magnus Group

International Conference and Expo on

CLINICAL MICROBIOLOGY

JUNE 17-18

VIRTUAL EVENT

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BOOK OF ABSTRACTS

INTERNATIONAL CONFERENCE AND EXPO ON

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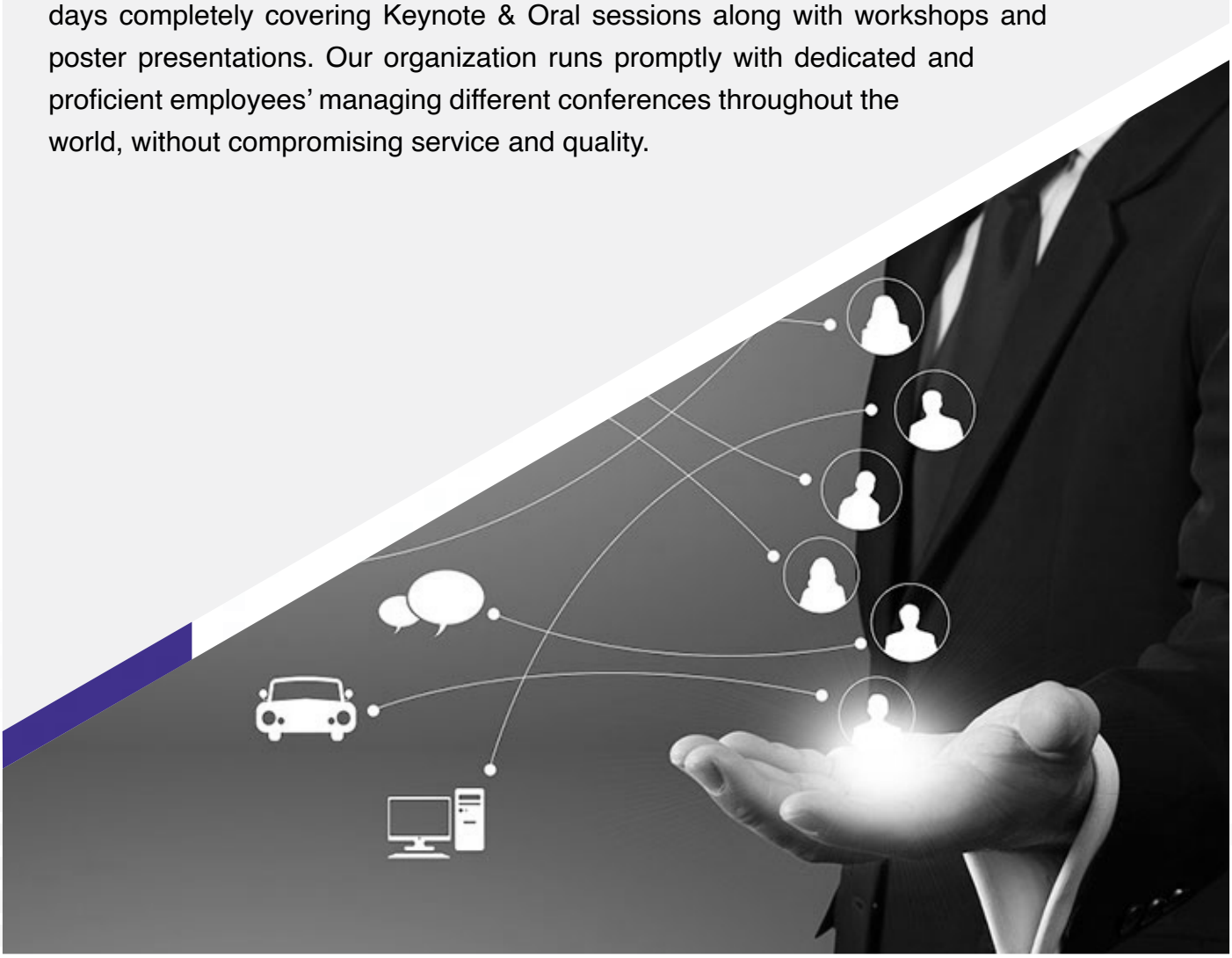
ABOUT MAGNUS GROUP

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 conference 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 ICCM 2022

With an earnest objective to congregate Microbiology professionals, researchers, scientists and microbiology industries, Magnus group cordially welcomes you to attend International Conference and Expo on Clinical Microbiology “ICCM 2022” going to be held from June 17-18, 2022 to discuss on Microbiology and Public Health concerns with the theme “*Scoping Out Innovations and Advancements in Clinical Microbiology*”. ICCM 2022 is an international platform for all health care professionals, experts, researchers, scientists, physicians,doctors, nurses and students working in various medical departments to share their views and to discuss on currentchallenges to achieve a better healthcare system to benefit the mankind.

This conference is designed with keynote, oral and poster presentations on various sessions and topics including the impact of COVID 19 on Public health.We are confident that our conference will provide you with an incredible chance to explore new horizons in your field and we hope to see you at ICCM 2022.

KEYNOTE FORUM

DAY 01

INTERNATIONAL
CONFERENCE AND EXPO ON

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17-18 JUNE

Giuseppina Mandalari*, Rosaria Gitto, Francesca Mancuso, Federica Bucolo, Teresa Gervasi, Giovanna Ginestra, Laura De Luca

University of Messina, Italy

The *in vitro* potential of novel carbonic anhydrase inhibitors against candida spp

Given the increased antimicrobial resistance, global effort is currently focused on the identification of novel compounds, both of natural and chemical origin. In immunocompetent subjects, Candida spp. are responsible for mucosal infections, including thrush and vaginitis, which could lead to invasive candidiasis in immunocompromised patients, especially with more species becoming multi-drug resistant.It is well-known that Candida spp. employ □-carbonic anhydrases (□-CAs) to accomplish the reversible hydration of CO2, an essential process to guarantee the survival of these pathogenic yeasts.Furthermore, small molecules bearing the sulfonamide moiety as zinc-binding group (ZBG) might be valuable agents reducing yeast virulence throughout the □-CA inhibition. In this study we screened an in-house library of arylsulfonamides against a range of Candida spp. Strains : Candida albicans ATCC 10231, Candida parapsilosis ATCC 22019, Candida glabrata DSMZ 70614, three clinical isolates of Candida albicans, two clinical isolates of Candida glabrata, two clinical isolates of Candida parapsilosis. The screening was performed by the determination of the Minimum Inhibitory Concentration (MIC).

Results showed

A fungistatic activity of arylsulfonamides against all tested strains with the exception of Candida glabrata DSM 70614 and one clinical strain of Candida glabrata at concentrations ranging between 0.125 and 1 mg/mL.A fungicidal effect was detected against Candida glabrata strain 33 e Candida albicans strain 16 at the concentration of 0.5mg/ml.The structural-function relationship has been explored through the synthesis of a series of compounds bearing a different aromatic tail as well as through the variation in the linking group. In order to confirm the role played by ZBG, an analog compound lacking the sulfonamide moiety was tested. These data could help provide novel therapeutics for topical use to treat fungal infections and increase the potential effectiveness of the association between novel compounds and commercial antifungals in order to combat drug resistance.

Audience Take Away:

- Candida spp. are responsible for mucosal infections, including thrush and vaginitis, which could lead to invasive candidiasis in immunocompromised patients.
- Carbonic anhydrase inhibitors are active against Candida spp. Novel synthetic compounds could therefore be used to treat drug resistance.

Biography

Giuseppina Mandalari is an Associate Professor in Microbiology and Clinical Microbiology at the University of Messina, Italy. She graduated in 2000 and obtained her PhD in 2003. During this period she joined various research groups at the Institute of Food Research in Norwich, UK. She has published more than 80 research articles in SCI(E) journals.

Jawad Alzeer

University of Zurich, Switzerland

Reduction of viral resistance and activation of the immune system through implementation of the le-chatelier principle

Attempts to improve prevention and develop cures are highly appreciated. Indeed, many approaches and models to prevent and cure diseases have been developed and pursued. However, a major challenge in research is to improve the effectiveness of existing drugs. For this purpose, many avenues and approaches have been explored, but fighting a viral infection remains a challenge, mainly because of the resistance of the virus to existing drugs or vaccines. The establishment of a compatible system and offering a reproducible response are favourable to achieve a well-organised and regulated health system. Permissible medicine "Halalopathy" has been introduced as a new model for building a compatible system between mind, and health system. Halalopathy provides a new approach to preventing disease by managing the entropic state and/or facilitating recovery by implementing the concept of permissible medicine. Halalopathy activates potential by creating a compatible relationship between therapeutic medicines and behaviours that can affect epigenetic traits such as lifestyle. The compatibility sets up a highly ordered system that has reduced entropy and enriched potential energy. Entropy was introduced by halalopathy as an essential element in the prevention and cure of disease. Potential energy dispersion and entropy enrichment can be used to prevent and/or cure COVID-19.The method is based on Le Chatelier's principle and utilises safe and available substances that can be easily taken by most patients. There is potential for the proposed method to reduce COVID-19 to a threshold level that might boost the patient's immune system and enhance recovery.

Keywords: Entropy, Potential Energy, Compatibility, COVID-19, Le Chatelier principle

Biography

Dr. Jawad Alzeer was born in Hebron, Palestine, graduated from Alhusein high school, and attended college at Karachi University, Pakistan, earning a B.Sc. in Chemistry, M.Sc. in Organic Chemistry, secured second position with distinction. In 1996, he received his PhD in Organic Chemistry from the Swiss Federal Institute of Technology (ETH) Zurich where he developed a cellulose analogue by replacing the glycosidic linkage with butadiyne units. After PhD, Alzeer joined Hoffmann La Roche as a postdoc and developed a new pharmacophore for antimalarial drug, then moved to Michigan University where he got involved in the discovery of new RT HIV inhibitor, following that he joined University of Zurich to become a Research Associate, during his stay at Zurich University he was involved in the design of chemical approach for targeted mutagenesis and evaluation of potential anticancer compounds that inhibit telomerase enzyme. From 2009 to 2010, Alzeer worked as a senior scientist at Swiss health care company, Lipomed. In 2010, Alzeer joined Halal Certification Service as a senior consultant, highly specialized in auditing pharmaceutical and other chemical companies.

Meanwhile Alzeer was appointed as an assistant Professor at Palestine Polytechnic University (PPU) during his stay at PPU, Alzeer was supervising a number of Master students and focused his research on the development of anticancer drug from Natural products. In 2014 founded Swiss scientific society for developing countries (SSSDC), as a neutral and non-profit organization devoted to promote communications, research, education and business between Switzerland and Developing countries. Alzeer is currently the director of SSSDC and the head of scientific board at Halal Certification Service, meanwhile Alzeer is a Senior Scientist at the University of Zurich, his research interest focused on rational use of natural product to design anti cancer drug and tackling different halal issues.

