome (deceased/survived). Kruskal-Wallis test was used to determine whether there was a statistical difference in modified Brixia score between groups of patients based on the disease severity (4 categories -mild, intermediate, severe, critical).

Results: Higher values of modified Brixia score were associated with higher mortality ($p<0.001$), with mean value of 12 in the group of patients who died vs. 6 in the group of patients who survived. Increased disease severity was followed by greater values of modified Brixia score ($p<0.001$; mean scores 5, 7, 11, 12, respectively). When comparing patients who developed acute respiratory distress syndrome (ARDS) to those who didn't, there was a difference in values od modified Brixia score between the two groups ($p<0.001$; mean score 12 vs. 8, respectively). Higher values of modified Brixia score were also associated with intensive care unit admission ($p<0.001$) and the need for mechanical ventilation ($p<0.001$).

Conclusion: Modified Brixia scoring system can be useful in evaluating patients who are at increased risk for developing more severe forms of COVID-19 pneumonia which can lead to ARDS and greater mortality. Our results suggest that increasing values of modified Brixia score correlates with disease severity. However, more research is needed, preferably on a larger group of patients, to confirm our findings.

Audience Take Away Notes

- Modified Brixia score could be useful and time-efficient tool for initial assessment of extent and severity of lung involvement in COVID-19 pneumonia, aiding clinicians in optimal patient management and potentially recognizing high risk patients that could develop ARDS
- In our study higher values of modified Brixia score were associated with higher mortality, suggesting that it could have an important role as a predictive factor for fatal outcome
- Due to relative simplicity of modified Brixia scoring system, it could easily be used in vast majority of clinical settings

Biography

Dr. Mehmedovic studied Medicine at the School of Medicine, University of Zagreb, Croatia and graduated in 2017. He is a recipient of Dean's Commendation for academic excellence in year 2015. He worked two years as a GP in health center of Zagreb county and currently is a 3rd year radiology resident at the University Hospital for Infectious Diseases Dr. Fran Mihaljevic and 1st year PHD student at the School of Medicine, University of Zagreb. He is a co-author of several scientific manuscripts and was awarded for the best abstract at the 8th Congress of Croatian Society of Gastroenterology, 2018, Split.

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Piringer kuchinka's lymphadenitis revealing visceral leishmaniasis in an immunocompetent: A case report

Background: Piringer Kuchinka's lymphadenitis is a non-specific histological entity with multiple etiologies. We present an atypical case of visceral leishmaniasis in immunocompetent adult.

A case report: 26-year-old male student in perfect health, living in an urban area, Presents a right inguinal adenopathy slightly painful on palpation. The other gonglioner areas are free, in particular hepatosplenic. Fine needle aspiration's diagnostic suggests large B-cell lymphoma. The immunohistochemical profile of the excisional biopsy concluded with piringer Kuchinka's lymphadenitis. Multiple etiologies have been evoked, refuted in front of negative assessments apart from visceral leishmaniasis, which is confirmed by a positive serology with the Western Blot, and a positive PCR on blood and marrow puncture slide. No immunodepression field is found. Treatment with liposomal amphotericin B 04 mg/kg /day for 5 days is received. Evolution is good

Conclusion: The molecular technique remains the cornerstone of the diagnosis of visceral leishmaniasis in its atypical presentation.

Cintia Gisela Cevallos*, Rosa Nicole Freiberger, Cinthya Alicia Marcela Lopez, Alex Guano Toaquiza, Franco Sviercz, Patricio Jarmoluk, Jorge Quarleri, M. Victoria Delpino

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SARS-CoV-2 viral load and replication in postmortem pulmonary and extrapulmonary tissues

Background: The novel coronavirus disease 2019 (COVID-19), caused by SARS-CoV-2 is severe and involves multiple organs in approximately 5%-10% of patients, leading to multi-organ dysfunction and failure.

Methods: Necropsy tissues (lungs, heart, liver, kidney, small-intestine) were obtained through minimally invasive autopsy from 15 cadaveric donors whose postmortem swabs tested positive for SARS-CoV-2 (median age: 69 years; females: 8; hospitalized: 7; vaccinated: 7). until use tissues were stored in RNAlater® at -70°C. SARS-CoV-2 RNA detection and viral load –VL– (as RNA copies/mL, for ORF1ab and N gene) were determined (RT-qPCR-DisCoVery); SARS-CoV2 infectivity was measured using VeroE6 cell culture and VL (in 7-day/cell culture supernatants).