Muhammad Morshed

University of British Columbia, Canada

Utilization of SARS-CoV-2 serology in public health and clinical uses

The SARS-CoV-2 virus causes COVID-19 disease, which was first diagnosed in late December 2019 among a few people with unknown respiratory illness in Wuhan city, Hubei province, China. Presumably this virus jumped from a natural host to human, and that occurred in one of the open food markets in Wuhan city, spreading very quickly to neighbouring provinces, neighbouring countries and eventually different continents. The World Health Organization declared the outbreak a Public Health Emergency of International Concern on 30 January 2020, and a pandemic on 11 March 2020.This virus killed over 5.5 million people globally as of 2021 and there is no sign of stopping with the latest addition of Omicron variant. However; SARS CoV-2 also forced us to invent new skills and technology not only to defeat it but also to propel ourselves forward. For instance, serological diagnostic tests in the form of Point of Care Test (POCT) format and regular EIA format become available in a couple of months instead of years.

Although molecular/ RT PCR become the test of choice for clinical diagnosis, serology has also limited uses for patient care in addition to Public Health (PH) uses. For PH, SARS-CoV-2 antibody testing is testing is essential for estimating population based seroprevalence and also to assess vaccine efficacy or responses which enable evidence-based decision making for public health recommendations. For clinical care, SARS CoV-2 antibody testing help select group of population where molecular/PCR test is negative. So it may help to increase case identification when used as an adjunct to routine molecular testing in those select cohorts; however, it is become challenging due to the emergence of new variants. So, in this presentation we will review serological testing of patients' blood against SARS Cov-2 virus and highlight pros and cons of uses of serological testing in public health and its uses of clinical diagnosis.

Biography

Dr. Morshed is a public health clinical microbiologist at the BCCDC Public Health Laboratory in Vancouver, British Columbia, Vancouver, Canada, where he is Head of the Zoonotic and Emerging Pathogens section. He is also a Clinical Professor in the Department of Pathology and Laboratory Medicine at the University of British Columbia. His area of interest is spirochaetal disease such as syphilis and Lyme disease and also working on SARS CoV-2.He has also added significantly to the general knowledge and understanding of these diseases with more than 120 refereed scientific publications. On his recognition, Dr. Morshed received an Excellence in Clinical Services Award from UBC's Department of Pathology & Laboratory Medicine in 2016, RBC Top 25 Canadian Immigrant Awards in 2017; Distinguished Microbiologists Award by the Canadian College of Microbiologists in 2018 and elected as an Expatriate Fellow of the Bangladesh Academic of Sciences in 2020.

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SPEAKERS

DAY 01

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Fei Deng*, Yi Li, Ewa M. Goldys
University of New South Wales, Australia

CRISPR/Cas12a-powered ultrasensitive immunosensing for the detection of single microorganisms

Waterborne pathogens, such as *Cryptosporidium parvum*, pose a major threat to public health globally, and this requires screening of drinking and environmental water for low number of contaminating microbes.However, current detection approaches generally require trained experts with sophisticated instruments, and not suitable for large-scale screening and rapid outbreak response. Recent advances in ultrasensitive CRISPR/Cas-based biosensing continue to expand the range of detectable molecular targets, but larger structures, such as single microbes, could not be directly detected so far. Here, we report an ultrasensitive CRISPR/Cas-based immunosensing method suitable for microbial detection which links antibody-based recognition with CRISPR/Cas12a amplification through an antibody-DNA conjugate.

This approach can detect whole 4 μm size *Cryptosporidium parvum* oocysts with a linear range from 6.25 – 1600 oocysts/mL, at a maximum sensitivity of single oocyst per sample. It can remain effective for various complex sample matrices. This method uses the same experimental setup as a conventional ELISA thus helping to avoid microscopy-based identification for *Cryptosporidium*, which represents the gold-standard but requires high level expertise and time-consuming manual counting. This work highlights the unexpected potential of CRISPR/Cas-based biosensing for ultrasensitive detection of large whole microorganism structures and opening a pathway towards sensing of new biologically and medically significant targets.

Audience Take Away:

- A CRISPR/Cas12a-based ultra-sensitive whole waterborne pathogen detection method.
- A hybrid single strand DNA oligo and antibody conjugate targeting the pathogen surface antigen.
- Capable with plate reader for conventional ELISA assay with same experimental setup.
- 3 orders of magnitude quantitative detection with maximum single microorganism sensitivity for *Cryptosporidium parvum* oocysts.
- Suitable for direct testing of diluted mud samples from water treatment plant.

Biography

Dr Fei Deng received his Ph.D. degree (specialising in precision diagnostics and Biomedical Engineering, 2021) from The University of New South Wales (UNSW), Sydney, NSW, Australia. He subsequently took up a postdoctoral research fellowship at the Graduate School of Biomedical Engineering (GSBmE), UNSW.Deng's research interests include point-of-care biosensing device, continuous biosensing device,CRISPR biosensing device and in vivo biosensing device.He is currently a key member of a multi-disciplinary team in GSBmE, leading the development of point-of-care biosensing device and real time continuous biosensing device.

Abduh Murshed
Tongji University, China

O-GlcNAcylation enhances sensitivity to RSL3 induced ferroptosis via the YAP TFRC athway in liver cancer

Ferroptosis is a form of regulated cell death characterized by iron-dependent accumulation of lipid hydro peroxide to lethal levels. YAP has been reported to play a pivotal role in controlling ferroptotic death, and the expression of YAP is enhanced and stabilized by O-GlcNAcylation. However, whether O- GlcNAcylation can increase the sensitivity of hepatocellular carcinoma (HCC) cells to ferroptosis remains unknown. In the present study, we found that OGlcNAcylation increased the sensitivity of HCC cells to ferroptosis via YAP. Moreover, YAP increased the iron concentration in HCC cells through transcriptional elevation of TFRC via its O-GlcNAcylation. With YAP knockdown or YAP-T241 mutation, the increased sensitivity to ferroptosis induced by O-GlcNAcylation was abolished. In addition, the xenograft assay confirmed that O-GlcNAcylation increased ferroptosis sensitivity via TFRC in vivo. In summary, we are the first to find that O-GlcNAcylation can increase ferroptosis sensitivity in HCC cells via YAP/TFRC. Our work will provide a new basis for clinical therapeutic strategies for HCC patients.

Audience Take Away:

- This work will help the audience and researches in development their researches and can use to expand their research or teaching, provide a practical solution to a problem that could simplify.
- Explore the treatments of Tumors and will open a prospects for a new development in science and medicine.
- Our work also will provide a new basis for clinical therapeutic strategies for HCC patients.

Biography

Dr. Abduh Murshed have studied Bachelor's degree at department of Medical Laboratory, Faculty of Medicine and Health Science, Sanaa University, Sanaa, Yemen after that win a scholarship to study Master degree in Medical Microbiology Dokuz Eylül University, Izmir, Turkey. When he finished his Masters study he directly win another scholarship to study Doctorate (PhD) in department of Clinical Laboratory Diagnostics in Medical School, Tongji University, Shanghai, China. His study will be completed around 2022. His Mother tongue is Arabic, he can speak English, Turkish and Chinese. He is published articles: 2 SCI paper as (co-first author) and 1 SCI paper as (co-author). He attended to 3 International conference and present orally in that conference. He win 1 ward (Tongji University President Scholarship award for good academic studies foryear2019/2020. Now; he is working in Tongji University in department of Clinical Laboratory Diagnostics as a PhD student.

Xu Yang
Shanghai University of Medicine and Health Sciences, China

Interpretation of non-responders to SARS-CoV-2 vaccines using who international standard

Coronavirus disease (COVID-19), caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), was declared a pandemic. Questions about non-responders to SARS-CoV-2 vaccines remain unaddressed. Here, we report data from people after administering the complete dose of SARS-CoV-2 vaccines using the World Health Organization International Standard for anti-SARS-CoV-2 immunoglobulin (Ig).Our study showed that immune cells such as CD4 cells, CD8 cells, and B cells and anti-spike IgG levels were significantly reduced in the elderly (60 years and older). There were 7.5% of non-responders in the age group of 18 to 59 years and 11.7% in the age group of 60 years and older. An individual with a titer of anti-SARS-CoV-2 spike IgG that is below 50 BAU/mL is considered a non-responder at 30 to 90 days after the last vaccine dose. Booster vaccination may be recommended for non-responders to reduce disease severity and mortality.

There are several potential strategies that are suggested to quickly end the COVID-19 pandemic : (1) increase the vaccination rate of the population; (2) develop vaccines against emerging and potential variants ; (3) administer booster vaccines for non-responders; (4) accelerate clinical trials of intranasal SARS-CoV-2 vaccines to prevent transmission; (5) assessment of humoral immune response in children, the elderly, and immunocompromised individuals within 1 to 3 months after administering the fourth dose; and (6) incorporate additional protective measures for individuals with persistent (fourth or fifth dose) negative humoral immune response after booster vaccination, such as injection of anti-SARS-CoV-2 immunoglobulins, antiviral drug treatment, and use of N95 masks in endemic areas.

Biography

Dr. Xu has been a full professor at Shanghai University of Medicine and Health Sciences for several years. He has contributed to many areas of clinical immunological research, including early detection of SARS *fingerprint* using immune-mass-spectrometry in 2003, special diagnosis in early stage of cancer,COVID-19 severity and mortality associated with the decrease in CD4, CD8 and B cells. He is the inventor of "a method for detection of severe COVID-19 caused by co-infection with influenza A and B viruses". *He* received *his PhD from the* Cornell University. He is the Secretary General of Global Immunity Surveillance Alliance & a national expert in China and recipient of numerous awards and honors.

Andrey Dmitrovskiy*[1,2], Marat Syzdykov[1], Tatyana Lyatomskaya[1], Nailya Ospanbekova[2]

[1]National Science Center for Extremely Dangerous Infections, Kazakhstan
[2]Kazakh-Russian Medical University, Kazakhstan

Diagnostics and clinical manifestations of listeriosis in Kazakhstan

The problem of Listeriosis is quite acute in the world. At the same time, in literature, Listeriosis is usually associated with a severe intestinal infection. As a result of more than 30 years of Listeriosis studying in Kazakhstan (the manual on Listeriosis we published in 1995,we have a clear idea of the epidemiology, spectrum of clinical manifestations and laboratory diagnosis of Listeriosis. So, in our view,Listeriosis exists in two “planes” as a zoonotic infection circulating in the numerous animal species, including mammals, birds, fish and reptiles on the one hand, and as sapronosis, when listeria can persist for a long time and even multiply in environmental conditions. Infection can occur alimentary and aerogenic and contact, including sexual and vertical, ways.At the same time, depending on the mechanism of infection, the following primary focal forms develop: cutaneous (infected through the skin), conjunctival (infected through the mucous membranes of the eyes), oropharyngeal (infected through the oral mucosa), intestinal / abdominal (when Listeria enters the stomach and intestines), genital (infected through the mucous membrane of the genital tract). Usually regional lymphadenitis developed. Listeriosis can be acute and chronical, while *Listeria* can persist for a long time and be found on the mucous membranes of the oropharynx / tonsils (chronic tonsillitis / pharyngitis), in the gallbladder and bile ducts (chronic cholecystitis / cholangitis), the urinary system (chronic pyelonephritis), the reproductive system (inflammatory processes in men and women). As a result of hematogenic dissemination, Listeria causes secondary foci in the lungs (pneumonia), liver (hepatitis), kidneys (pyelonephritis), central nervous system (meningoencephalitis), secondary skin lesions and other.

Laboratory diagnostics should consist of classical bacteriological study of clinical material from primary or secondary foci of infection, and punctate of enlarged lymph nodes. PCR is useful.Interpretation of serological examination (ELISA) is more complicated, because in the absence of IgM and the presence of IgG only, it is necessary to determine the activity of the infectious process.In this presentation, we also wanted to demonstrate the features of skin lesions in listeriosis, since this side of listeriosis is little known to the general medical community. Characteristic skin manifestations develop with a cutaneous or ulcerative form of infection, passing through the stages of development of a spot - papule - vesicle - ulcer. The most informative method of diagnosing the skin form is bacteriological examination of the skin affect. Skin effects develop at the site of listeria penetration through skin damage (even at the site of mosquito bites). They can be either single or multiple.On the other hand, skin lesions, in the form of multiple skin affects (secondary), can occur during the generalization of the process, as manifestations of secondary foci.Thus, the material from skin lesions should also be examined for listeria (bacteriological or PCR) with an appropriate clinical manifestations, among other etiological factors of infection. Listeria isolated in Almaty more often had sensitivity to the following antibacterial drugs : Fluoroquinolones (ciprofloxacin – 85 - 88%), cephalosporins (ceftriaxone, cefaclor - 85%).

Audience Take Away:

- Participants will learn the spectrum of listeriosis clinical manifestations, the features of skin manifestations and the informative value of methods for diagnosing listeriosis.
- The results obtained by us can be used by the participants for teaching in the field of microbiology, epidemiology and infectious diseases.
- The presented data provide a practical solution to the problem of diagnosing a number of syndromes and improve laboratory diagnostics and treatment of listeriosis.

Biography

Andrey Dmitrovskiy was born in 1950, in Almaty, Kazakhstan, graduated from Almaty Medical University in 1973, he worked as infectious disease specialist,completed residency at Kazakh Institute of Microbiology.He worked for 20 years at Kazakh Anti-Plague Institute, defended PhD (Yersinioses) and doctor of science (Plague) dissertations, worked at CDC CAR, AECOM. Professor of Kazakh National Medical University. Participated in the diagnostics and anti-epidemic measures for outbreaks of typhoid fever, brucellosis, anthrax, plague, hemorrhagic fevers, cholera, yersinioses, leptospirosis, listeriosis. Currently, he is head of laboratory of NCB (CRL) and chief research of the National Center for Extremely Dangerous Infections.

Abderrahmen Merghni
University of Tunis El Manar, Tunisia

Antibacterial and antibiofilm activity of turpentine nanoemulsion against methicillin-resistant Staphylococcus aureus

Turpentine essential oil (TEO) is a commercially available product having various application due to its ethno-botanical and ethnopharmacological properties.In the present study, we performed chemical composition of TEO by Gas Chromatography-Mass Spectrometry (GC-MS). Further, TEO was nanoemulsified, encapsulated and characterized by droplet size, PDI, Zeta potential and transmittance. The obtained turpentine nanoemulsion (TNE) was investigated for its antibacterial and antibiofilm potentiality against methicillin-resistant Staphylococcus aureus (MRSA), a model biofilm-forming microorganism. Small micellar TEO nanoparticles were successfully formed with a mean droplet size ranging from 22.52 to 26.54nm.Thermodynamic stability studies revealed homogeneous dispersion of the droplets size confirming the stability of TNEs. The developed nano-emulsions displayed two fold enhanced antagonistic activity against S. aureus in comparison with TEOs, with minimum inhibitory concentration (MIC) values at 0.039% (v/v) against MRSA. Additionally, TNEs displayed potent antibiofilm activity against MRSA strains with percent biofilm disruption of around 70.83%. Findings from this study validates the phytomedicinal significance of turpentine nanoemulsions and envisage its exploration as a natural and cost-effective strategy against bacterial biofilms in medical and industrial sectors.

Audience Take Away:

- Preparation of Nanoemulsion from Turpentine essential oil (TEO).
- Characterization of Turpentine Nanoemulsion (TNE).
- Evaluation of antibacterial efficacy of TNE (compared to the TEO) against methicillin-resistant Staphylococcus aureus.
- Assessment of antibiofilm potential of TNE.
- TNE can be used as an effective agent to prevent surface contaminations with bacterial biofilm in various sectors (valorization of TEO as a disinfectant).

Biography

Dr. Abderrahmen studied Biotechnology at the Monastir University, Tunisia and graduated as MS in 2009. He then joined the research group of Prof. Mastouri at the Faculty of Pharmacy of Monastir, at the Monastir University. He received his PhD degree in 2016 at the same institution. After one year he obtained the position of an Associate Professor of Microbiology at the Faculu of Medicine of Tunis, Tunisia. He has published more than 23 research articles in SCI(E) journals.

Marat Syzdykov*[1], Andrey Dmitrovskiy[1,2], Svetlana Daulbayeva[2], Veronica Sadovskaya[1]

[1]National Science Center for Extremely Dangerous Infections, Kazakhstan
[2]Kazakh-Russian Medical University, Kazakhstan

Analysis of the dynamics of COVID-19 cases in Kazakhstan, 2020

The first cases of COVID-19 in Kazakhstan were imported on March 13, 2020 to the cities of Almaty and Nur-Sultan from Germany and Italy. After March 20, cases of COVID-2019 began to be registered in other regions of the country. To assess the spatial patterns of the spread of COVID-19 in various administrative territories of Kazakhstan, we conducted a descriptive cross-sectional study in 14 regions. GIS analysis of confirmed COVID-19 cases was carried out throughout Kazakhstan at the district level. For each district, the number of cases (in the form of dots) was calculated for spatial analysis. Conceptualization of spatial relations (analysis of the average nearest neighbor) was used to evaluate clustering in districts. This study is aimed at conducting a spatial analysis of the COVID-19 epidemic in Kazakhstan to better understand the current features of the spread of the virus and study its geographical patterns, especially its spatial clustering.

We included in the study 6165 confirmed cases of COVID-19 of which 45.3% were women and 54.7% were men, the average age of the patients was 36.2 ± 16.6 years; 405 of them were children under 14 years old.83% COVID-19 cases were hospitalized, 0.52% died. In the period of 14 days before the onset of the disease, 4.25% of people flew by plane, 0.47% - traveled by train, and most of the COVID-19 patients apparently occurred at the place of residence. The largest number of cases were registered in the south-eastern part of the country (Almaty and Turkistan regions) and in the capital Akmola region.During the analysis, we found clustering of COVID-19 cases in the regions, while mostly the points of cases are scattered and distributed not randomly. Clusters of COVID-19 cases were identified in two regions of Kazakhstan: Almaty (Ili, Karasai, Raiymbek, Talgar districts and Almaty city) and Akmola (Arshali, Yerementau and Shortandy districts).By calculating population density and using this variable to measure its impact on the spread of COVID-19, we have shown that high population density is a risk factor for the spread of COVID-19.Thus, GIS methods of analyzing cases of infection helps to determine the occurrence of random and regular cases of infection on the territory, which can help in solving tasks to determine priority areas in surveillance and management decision-making.

Audience Take Away:

- The audience will use GIS method in surveillance for infectious diseases.
- The presented materials will help in understanding the mechanism of the spread of the epidemic and the development of effective anti-epidemic measures and can be useful in training.

Biography

Marat Syzdykov, was born in 1947 in Karaganda region, Kazakhstan.Graduated from Karaganda Medical University in 1971. Since 1974, he worked at Infectious Diseases Department of the Karaganda Medical University. Since 1991 he worked at the Kazakh Institute of Microbiology as a senior researcher, Almaty, Kazakhstan. Since 1998, he worked as a head of brucellosis laboratory at Kazakh Anti-Plague Institute.Since 1995, - Professor of Epidemiology Department of Kazakh National Medical University, since 2005 - Professor of Microbiology Department of Kazakh-Russian Medical UniversityCurrently, he works as a BS&S Department Chief Researcher of the National Science CenterforExtremelyDangerousInfections. Sphere of interests - zoonotic and extremely dangerous infections, diagnostics and epidemiology.

J.A.A.S. Jayaweera* , W.W. Kumbukgolla
Rajarata University of Sri Lanka, Sri Lanka

The importance of timely introduction of vancomycintherapy against methicillin resistant staphylococcus aureus (MRSA) bacteremia and severity of MRSA bacteremia at teaching hospital, Anuradhapura, Sri lanka

Aim: Worldwide, an estimated 2 billion healthy people carry Staphylococcus aureus (SA) and of these, up to 53 million are thought to carry methicillin-resistant SA (MRSA). MRSA bacteremia patients are more critical to manage and timely introduction of antibiotics is life-saving. The aim of the study was to elucidate the prevalence of MRSA bacteremia in different units of Teaching Hospital, Anuradhapura (THA), and Sri Lanka and assess the clinical characteristics and associated mortality related to timely introduction of vancomycin therapy.

Materials and Methods: The data on MRSA bacteremia which were obtained from THA, for the period of March 2012 to December 2013 were statically analyzed emphasizing the unit-wise prevalence, severity, and comorbidity and timely introduction of vancomycin therapy.