Results: SARS-CoV-2 RNA was detected in lung (8/15), heart (6/15), liver and kidney (4/15), and small-intestine (4/9). The highest VL level (median values in copies/mL for ORF1ab/N gene) was measured in lung samples (1.5x104 /1.9x104; range: 1.01x102 to 1.14x108) but without significant differences against extrapulmonary tissues (liver: 5.6x102 /1.6x102, heart: 5.5x102 /4.4 x102, kidney: 1.3x103 /9.1x102, and small intestine: 9.4x103 /1.6x102). Median VL measured in tissues from non-hospitalized vs. hospitalized cases was slightly lower (5.5x101 vs. 3.0x103 copies/mL; p=0.1). Infectious SARS-CoV-2 was demonstrated in different tissues (lung: 8/15, heart: 11/15, liver: 4/15; kidney: 3/15; small-intestine: 2/9) but the VL (as RNA copies/mL) was significantly higher ($p < 0.05$) in the lung (1.4x106) and heart (1.9x106) samples than other tissues.

Conclusions: The postmortem presence of infectious SARS-CoV-2 is demonstrated in pulmonary and extrapulmonary tissues even among vaccine-recipient decedents. Autopsies of COVID-19 cases are associated with a consistent biological risk. These findings support initiatives that make transplants safe by reducing the potential for transmission of SARS-CoV-2.

Biography

My name is Cintia Cevallos from Argentina and I will proceed to describe briefly my academic and professional training.
2010: I started an internship as an undergraduate student to obtain a bachelor's degree at the School of Chemistry, Biochemistry and Pharmacy, University of San Luis, Argentina. Research topic: Effects of exposure to cadmium in drinking water on parameters related to oxidative stress in the small intestine of rats. Supervisor: Dr. Larregle Ethel Viviana.
2012: I got a BSc. in Molecular Biology from the School of Chemistry, Biochemistry and Pharmacy, University of San Luis, Argentina.
2013: I started my doctoral studies when the National Research Council from Argentina (CONICET) awarded me with a fellowship. Research project: Study of the evolution of the Human Immunodeficiency Virus (HIV) in Men who have sex with men in Argentina (2000-2013) at the Institute for Biomedical Research on Retroviruses and AIDS (INBIRS, School of Medicine, University of Buenos Aires). Supervisor: Dr. Maria Mercedes Avila and co-supervisor: Dr. Jorge Quarleri.
2019: I got a PhD. in Medical Science from the School of Medical Sciences, University of Buenos Aires, Argentina. In this year I also worked as a Forensic expert for the Scientific Police Department of Buenos Aires city in the forensic genetics area.

2020: I started my post-doctoral studies when the National Research Council from Argentina (CONICET) awarded me with a fellowship. Research project: Cellular cross-talk and modulation of the hepatic profibrotic profile in the context of HIV-HCV coinfection. Supervisor: Dr. Jorge Quarleri. Furthermore, since the COVID-19 outbreak, I also started to participate in the diagnosis area of INBIRS Institute processing a large number of samples (nasopharyngeal swabs) for SARS-CoV-2 detection, working under ISO9001 requirements.
2021: In the context of the SARS-CoV-2 pandemic as a postdoctoral student I joined to work on a research project focused on evaluating the direct mechanisms of pathogenesis cells associated with the coronavirus SARS-CoV-2.