Results: The laboratory records of total 13,260 blood cultures were analyzed. Of those, MRSA bacteremia was detected in 61 cultures (9.3%). The highest prevalence of MRSA bacteremia was observed in the nephrology unit. The survival rate of the patients when the vancomycin therapy started before 24 h of receiving the blood culture report was 94.9% and in the instances of the treatment started after 24 h of blood culture report, the survival rate decreased down to 50%. High Pitt Bacteraemic score (PBS) ($p<0.05$) and initiation of vancomycin therapy after 24 h following the receipt of blood culture report ($p<0.05$) independently affected the MRSA bacteremic patient's 7th day mortality. Having comorbidities have not shown significant impact on 7th day mortality.

Conclusion: The start of vancomycin therapy as earlier as possible following arrival of antibacterial susceptibility test reduces the likelihood of mortality.

Audience Take Away:

- Management of MRSA bacteremia is time critical.
- Proper anti-MRSA antimicrobials has a role and timely introduction would be life-saving.

Biography

Dr. J.A.A.S. Jayaweera acquired his MD in medical microbiology and MPhil in medical virology. Dr. Jayaweera has over ten years of research experience in microbiology, biochemistry, nano-biotechnology, complementary and alternative medicine, and biostatistics. He has so far published more than 30 research articles in international peer-reviewed journals. He has won several international awards, and he is serving as a reviewer for many reputed groups of journals in the Global Journal of Medical Research and BMC antimicrobials and infection control. Further, he is an honorary editor in the Annals of clinical immunology and microbiology journal and the chief editor in Asian journal of dermatological sciences.

Shikhar Tripathi*, Atul Kakar
Sir Ganga Ram Hospital, India

Opsoclonus myoclonus ataxia syndrome in a HIV patient as a rare presentation of CSF escape

CSF escape is an uncommon phenomenon seen in patients where there is discordance in Plasma and CSF viral load. Its presentation can vary from being asymptomatic to cognitive dysfunction and can also be associated with opportunistic CNS infection. Opsoclonus Myoclonus Ataxia is very rare entity usually associated with neuroblastoma and viral illness. This syndrome has not been describes as a presentation of CSF Viral escape. Here, we present a case of Opsoclonus Myocolnus Ataxia Syndrome (OMAS) in People Living with HIV/AIDS (PLHA), associated with CSF Escape. Moreover, in this lecture, we're providing a postulation for the plausible cause behind CSF escape leading to the OMAS.

Audience Take Away:

- The audience will learn about Opsoclonus Myoclonus Ataxia syndrome, which in itself is a rare presentation.
- The audience will learn about CSF escape, which is an even rarer finding, especially for HIV infection.
- This presentation will focus on our case where we analyse and review the data and literature available on the topic, which shall definitely help the audience with their future researches.
- This presentation will include hypothesis/theory for the mechanism of precipitation of this rare phenomenon, that has only been reported a handful number of times in the history of medical research.
- This presentation will be providing an amalgamation of essential information on the a for mentioned topic, that shall prove to be very helpful for the audience.

Biography

Shikhar Tripathi is a medical student, a researcher and an author. Even as a student, he has published multiple research as well as review articles, which have received global acclaim, and has authored two medical reference books. One of his articles, where he gave a hypothesis on vertical transmission of COVID-19 from pregnant mother to fetus, was well acclaimed world wide and even got featured by Johns Hopkins Bloomberg School of Public Health in their repository and also got featured amongst the references on COVID-19 researches, on Wikipedia. He has been a guest speaker for the Young Researcher's Forum at International Conference on Diabetes, Hypertension and Metabolic Syndrome 2020, International Conference on COPD and Asthma 2021, International Conference on Clinical Microbiology and Infectious Diseases, 2021 and Diabetes Conclave, 2021.

Chandan Kumar*[1], Pankul Parnami[2], Pal Satyajit Singh Athwal[3], Sima Kumari[4], Piyush Puri[5], Yogita Suri[6]

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[2]Jawaharlal Nehru Medical College, IND
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[4]Patna Medical College, IND
[5]Rama Medical College Hospital & Research Center, IND
[6]Saraswathi Institute of Medical Sciences, IND

Reactivation of Herpes Zoster during COVID-19 infection

During the coronavirus 2019 (COVID-19) pandemic, sundry dermatological conditions related to COVID-19 pneumonia have been published.COVID-19 primarily affects the respiratory system, but secondarily it also affects the heart, kidney, brain, skin, spinal cord, etc. Herpes Zoster (HZ) is considerably important morbidity associated with COVID-19 pneumonia.Recrudescence of HZ occurs because of the latent varicella-zoster virus (VZV) predominantly because of the decline in cell-mediated immunity (CMI).Abating CMI is due to the increasing age, but could also occur if the patient is suffering from an immunosuppressive disease or is using immunosuppressive drugs. In our case, the patient had no lymphopenia unlike the other cases, yet still, he developed HZ. The median time to be diagnosed with COVID-19 and shingles was 5.5 days and acyclovir resolved the lesions after 10 day Herpes zoster has recently resurfaced, and the inactivated COVID-19 vaccine has been implicated, especially with CoronaVac which carries an inactivated portion of coronavirus. In addition, there was a 5-day latency period between the onset of herpes zoster and the administration of the inactivated COVID-19 vaccination.

Audience Take Away:

- COVID has impact in reactivation of herpes zoster without lymphopenia.A possible explanation may modulation of immunity.
- COVID morbidity is not limited to COVID pneumonia.

Biography

Dr Chandan Kumar, completed MBBS from Ranchi university(Rajendra Institute of medical science), India in 2012.Then completed his MD (Internal Medicine) from VMMC Safdarjung hospital New Delhi.Then pursued his sub-speciality in medical gastroenterology (DM Medical gastroenterology) from All India institute of medical sciences, Bhubaneswar Odisha India (2019-2022). Now he is practicing gastroenterology.

Vijay Prabha* and Harpreet Vander

Panjab University, India

Evaluation of pregnancy outcome as a consequence of intravaginal inoculation with various microorganisms in mouse model

The concept of infertility as a result of asymptomatic microbial colonization of the female reproductive tract has been neglected to date.However, increasing incidence of infertility and advanced research has drawn attention towards this idea. Many of these micro-organisms have been reported to bring about adverse changes in sperm parameters viz. motility, viability Magnesium dependent ATPase activity and acrosome reaction in vitro, but their in vivo potential to cause infertility is still a controversy. The present study indicates that colonization of mouse vagina with microorganisms possessing sperm impairing property could result in infertility whereas non sperm impairing microorganisms failed to do so. When the intravaginal inoculation of sperm impairing microorganisms was carried out into female BALB/c mice for 10 consecutive days with mating of mice on day 12, 100% decrease in fertility was observed in all the groups as compared with control mice receiving PBS alone. Furthermore no clinical or histopathological changes could be observed viz. ovary, uterus and vagina suggesting that colonization of the genital tract with sperm impairing microorganisms is not accompanied by signs of inflammation. Thus this study tends to align with the opinion that presence of sperm impairing microorganisms in female genital tract might be altering the vaginal milieu due to release of microbial components which in turn impair sperm parameters thereby leading to infertility.

Audience Take Away:

- The audience will get deeper insights into the relationship between microorganisms and female infertility.
- This research can be used further to better understand the mechanisms of infertility caused by microorganisms.
- New therapeutic measures can be exploited to ameliorate the infertility caused by various microorganisms.

Biography

Dr. (Mrs) Vijay Prabha is working as Professor in the Department of Microbiology, Panjab University, and 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 90 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.

Anderson Santos*[1], Getúlio Pereira[1] and Preetam Ghosh[2]

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[2]Virginia Commonwealth University, USA

A bridging centrality plugin for gephi and a case study for Mycobacterium tuberculosis H37Rv

Bridging Centrality (BriCe) is a popular measure that combines the Betweenness centrality and Bridging coefficient metrics to characterize nodes acting as a bridge among clusters. However, there were no implementations of the BriCe plugin that can be readily used in the GEPHI software or any other software dedicated to graph-based studies. In this paper, we present the BriCe plugin for GEPHI. It is available as a third-party functionality from the native GEPHI interface as a handy plugin to add; hence, no additional download and installation process is necessary. The BriCe plugin for GEPHI is open-source, and one can access the code through the GEPHI GitHub repository. As a use case of the BriCe plugin, we analyzed the genome of *Mycobacterium tuberculosis* H37Rv to identify biological explanations on why some proteins were ranked with top BriCe values? For instance, we were able to formulate a new hypothesis combining the predicted sub cellular localization and high BriCe values concerning lipopolysaccharides (LPS) exportation. Our hypothesis provides a possible link among proteins of a glycosyltransferase group and the type VII Secretion System.

The Bridging Centrality plugin for GEPHI is an easy to use tool for analyzing complex graphs and draw novel insights from graphical data. Moreover, for situations where there is no reliable interaction network for your genomes of interest, we developed GENPPI software for the ab initio prediction of interaction networks using predicted proteins from a genome. In our case study, we employed 50 genomes of the genus *Corynebacterium*. Based on the PP relationship, GENPPI differentiated genomes between the ovis and equi biovars of the species *Corynebacterium* pseudotuberculosis and created groups among the other species analysed. If we inspected only the CN relationship, we could not entirely separate biovars, only species. Our software GENPPI was determined to be efficient because, for example, it creates interaction networks from the central genomes of 50 species/lineages with an average size of 2200 genes in less than 40 min on a conventional computer. Furthermore, the interaction networks that our software creates reflect correct evolutionary relationships between species, which we confirmed with average nucleotide identity analyses.

Audience Take Away:

- The audience will be able to use the methodology explained in my presentation because I published and open-sourced both software tools. Moreover, the software is handy, has plenty of documentation, and I comprehensively explained it. The first one is a GEPHI plugin to analyze interaction networks in the light of bridging nodes for bacterial proteins (Bridging centrality) (Pereira et al., 2021). The second one is a software tool called GENPPI to generate interaction networks if a particular one is not available in public databases (Anjos et al., 2021).
- To spot conserved interaction among proteins in a bacterial genome can be crucial to focus on the leading vaccine and diagnosis candidates against infectious diseases like Tuberculosis or Diphtheria, both re- emerging diseases.
- Anyone can access and use these tools freely, so our methodology is reachable to everyone.
- We can think about our method to find target proteins against infectious disease agents as a complement to reverse vaccinology (RV). Besides the classical RV, we extend the search dimension, including a topological one. We can use several topological measures. However, we need to find a link between topological statistics and their biological meaning. We have no difficulties explaining the relationship between the Bridging centrality statistic and its possible meaning for bacterial infection agents' proteins.
- Our method of generating and analyzing both interaction networks and potential candidates for vaccine and diagnosis

could shed light on the difficult task of selecting a few promising proteins for further studies. We offer not only a pool of exported proteins or the more immunogenic ones but a new point of view: proteins evolutionary correlated as bridging among clusters of related molecular processes.

- Likewise, as long a researcher starts using our method, many other possibilities are over the board. For instance, to study hub proteins (highest Degree Centrality), more traversed (Betweenness Centrality), peripheral ones (inverse of highest Degree Centrality), proteins present in the bulkiest connected component, and more. In this new scenario, the imagination and knowledge of a researcher are the limits for further insights.

Biography

Anderson Santos graduated in Computer Science (1995), Masters in Computer Science with an emphasis in Artificial Intelligence (1999), and a Ph. D. in Bioinformatics (2012). Significant participation in the assembly and annotation of the first genome project conducted entirely in the state of Minas Gerais (Brazil) about the bacterium *Corynebacterium pseudotuberculosis* and experienced in the use of Computer Science for assembly and annotation of genomes. He also has practiced coordinating multidisciplinary teams for the assembler, annotation, and analysis of several bacterial genomes. He has been a professor at the Federal University of Uberlândia, Faculty of Computing, Brazil, since 2013.

Amira A. Moawad*, Heinrich Neubauer

Friedrich-Loeffler-Institut (Federal Research Institute for Animal Health), Germany

WGS-based analysis of bovine mastitis-related MRSA in thuringia, Germany

In animal husbandry, acute and chronic staphylococcal mastitis cause massive financial losses for the producer due to the reduced milk yield of the infected cow, price reductions due to reduced milk quality up to a ban on milk sales and significantly increased premature loss of animals. A multi-parametric staphylococcal rapid test is to be developed to match this one-health problem. The probability that a dairy cow will be culled increases significantly after three udder treatments. A major cause of these infections is Staphylococcus (S.) aureus. In the case of sanitation, the quarter milk samples from 10% of the animals in a herd (assumed infection rate of approx. 25%) with cell counts greater than 250,000 cells/mL milk must be examined, as well as dry cows, heifers and newcomers.

The aim of the study was to compare the genotypes, antimicrobial resistance profiles, and virulence factors of MRSA strains from clinical and subclinical bovine mastitis in dairy farms in Thuringia, Germany. Whole-genome sequencing (WGS) of strains was conducted and the sequence data were analyzed regarding antimicrobial resistance and virulence associated genes to draw conclusions for a current situation of bovine clinical and subclinical mastitis infections in dairy herds in the state and the potential public health risk. Furthermore, mapping the possible phylogenetic relations between MRSA strains from various farms as well as within one farm.

Audience Take Away:

- Audience will expand their knowledge about current situation of bovine mastitis in Germany.
- Audience will get a knowledge about the important resistance genes in bovine mastitis associated pathogens.
- Provide new information to assist in a study-design to solve mastitis problem in dairy herds.

Biography

Dr. Amira Moawad is currently working as Ass. Professor at Animal Health Research Institute. She became from 2016 until now a scientific researcher at Friedrich-Loeffler-Institute. Her PhD was on different mechanisms of antimicrobial resistance in pathogens of human and animal origin. She practices research in Microbiology and Molecular Biology. Since 2017, she has cooperated in international Projects funded by German federal foreign Office. She is now working on a project to develop a rapid pen-side device for rapid diagnosis of mastitis direct in the dairy farms.

Yinghui Huang*, Jie Zhou, Shaobo Wang, Jiachuan Xiong, Yin Chen, Yong Liu, Tangli Xiao, Yi Li, Ting He, Yan Li, Xianjin Bi, Ke Yang, Wenhao Han, Yu Qiao, Yanli Yu, Jinghong Zhao

Army Medical University, China

The intestinal microbiota metabolite indoxyl sulfate induces intestinal barrier injury through IRF1-DRP1 axis-mediated mitophagy impairment

Rationale: The dysfunctional gut-kidney axis forms a vicious circle, which eventually becomes a catalyst for the progression of chronic kidney disease (CKD) and occurrence of related complications. However, the pathogenic factors of CKD-associated intestinal dysfunction and its mechanism remain elusive.

Methods: We first identified an intestinal microbiota metabolite, as well as a protein-bound uremic toxin indoxyl sulphate (IS) as a possible contributor to intestinal barrier injury by using 16s ribosomal RNA (rRNA) sequencing. Trans epithelial electrical resistance, permeability assay and transmission electron microscopy were carried out to evaluate the damaging effect of IS on intestinal barrier in intestinal epithelial cells, IS-injected mice and CKD mice. In vitro and in vivo experiments were performed to investigate the role of IS in intestinal barrier injury and the underlying mechanism. Finally, CKD mice treated with AST-120 (an oral adsorbent for IS) and gene knockout mice were used to verify the mechanism and to explore possible interventions for IS-induced intestinal barrier injury.

Results: Trans epithelial electrical resistance and the expressions of tight junction-related genes were significantly suppressed by the intestinal microbiota metabolite IS in intestinal epithelial cells. In vitro experiments demonstrated that IS inhibited the expression of dynamin-related protein 1 (DRP1) and mitophagic flux, whereas DRP1 overexpression attenuated IS-induced mitophagic inhibition and intestinal epithelial cell damage. Furthermore, IS suppressed DRP1 by upregulating the expression of interferon regulatory factor 1 (IRF1), and IRF1 could directly bind to the promoter region of DRP1.Administration of AST-120 or genetic knockout of IRF1 attenuated IS-induced DRP1 reduction, mitophagic impairment and intestinal barrier injury in mice.

Conclusions: These findings suggest that reducing IS accumulation or targeting the IRF1-DRP1 axis may be a promising therapeutic strategy for alleviating CKD-associated intestinal dysfunction.

Audience Take Away:

- We identified the intestinal microbiota metabolite, indoxyl sulphate (IS), as a possible contributor to intestinal barrier injury by using 16s rRNA sequencing and experimental validation.
- In vitro and in vivo experiments were performed to investigate the role of IS in intestinal barrier injury and the underlying mechanism.
- Reducing IS accumulation or targeting the IRF1-DRP1 axis may be a promising therapeutic strategy for alleviating CKD-associated intestinal dysfunction.

Biography

Dr. Yinghui Huang received his PhD degree majoring in Nephrology from the Army Medical University in 2020. He obtained the position of Associate Chief Physician and Associate Professor in Xinqiao Hospital of the Army Medical University in 2021. He has published 7 research articles including Gut, Nature communications and Theranostics in SCI(E) journals.

Iti Saraav*[1], Philipp Olias[1], Luisa Cervantes-Barragan[2], Qiuling Wang[1], Leran Wang[1], Yi Wang[1], Matthias Mack[2], Megan T. Baldridge[1], Thaddeus Stappenbeck[1], Marco Colonna[2], L. David Sibley[1]

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[2]University of Regensburg, Germany

Long term infection with Toxoplasma activates monocytes leading to enhanced susceptibility to colitis

Previous studies have shown that acute *Toxoplasma gondii (T. gondii)* infection in mice causes microbial dysbiosis and ileitis both of which return to normal condition during chronic infection. There are studies in the field that suggest latent toxoplasmosis play role in the pathogenesis of other diseases characterized by excessive inflammation. However, whether prior toxoplasma infection leaves a lasting effect on mucosal responses or not remained an open question in the field. Using chemically induced colitis model, we found that chronically infected mice showed greater damage in the colon following treatment with DSS. Infected mice also showed blunted wound healing response in the colonic mucosa due to defect in stem cell regeneration. Given that acute *T. gondii* infection results in microbial dysbiosis in the gut, we investigated whether changes in the microbiota also occur during chronic infection and following DSS treatment. Our data suggest that differences in the microbiota composition do not play a major role in the increased severity of DSS treatment in chronically *T. gondii*–infected mice. Enhanced susceptibility to DSS was also not related to changes in regulatory T cells that were unaltered in chronically infected mice. Rather, chronically infected mice showed persistently higher levels of IFN-γ in CD4+ and CD8+ T cells and systemic activation of inflammatory monocytes that migrate to the site of the infection and produce inflammatory cytokines. We found that enhanced tissue damage was attributable to pathogenic inflammatory monocytes that emerge from bone marrow in pre-activated form and release inflammatory mediators like nitric oxide upon reaching the inflamed tissue sites. We further observed that blocking recruitment of monocyte or using $Nos2^{-/-}$ mice which lack inducible nitric oxide synthase, protected chronically infected mice from DSS associated intestinal damage. Although heightened innate immunity provides protection to the host, but our study demonstrate that such immune responses are not always beneficial and may have detrimental effect as in our study we found pre-activated monocytes to be responsible for increased tissue damage in response to DSS. Together, our work uncovers the pathogenic role for inflammatory monocytes in an acute experimental colitis model that is further exacerbated in chronically *T. gondii*–infected mice that may increase the risk of severe outcome to environmental irritants, underlying genetic susceptibilities, or other enteric infections that are implicated in intestinal diseases such as sepsis, celiac disease, and autoimmunity.

Audience Take Away:

- The audience will learn the disadvantage associated with enhanced trained immunity.
- Our study can be used further in other infectious model to study the consequence of prior chronic infection to secondary insult.

Biography

Dr. Iti Saraav did her Ph.D. from the Department of Zoology, University of Delhi, India, where she studied host immune response to Mycobacterium tuberculosis. She then moved to Washington University in St Louis, USA for her Postdoctoral research where she joined Dr. L. David Sibley lab. In his lab, she was able to identify antigens that can be used in IFN-γ based diagnostic assays to detect Toxoplasma infection. She has two patents for this work. Dr. Saraav further published a study in 2021 in PNAS where she demonstrated why chronic Toxoplasma infection enhances susceptibility to colitis.As a Staff scientist, she continues to work on parasites. She has published several research, review articles and presented at various national and international conferences.

Adnan Alrubaye
University of Arkansas, United States

Staphylococcus agnetis as a model microorganism to induce bacterial chondronecrosis with osteomyelitis in broiler chickens

We have isolated Staphylococcus agnetis from lame birds and used one isolate to induce lameness in broilers, which resulted in 50-60% of lameness. In addition, we are identifying the virulence factors in S. agnetis, so we can understand the pathogenicity of this emerging pathogen. *S. agnetis* is a relatively newly identified bacterial species that causes Bacterial Chondronecrosis with Osteomyelitis (BCO) lameness cases in broiler chickens. BCO lameness is a major animal welfare and food safety issue that affects the poultry industry worldwide resulting in hundreds of millions of dollars in lost revenue. Our research group isolated *S. agnetis* from infected bones and blood samples from birds raised on either wire or wood shaving flooring. Identifying bacterial species that cause BCO lameness in chickens helps us understand the transmission and pathogenesis of the disease. *S. agnetis* is a Gram positive, non-motile, non-spore forming, and coagulase negative species that was known for causing mastitis cases in bovine.