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Molecular identification of babesia and borrelia species that are potential cause of babebiosis and lyme disease: A one-health concept study of wild ticks

Ticks are second to mosquitoes in disease transmission yet, significant gaps remain in our knowledge of how ticks transmit pathogens to wild animals and even humans. According to the one-health concept, wild ticks may contribute to the transmission of tick-borne diseases such as Babesiosis and Lyme disease. This project focused on identifying ticks in the genera *Ixodes*, *Haemaphysalis*, and *Rhipicephalus* that are associated with *Babesia* and *Borrelia* species sampled from the wild animals. This was to add to the knowledge of transmission as wild ticks could be reservoirs of *Babesia* and *Borrelia* species capable of causing Babesiosis and Lyme disease. Conventional and nested PCR was done using general Babesia primers and specific Borrelia primers to detect Babesia and Borrelia species. The data showed that wild ticks in the genera *Ixodes*, *Haemaphysalis*, and *Rhipicephalus* may be reservoirs of disease-causing *Babesia* species group and *Borrelia burgdorferi* clade, noticeably for causing Babesiosis and Lyme disease in wild animals and even humans. These pathogens were found in all tick species. This may be due to the life cycle of ticks and their parasitic-feeding relationship with their wide range of mammalian bushmeat, including *Civettictis civetta*, *Thryonomys swinderianus*, *Tragelaphus scriptus*, and *Cricetomys gambianus*. In future work, there are plans on sequencing and do phylogenetic analysis on the 16S gene of the ticks, the 18S ribosomal DNA gene of the Babesia species, and the gene encoding for Flagellin B of the *Borrelia burgdorferi* which will be compared to the data of *Babesia* and *Borrelia* species found in ticks on domestic mammalian animals

***Keywords*: *Borrelia burgdorferi*, *Babesia* species, ticks, mammalian bushmeat**

Audience Take Away Notes

- This study will contribute to data on ***Babesia*** and ***Borrelia*** species transmission from ticks as ticks are second to mosquitoes in disease transmission among humans
- There is a gap in knowledge about the transmission of *Babesia* and *Borrelia* species from wild animals to humans, so this study will give information on the transmission of *Babesia* and *Borrelia* species (a one-health concept study). This is the first study to be done in Ghana
- This study targets bushmeat as it is highly consumed in Ghana. Market women may have contact with ticks that are reservoirs and vectors of disease-causing pathogens including *Babesia* and *Borrelia species*
- This study has addressed the potential transmission of Babesiosis and Lyme disease from wild ticks

Biography

I am Emmanuel Boafo, a postbaccalaureate in 2021 at the University of Ghana, and offered Animal Biology and Conservation Science in my undergraduate study. I am a research assistant at Noguchi Memorial Institute for Medical Research, University of Ghana at the Department of Immunology with two years of experience in biomedical research. I joined Professor Ben Gyan's research group, working as a research assistant on the study Blood-Brain Barrier, Cerebral Malaria and Exosome Study. I have done multiple oral and poster presentations during my biomedical research exploration.

Zeineb Denden[1], Houda Limam[2*], Sahar Sallem[1], Ameni Bellaaj[1], Helmi Ernandez[1]

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Osteoarticular brucellosis in an endemic region: Epidemic-clinical aspects, diagnosis, and treatment of 49 cases

Background: Brucellosis is a common bacterial zoonotic disease with a broad spectrum of clinical manifestations. Osteoarticular involvement is frequent, with a reported prevalence ranging from 27% in no endemic regions to 36% in endemic regions. The sacroiliac and spinal joints are the most common affected sites. The aim of this study was to determine the epidemiological characteristics, clinical manifestations, diagnostic tools, and outcome of Osteoarticular Brucellosis (OAB) in an endemic region.

Method: We conducted a retrospective analysis of records of the patients diagnosed as OAB and attending the infectious diseases department from 2017 to 2022. A diagnosis of OAB was established in all patients with compatible clinical and radiological findings in the presence of an antibody titer of 1/80 or more in Standard Tube Agglutination (STA) test or by a positive culture.

Results: A total of 49 patients with OAB (34 males, 15 females) were enrolled. Median age was 55 years (age range, 14-82 years). Forty patients (82%) lived in rural areas and 26 patients (53%) had a history of handling animals or animal excretions. Forty-two patients (86%) reported consuming unpasteurized milk and/or dairy products. Median diagnostic delay was 90 days (IQR 33-165). The most frequent complaints were fever (86%), sweats (71%) and asthenia (51%). Spondylodiscitis was the most frequent manifestation of OAB (75%). The lumbar spine was the most commonly affected spinal site (n=29), followed by thoracic (n=13) and cervical segments (n=7). Spondylodiscitis was followed by sacroiliitis (n=7) and peripheral arthritis (n= 2). One patient had a septic loosening of total knee Arthroplasty. Multiple joint involvements was noted in 4 cases.