No prior correlation was established between *S. agnetis* and BCO prior to the research conducted by our group at the University of Arkansas. We have used *S. agnetis* as a model for the epidemiology of BCO. In addition, we used selected probiotics and prebiotics mixes to decrease the incidence of BCO in chickens.Broiler chickens get the *S. agnetis* infection from the environment and the bacteria gain access to the blood via the gastrointestinal tract, respiratory system, and/or the skin. After entering the blood stream, *S. agnetis* bacteria colonize the proximal femoral and tibial heads eliciting necrosis, which results in lameness.Lameness is caused by many bacterial strains that vary according to the geographical region.We have established that *S. agnetis* is one of the main causes of lameness in our poultry research farm. Our group published the full genome sequence for multiple *S. agnetis* isolates from chicken and cattle. The chicken isolates cluster within the cattle isolates, suggesting a recent host transition, with very different etiology. Understanding the determinants of host adaptation, and virulence will be critical to understanding this transition.

Audience Take Away:

- The audience will learn about the Bacterial Chondronecrosis with Osteomyelitis BCO lameness in broiler chickens.
- BCO lameness is a major animal welfare and food safety issue that affects the poultry industry worldwide resulting in hundreds of millions of dollars in lost revenue.
- Identifying bacterial species that cause BCO lameness in chickens helps us understand the transmission and pathogenesis of the disease.
- Our research group isolated Staphylococcus agnetis from infected bones and blood samples from birds raised on either wire or wood shaving flooring.
- We are now using to induce BCO lameness in broiler chickens. This model helps test feed additives impact on the incidence of BCO lameness in broiler chickens.

Biography

Dr. Adnan Alrubaye was born and raised in the South region of Iraq, traveled to the U.S. in 2008.He completed his bachelor's degree in veterinary medicine from the College of Veterinary Medicine at the University of Baghdad in 2000.He earned his master's degree in medical microbiology from the College of Medicine at the University of Baghdad in 2003,Master's and PhD from the University of Arkansas.Dr. Alrubaye is now an assistant professor of poultry science, and the associate director of the Cell and Molecular Biology Graduate Program.

magnus Group

POSTERS

DAY 01

INTERNATIONAL CONFERENCE AND EXPO ON

CLINICAL MICROBIOLOGY

17-18 JUNE

Noha Tharwat Abou El-Khier*, Samah Sabry El-Kazzaz
Mansoura University, Egypt

Effect of the lantibiotic nisin on inhibitory and bactericidal activities of antibiotics used against vancomycin-resistant enterococci

Objectives: Antibiotic resistance is a serious issue facing clinicians all over the world. Vancomycin- resistant enterococci (VRE) are amongst the most common resistant pathogens that are isolated from patients suffering from infections in our locality. New antimicrobial agents such as the lantibiotic nisin have been previously examined against resistant bacteria as it has strong antibacterial action with no chance of resistance development. This study aimed to explore the effect of nisin in combination with the conventional antibiotics against VRE, with a view to using it as an auxiliary therapy with such antibiotics for combating resistant isolates.

Methods: Twenty-three VRE had been examined for the combined effect of nisin with the routine sets of antibiotics using the microplate dilution technique for minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) testing. Checkerboard microbroth assay was conducted for inspection of synergism between nisin and either ampicillin or chloramphenicol.

Results: An obvious improvement of inhibitory and bactericidal activities of the tested antibiotics after addition of lantibiotic nisin was observed, with a remarkable reduction in the MIC values of vancomycin against all of the isolates. Nisin recorded a synergistic outcome when combined with either ampicillin or chloramphenicol using the checkerboard assay.

Conclusion: Nisin could be effectively considered as a supplementary agent to traditional antibiotics in the management of VRE-associated infections, as it had a synergistic outcome with commonly prescribed antibiotics such as ampicillin and chloramphenicol.

Audience Take Away:

- Explore the effect of nisin in combination with the conventional antibiotics against VRE.
- Consider nisin as a supplementary agent to traditional antibiotics in the management of VRE-associated infections.

Biography

Noha Tharwat Abou El-Khier studied at Faculty of Medicine, Mansoura University, Egypt and graduated as MS in Medical Microbiology & Immunology .She received her PhD degree in 2011 at the same institution.she obtained the position of Professor of Medical Microbiology & Immunology in 2021. She has published more than 40 research articles in different journals.

Luana L.S. Rodrigues*[1,2], Mariza G. Morgado[2], Vikrant V. Sahasrabuddhe[3], Katrini G. Martinelli[4], Vanessa S. De Paula[5], Lyana R. P. Lima[5], Nathália S. Oliveira[6], Diane M. Da Silva[7,8], W. Martin Kast [7,8,9], Justin Hardick[10], Charlotte A. Gaydos[10], Alcina F. Nicol[11], José H. Pilotto[2]

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[11] Instituto Nacional de Infectologia Evandro Chagas, INI-FIOCRUZ, Brazil

Anal HPV, diversity and concordance with genital infection in women living or not with HIV -1 in the tapajós region, Amazon, Brazil

Published scientific data on human papillomavirus (HPV) are predominantly related to genital infection. Studies on anal HPV, diversity and concordance with genital infection are scarce. Cervical cancer screening might contribute to the prevention of anal cancer in women as secondary prevention programs for the prevention of anal cancer. This study was supported by previous studies, which evaluated the acceptability of the cervico-vaginal self-collection, HPV and other STIs testing, and sociodemographic data in women living (WLWH) or not (WNLWH) with HIV in the Tapajós region. The overall prevalence of anal HPV infection was 49.0% (75/153), and by group of participants was 31.3% (35/112) for WNLWH and 97.6% (40/41) for WLWH. Only WLWH had cervical cytological abnormalities (12.2%). A high diversity of anal HPV genotypes has been identified in the anal scraping of both groups participating in the study. HPV anal types of the genus Alphapapillomavirus and Betapapillomavirus were identified, considering the predominant tissue associations and the typical relationships between HPV type and disease caused. The overall HPV prevalence was 53.3% (40/75) for single anal infections and 46.7% (35/75) for multiple anal infections by HPV types in the participants. Among the WNLWH, 97.0% (34/35) had single anal infections and 3.0% (1/35) multiple anal infections. However, among WLWH, multiple HPV anal infections were much more prevalent, at 85.0% (34/40), and single anal infections accounted for 15.0% (6/40).

Anal HPV types found in the participants were predominantly of the genus Alphapapillomavirus. Overall, anal HPV types found in the participants were predominantly of the genus Alphapapillomavirus and included samples grouped into high-risk, “probable” or “possible”, and low-risk carcinogenic groups. In WLWH, 42.9% (15/35) of anal hrHPV infection was detected, and HPV-18 (6) and HPV-16 (5) were the most frequent anal hrHPV types, representing 73.3% (11/15) of the total anal hrHPV types genotyped in this group. In WNLWH, 75.0% (30/40) of hrHPV anal infection was detected, and HPV-51 (12), HPV-59 (10), HPV-31 (9) and HPV-58 (9) were the most frequent anal hrHPV types, representing 59.7% (40/67) of the total anal hrHPV types genotyped in this group. The anal hrHPV infections were significantly more prevalent in the WLWH than WNLWH (Chi-square test $p < 0.001$). The Kappa test was performed for concordance analysis between anal and genital HPV infection and we consider categorizing in the absence and presence of high and low-risk HPV types. The concordance analysis proved to be moderate for HPV considering the oncogenic risk classification, Kappa value 0.44.

Audience Take Away:

- High overall prevalence of anal HPV infection, 49.0% (75/153), in women living (WLWH) or not (WNLWH) with HIV in the Tapajós region, Amazon, Brazil.

- High prevalence, 97.6% (40/41), of anal HPV infection in WLWH.
- High diversity of anal HPV genotypes has been identified in the anal scraping, including HPV types of the genus Alphapapillomavirus and Betapapillomavirus.
- Among the WNLWH, 97.0% (34/35) had single anal infections and 3.0% (1/35) multiple anal infections. However, among WLWH, multiple HPV anal infections were much more prevalent, at 85.0% (34/40), and single anal infections accounted for 15.0% (6/40).
- The anal high-risk HPV (hrHPV) infections were significantly more prevalent in the WLWH than WNLWH, in which HPV-18 and HPV-16 were the most frequent anal hrHPV type. The concordance analysis proved to be moderate between anal and genital HPV infection considering the oncogenic risk classification, Kappa value 0.44.
- Cervical cancer screening might contribute to the prevention of anal cancer in women as secondary prevention programs for prevention of anal cancer.
- When evaluating the utility of cervical screening results to stratify anal cancer risk, an important consideration should be given to HIV status, cervical cytological abnormalities, age-specific shifts, types of oncogenic HPV, single or multiple HPV infections, among other factors to be better investigated.
- More studies are needed to understand the influence of factors related to anal HPV infection on the development of anal cancer and how these results can improve cancer screening policies.
- However, the status of HIV infection in the development of cancer is already well evidenced in the scientific literature. This study adds to the body of evidence in the specialized literature by showing unpublished data on the prevalence of anal HPV, non-HPV STIs diversity, and concordance with genital infection in women non-indigenous in the Amazon, Northern region of Brazil, where cervical cancer continues to be the type with the highest incidence and mortality among women.

Biography

Dr. Rodrigues is Graduated in Pharmacy with a qualification in Clinical Analysis Laboratory. She received a Ph.D. in Tropical Medicine from the Oswaldo Cruz Institute of the Oswaldo Cruz Foundation (FIOCRUZ - Brazil). She had a doctoral fellowship at the Division of Infectious Diseases at Johns Hopkins University and at the Department of Molecular Microbiology and Immunology, University of Southern California (USA). Currently, Dr. Rodrigues is a professor and coordinator of the Postgraduate Program in Health Sciences at the Institute of Collective Health of the Federal University of Western Pará. Dr. Rodrigues has experience in microbiology, with an emphasis on virology.