Cases: sacroiliitis plus spondylodiscitis in 3 cases and sacroiliitis plus peripheral arthritis in one case. STA test was positive in 48 patients. Blood cultures yielded Brucella spp in 4 cases. Disco-vertebral needle biopsy was performed in 5 patients with spondylodicitis. Only 2 biopsy specimens yielded positive culture results. All patients received antibiotic treatment with a combination of two (77%) or three agents (23%). The most commonly used antimicrobial combination therapy was rifampicin plus doxycycline (53%). Median duration of antimicrobial treatment was 143 days (IQR 98-180). Surgical treatment was performed in 5 patients. Median follow-up period was 210 days (IQR 120-315). Relapse occurred in 4 cases.

Conclusion: In our study, spondylodiscitis was the most common form of OAB. The lumbar spine was the most frequently involved. Early symptoms are non-specific, leading to delayed diagnosis and late onset of treatment. Brucellosis should be considered in all patients with unexplained fever and osteoarticular complaints in endemic areas or in patients visiting such areas.

Audience Take Away Notes

- The spine and sacroiliac joints tend to be the most commonly affected sites of osteoarticular brucellosis
- The isolation of *Brucella* from bone biopsy or blood culture may be difficult, and therefore diagnosis is mainly based on serologic testing
- Patients with osteoarticular brucellosis need a long-term antimicrobial treatment

Biography

Dr Houda Limam is a senior resident doctor (infectious diseases) in Tunisia.

Rachida Belhadj Aissa*, N. Haddag, M Limane, F/Z Amani, F Taicha, M Djema, N Ait Kaci, R Hamiche, F-Z Chabani, M Mebarki, H Cherabit, A Tebani, F Djani, K Saighi, H Zane, B Bouzouidja, F-Z Djermoum, M Boumaaza, I Maazouz, K Yahouni, H Ferdjani, N Chaib, F-Z Athmani, M Yousfi

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Therapeutic challenges of cryptococcosis in immunocompetent and people living with hiv in boufarik, Alegria: A retrospective analysis

Cryptococcosis is a fungal potentially fatal infection, especially in its meningeal location. It's most often due to Cryptococcus neoformans (Cn). Cellular immunosuppression, in particular the advanced stage of HIV infection, is a frequent risk factor for the onset of the disease in Third World countries.

We present a retrospective analysis of patients treated for Neuromeningeal Cryptococcosis (NMC) or Antigenemia Alone (AGC); from January 2018 until April 2023, in the infectious diseases department of the Public Hospital Establishment (EPH) Boufarik, Algeria.

Findings: Twenty patients collected. Male were the more affected (65%). The mean age was 43.3 ± 15.7 years. The risk factor associated with cryptococcosis was mainly AIDS (95%) with a CD4 count < 100 cells / µl in 63%. No immunosuppression field was found in one patient. NMC was the predominant clinical form (60%), of which, one was associated with chorioretinitis. The therapeutic regimens are guided by national and international recommendations: for NMC the combination of amphotericin B (amphB) + fluconazole (only association available in country) is used in 84% either amphotericin B deoxycholate (30%) or AmphB liposomal (70%); fluconazole 800 mg/d - 1200 mg/d alone in induction therapy was also used (16%) . the mean duration of induction therapy was 25.8 ± 13 days. The transition to consolidation regimen is conditioned by tolerance to AmphB, the availability of the drug and the negativity of the CSF culture. However, there is discordance in vitro/in vivo Cn's antifungal susceptibility with a delay in LCS culture negativation. Pre-emptive treatment (fluconazole 400mg/day) for AgC was prescribed in 37,5%. relapse of CNM is noted in 2 patients after discontinuation of prophylaxis. The association with other opportunistic infections, namely tuberculosis (5), CMV viremia (4) worsened the prognosis. Death affected 35% of patients.

Conclusion: Despite increasing access to retroviral therapies, persons presenting with advanced HIV disease remains commen. Although cryptococcosis remains rare in immunocompetent patients, new molecules and therapeutic strategies must be developed regardless of the underlying terrain.

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