Adriano Alberti*, Clarissa Martinelli Comim
Southern University of Santa Catarina (PPGCS-UNISUL), Brazil

Obesity in people with diabetes in COVID-19 times : Important considerations and precautions to be taken

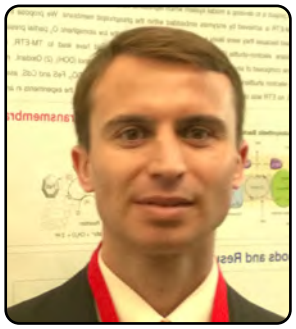
At the end of 2019, a new disease with pandemic potential appeared in China. It was a novel coronavirus called coronavirus disease 2019 (COVID-19). Later, in the first quarter of 2020, the World Health Organization declared the outbreak of this disease a pandemic. Elderly people, people with comorbidities, and health care professionals are more vulnerable to COVID-19. Obesity has been growing exponentially worldwide, affecting several age groups. It is a morbidity that is associated with genetic, epigenetic, environment factors and/or interaction between them. Obesity is associated with the development of several diseases including diabetes mellitus, mainly type 2.Diabetes affects a significant portion of the global population. Obesity and diabetes are among the main risk factors for the development of severe symptoms of COVID-19, and individuals with these conditions constitute a risk group. Based on a literature review on obesity in people with diabetes in the framework of the COVID-19 pandemic, this study presents updated important considerations and care to be taken with this population.

Audience Take Away:

- People can better understand how covid-19 works in diabetic and obese people.
- This article could help research on diabetes, covid-19 and obesity.

Biography

Adriano Alberti has a degree in physical education, as well as a master's and a doctorate (PhD) in health sciences. He is currently a postdoctoral student in health sciences at Universidade do Sul de Santa Catarina, Brazil. He is a researcher and author, with articles and books published in the areas of neuroscience, epigenetics, genetics, and obesity.



A. Guillermo Bracamonte*[1,2], Luna R. Gomez Palacios[1], Carina Salinas[1], M. Valeria Ame[3]

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Ultra luminescent bio photonics assays for in flow Escherichia coli bacteria detection and counting towards perspectives on single bio structure analysis at molecular level

In this presentation it is showed Research and Development related with the design and synthesis of Ultraluminescent Nano-emitters based on Metal Enhanced Fluorescence (MEF) phenomena. It is showed gold Core-shell Nanoparticles with silica spacers and modified Fluorescent Silica shells with Enhanced and stable Luminescent properties.These Nano-emitters were used as Nanolabellers for Escherichia Coli bacteria. In this manner it was achieved Bright and Ultraluminescent Nano-Biostructures that afforded to faster detection within low bacteria concentrations at the level of single bacterium detection by Laser Fluorescence Microscopy.In this context it is highlighted and discussed the importance of the Optical properties of Nano-labellers and Biostructures for targeted applications from the Nano-Biostructure formation.Thus, it is showed In Flow Cytometry detection of Nano-Biostructures at varied levels of concentrations.In addition, it is discussed perspectives about how it could be managed these Hybrid Nano-Biostructures to record additional information from single Biostructure analysis.In this manner it is leaded to new potential approaches within Biophotonics by Targeted Light Delivery through Biostructures that just not improve only Biodetection,but as well it increases the power of analysis towards Single Cells applications.

Audience Take Away:

- In the presentation the audience could incorporate proofs of concepts and new approaches from the control of the Nanoscale toward developments within Nanophotonics and Biophotonics.
- In this manner, the design and synthesis of functional Nanoparticles could lead to Nano-Biolabelling with improved imaging resolution.
- Ultraluminescence generation based on Metal Enhanced Fluorescence (MEF) is discussed for faster detection and counting of Escherichia Coli bacteria.

Biography

A.G. Bracamonte studied in Faculty of Chemical Sciences at National University of Cordoba (UNC) Argentine; where he obtained his bachelor in Chemistry and PhD in Chemical Sciences.Then, it was associated as Postdoctoral Researcher at Laval University, Québec, Canada. Moreover, he holds a second Postdoctoral Research at University of Victoria, British Columbia, Canada. He was Lecturer in Professor Burkhard König Group at Universitat Regensburg, Germany. And, he holds a Postdoctoral Researcher position at University of Akron, and NASA Astrobiology Institute, Ohio, United States. Actually, he is Researcher and Assistant Professor at UNC.Argentine.

KEYNOTE FORUM

DAY 02

INTERNATIONAL
CONFERENCE AND EXPO ON

CLINICAL MICROBIOLOGY

17-18 JUNE

Shailesh R Dave*[1] and Devayani R Tipre[2]

[1]Xavier's Research Foundation, India

[2]Gujarat University, India

Urban biomining of precious and hazardous metals a green circular economy model

Urbanization, economic growth, a desire for novelty, and rapid innovation have resulted in shorter-lasting products in general and electrical and electronic equipment (EEE) in particular. This resulted in an exponential rise in the production of EEE waste (EEEW) around the world. Presently, more than 660 varieties of EEE are used and sold in the global market. Televisions, computers, printers, refrigerators, temperature exchangers, driers, washing machines, cell phones, smart mobile phones, as well as other electrical and electronic devices fall into this category. Globally, about 57.4 million tonnes of EEEW were produced in 2021, and it will reach 74 million tonnes by 2030 and 120 million tonnes by 2050. EEEW is the fastest-growing fraction of municipal solid waste. EEEW has as many as 60 elements from the periodic table along with glass, plastic, flame retardant and several organic pollutants. Despite this, EEEW is poorly collected and not properly recycled, resulting in serious aquatic, terrestrial, and atmospheric pollution as well as even threats to public health. But if the EEEW is considered in terms of the source of base metals, precious metals, platinum group metals (PGM), and rare-earth elements (REE), it is economically valuable. The estimated value of the EEEW produced in 2019 (53.6 million tons) is about the US $57 billion. But currently, only 20% of total EEEW is recycled or processed scientifically, and the rest of the waste is either incinerated or disposed of as a landfill.

That has created several environmental and health problems. Pyrometallurgy and hydrometallurgical processes are commonly used for the recovery of metals and REE, but they are energy and cost-intensive, as well as generate secondary pollutants. Bio-hydro-metallurgical methods have recently replaced traditional processes because they are more environmentally friendly, economically viable, and operate at lower temperatures and pressures than pyro- and hydro-metallurgical processes. A consortium of iron oxidizers, sulphur oxidizers, and cyanogenic microorganisms is playing a critical role in the enhanced and rapid extraction of the base, critical, and precious metals as well as REE from a variety of EEEW pre-treatments and applications. Applications of cost-effective technology are among the top priorities in bio-hydrometallurgy for the recovery and recycling of critical, valuable, and toxic elements from the EEEW due to the rapid depletion of their natural resources and serious harmful effects on health and the environment. Given the complexity and diversity of EEEW, effective treatment requires integrated technology with a clear focus on recovering or recycling valuable metals, critical metals, REE, and even hazardous materials to contribute to resource recovery, pollution reduction, environmental conservation, and long-term economic development. Based on the available data on bioprocesses, the replacement of conventional steps used in EEEW recycling with bio-based technological processes can be possible. The current talk will provide insights into the integrated approach to biobased economy and EEEW treatment in this context.

Audience Take Away:

- The audience will learn about the generation of e-waste along with its harmful and economic values.
- Conventional methods used for e-waste treatment, and their limitations.
- Will know the concept of biomining or biohydrometallurgy and their beneficial role in e-waste treatment.
- Will also learn that if e-waste is properly handled it is a rich source of the base, critical, and valuable metals as well as rare earth elements.
- Learn new reactor design and bio-regeneration of ferric for the circular economy.
- Will learn the critical evaluation of pre-treatments and their benefits.
- Also, know the importance of an application of a developed consortium and its significance.

Biography

Shailesh Dave is Admin director at Xavier's research foundation, LCRD, Ahmedabad. He is a UGC Emeritus professor, former Director of School of Sciences, and former Head, P.G. Department of Microbiology and Biotechnology, at Gujarat University, Ahmedabad, Gujarat. He has 42 years of teaching and research experience in Microbiology and Environmental Biotechnology. 38 and 50 students have been awarded PhD and M. Phil degrees under his guidance. He has published more than 130 papers in journals. He has handled 19 research projects funded by various funding agencies. Prof. Dave is a fellow of FAEB, FGSA, FISBT, FBRS, and FAMI. He has filed 4 patents two of them are awarded and two are waiting for the final decision.

Andrzej Babuchowski*, Aleksandra Grzeskiewicz

Dairy Industry Innovation Institute, Poland

Rapid method for detecting pathogenic microorganisms in food

Reference methods for the detection of pathogenic microorganisms *Salmonella* spp. in accordance with PN-EN ISO 6579-1: 2017-04 or *Listeria monocytogenes* and *Listeria* spp. in accordance with PN-EN ISO 11290-1: 2017-07 are labour-intensive and time-consuming.These classic methods for detecting *Salmonella* spp. in food takes 3 to 5 days, while for detecting *Listeria monocytogenes* in food takes 5 to 7 days. Alternative methods for the shortest possible detection time of these microorganisms are constantly being sought in order to be able to release food products from the processing plant as quickly as possible.One of such methods is LAMP (Molecular Detection System 3M) method. This method uses Loop-mediated Isothermal Amplification system to rapidly amplify nucleic acid sequences with high specificity and sensitivity, combined with bioluminescence to detect amplification.Positive results are reported in real time, negative results are displayed after the test is completed. Positive results must be confirmed with a reference method.The analysis with this method takes 22-26 hours depending on the tested microorganism.

The Microbiological Research Laboratory of the Dairy Industry Innovation Institute has validated and accredited the *Salmonella* spp., *Listeria monocytogenes* and *Listeria* spp. detection method using the LAMP molecular method in environmental samples from the area of food processing, distribution and marketing in different dairy products. During the validation tests, the laboratory analysed 364 samples for *Salmonella* spp., 360 samples for *Listeria monocytogenes* and 360 samples for *Listeria* spp. The validation process revealed the equivalence of the alternativemethodtothereferencemethod.The RT-LAMP (reverse transcription loop-mediated isothermal amplification) method of nucleic acid amplification can be also used to detect the RNA of the SARS-CoV-2 coronavirus in food production and distribution environment. The Microbiological Research Laboratory of the Institute of Dairy Industry Innovation has accredited this method for the detection of SARS-CoV-2 coronavirus RNA in environmental samples from the area of food production and distribution, in environmental samples from the surface of packaging and in dairy samples such as UHT milk, powdered products, cheese.

Audience Take Away:

- A new method for detection of pathogenic microorganisms in food, a comparison of new and reference methods, use the RF-LAMP method to detect SARS-CoV-2 virus in food production environment.
- To widen area of their expertise and possibly to apply new method.

Biography

Prof. Dr. Andrzej Babuchowski graduated with Honour in Food Technology in 1973 on University of Agriculture in Olsztyn, Poland. In 2003, he was granted a Titular Professor. From 1976 till 2017 he was working at University of Warmia and Mazury in Olsztyn, Poland and in different research institutions abroad. In years 2005-2009, he was Head of the Department of Industrial and Food Microbiology at the University. All his academic activities were related to food and dairy technology, fermentation technologies, technical biotechnology, food safety and quality, food and nutrition. Currently he is a President of Dairy Industry Innovation Institute as from 2015.

A. C. Matin

Stanford University, United States

Managing bacterial eradication in disease and survival for life support systems on earth and space

Bacteria like *Escherichia coli* cause disease but are also beneficial in resource regeneration. Its UPEC strain causes cystitis, which is treated by gentamicin.The protein s,encoded by the *rpoS* gene, controls *E. coli* resistance to antimicrobial agents.We discovered that rpoS deletion mutation renders UPEC more sensitive to Gm and other bactericidal antibiotics;proteomic analysis suggested a weakened antioxidant defense as the cause. Reactive oxygen species (ROS) detectors (psfiA gene reporter, and appropriate chemicals)indicated greater ROS generation by Gm in the mutant. When administered along with an antioxidant,or under anaerobic conditions (that prevent ROS formation),Gm was less lethal to the mutant. *In vivo* studies of treating UPEC infection of mice bladder gave similar results. Thus, oxidative stress produced by insufficient quenching of metabolic ROS accounted for greater sensitivity of the mutant. Gm exposure to other *E. coli* mutants, missing antioxidant proteins, also resulted in greater ROS production and lethality; these lacked the ROS quencher proteins, (e.g., SodA/SodB; KatE/SodA),or the pentose phosphate pathway proteins, which provide NADPH (e.g., Zwf Gnd; TalA) required by the quencher proteins. Use of a microfluidic device indicated that the results applied at a single cell level. Gm's lethality in bacteria is due to inhibition of protein synthesis, but most current UPEC patient isolates can overcome this (reflecting the larger problem of growing bacterial antibiotic resistance). Therefore, these findings provide a timely means of restoring Gm effectiveness by curbing bacterial antioxidant defense.

Using bioinformatics, we have identified several small molecules that inhibit s and can overcome bacterial Gm resistance. In space flights, astronauts often suffer from cystitis; further, bacterial antibiotic resistance is a greater threat to them as microgravity (MG) impairs human immune response.Bacterial gene regulation can differ in normal vs.MG. However, the "EcAMSat" Stanford/NASA mission showed that s controls Gm resistance also in MG. This work employed a free flying "nanosatellite" equipped with a sophisticated microfluidic system, which autonomously analysed UPEC sensitivity to Gm in space flight over several days and transmitted the results by telemetry to Earth in real time. Bacterial multidrug resistance, such as the one regulated by the emrRAB operon and the EmrR protein, is a major public health problem. Its activation is due to alteration in the EmrR protein structure by antibiotics, which too can be prevented by small molecules and bioinformatic approaches. For long-term space flights and space colonization, ecosystems need to be established for resource regeneration and waste recycling, processes in which *E. coli* is important. Manipulation of s levels and the resistance proteins it controls hold the key for stabilizing this bacterium under MG conditions. Several scientists have contributed to this work; they will be recognized in the presentation.

Biography

Dr. Matin has been a full professor at Stanford University for several years and is affiliated with several programs, including the Stanford Cancer Research Institute.He has contributed to many areas of biological research, including discovery of new drugs and therapeutic enzymes and their improvement as well as their specific targeting to cancer (and other diseases).He did his Ph. D. at UCLA, spent some years in the Netherlands(State University of Groningen),where he directed a research group, before joining Stanford. He is recipient of numerous awards and honors.

magnus Group

SPEAKERS

DAY 02

INTERNATIONAL CONFERENCE AND EXPO ON

CLINICAL MICROBIOLOGY

17-18 JUNE

Dimple Sethi Chopra*[1], Abhishek Gupta[2], Dhandeep Singh[1], Nirmal Singh[1]

[1]Punjabi University, India

[2]University of Wolverhampton, Walsall

Multidrug resistance in burn patients

Staphylococcus and Pseudomonas spp. are the most common cause of infection in patients suffering burn injuries. As burn patients have lost their primary protective barrier ie skin, they are susceptible to colonization by both endogenous and exogenous micro-organisms. The thermal injury itself decreases host resistance and increases the body's natural inflammatory response. The burn eschar provides an environment conducive to bacterial growth because of its protein richness, release of toxic substances, and avascularity, which impedes the delivery of antimicrobial drugs. In the first five days, post-burn the most common pathogens are gram-positive, whereas gram negative bacteria increase in prevalence after five days.The most common pathogens in the early phase are Staphylococcus aureus, Haemophilus influenza, Escherichia coli, and Klebsiella.The most common late-phase pathogens include S. aureus and Pseudomonas aeruginosa. Yeast and fungal infections typically occur, around 7–14 days, post-burn, followed by multi-drug–resistant (MDR) infections.The crucial risk factors for Multidrug bacteria, include length of stay in hospital, previous antimicrobial therapy, inadequate burn excision, and use of invasive medical devices.Although, intravenous (IV) and intra-arterial catheters are used in burn patients to provide access for fluid resuscitation, parenteral nutrition, and administration of medications. But, they increase the risk of central line-associated blood stream infection (CLABSI). Diagnosis of MDR is difficult, as colonization usually precedes infection.Because of empiric treatment with broad-spectrum antibiotics during the initial burn treatment, resistance patterns and sensitivities vary. Pathogens of utmost concern are MDR strains of P. aeruginosa, Stenotrophomonas maltophilia, Acinetobacter, and methicillin-resistant S. aureus (MRSA). There also have been reports of outbreaks of carbapenem resistant Enterobacteriaceae in burn unit.

Audience Take Away:

- Awareness about Multi Drug Resistance.
- Burn wounds are different from other wounds. Their healing mechanism is also different.
- Burn wound patients should be strictly prevented from secondary infection.
- Initial management of burn patients decides their length of stay in the hospital.
- Trained Paramedical staff to deal with Fire disasters are need of the hour.

Biography

Dr. Dimple Sethi Chopra is presently working as Associate Professor (Pharmaceutics) in Department of Pharmaceutical Sciences and Drug Research (DPDSR), Punjabi University, Patiala. She did her graduation and post-graduation from UIPS, Panjab University, Chandigarh. She joined DPDSR in 1998. She did her Ph.D under guidance of Professor Manjeet Singh. She has published several research papers in national and international journals of repute. She has been granted two Indian patents on brain permeable nanoparticles. She is a member of American Nano Society. She recently Edited a book published by IGI Global " Strategies to Overcome Superbug Invasion".

Hem Chandra Jha*[1], Budhadev Baral[1], Shweta Jakhmola[1], Omkar Indari[1], Dharmendra Kashayap[1], Nirmal Kumar Mohakud[2]

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[2]Kalinga Institute of Medical Sciences, India

COVID-19 pandemic ; A complex mixture of co-infection and comorbidity

The COVID-19 pandemic has gravely affected people of all age groups globally. However, one of our studies concerning data of the initial days of the COVID-19 pandemic revealed that population groups of 20-49 years and 50 years above were most vulnerable to infection. Higher population of the deceased were reported in 50 years-above age group in all countries. Interestingly, the 20-49 years of age group from India were most affected.The epidemiological data from India and South Korea provided clues that BCG and JE vaccines may be responsible for non-specific immunity against SARS-CoV-2. Further, the mutational analysis of the virus shed light on the reasons for high SARS-CoV-2 virulence. Our analysis found that mutations in E, M, and S proteins of the virus resulted in modification sites like PKC phosphorylation and N-myristoylation. Moreover, the structural analysis revealed that the D614G mutation and Arg-Gly-Asp tripeptide played an important role in viral pathogenesis. We also speculated crucial host pathways which the mutated isolates of SARS-CoV-2 may alter, like PKC, Src, and integrin-mediated signaling pathways. Additionally, the myristoylated proteins might activate NF-κB, a master inflammation molecule.Although COVID-19 is an inflammation-mediated disease,the role of comorbidities is crucial in disease progression.

Our observational analysis revealed that deaths associated with cardiovascular diseases and diabetes were highly significant ($p < 0.0001$) compared to hospitalized individuals in Italy, France, and Spain, unlike the Netherlands. Deaths from kidney diseases (Italy- $p < 0.0001$; Sweden- $p < 0.0001$; Netherlands- $p = 0.0001$; France- $p = 0.0033$) and neurological ailments (France $p = 0.0001$; Netherlands- $p < 0.0001$) were significantly higher than the total hospitalized patients affected by the comorbidity. Neurological disorders increase the complications in the COVID-19 situation. We also found that COVID-19 could cause neurological manifestations like meningitis. The probable routes of virus entry into the nervous system include the hematogenic pathway through the vagus, the olfactory nerve, or the enteric nervous system. Besides the traces of SARS-CoV-2 RNA have been found in gastrointestinal cells. ACE2 receptors such as sialic acid and CD147 may facilitate the virus entry exclusively in the GI tract. Co-infection of SARS-CoV- 2 with other pathogens can further change the course of the disease progression. We found that co-infection of plasmodium could increase the disease severity in a short period. Besides occurrence SARS-CoV-2 infection in cancer patients can increase the complications specifically in the patients receiving chemotherapy.

To alleviate the symptoms of COVID-19 various drugs are under investigation. Drug repurposing is a practical approach for rapidly discovering frontline arsenals to fight against COVID-19.However, the common repurposed drugs like chloroquine, hydroxychloroquine, remdesivir, lopinavir- ritonavir, favipiravir, ribavirin, azithromycin, umifenovir, oseltamivir need to be studied thoroughly for long term uses. In one of our studies, we found some of the FDA approved kinases inhibitors like Baricitinib, Brepocitinib, Decernotinib, Fasudil, Filgotinib, GSK2606414, Peficitinib, Ruxolitinib, Tofacitinib, Upadacitinib, Pamapimod, and Ibrutinib can potentially target the Ni-Ren domain of the SARS-CoV RdRp protein hence can be used as a drug against the virus.We have also found potential anti-SARS-CoV-2 activity in some plant-derived compounds like Withanolide D, Withaferin A.

Keywords: COVID-19, SARS-CoV-2, Comorbidity, Drug-repurposing, Natural-compounds.

Audience Take Away:

- Association of Comorbidity with COVID-19 may depends on various factors.
- Mutations in SARS-CoV-2 is needed to understand carefully before defining treatments regimes.
- Natural compounds may also preventive and delay the progression of COVID-19 severity.
- Treatments may divide based on viral infection stage into host.

Biography

Dr Hem Chandra Jha did his PhD in 2010 from Institute of Pathology in Delhi with Dr. Aruna Mittal, where he worked on Molecular Diagnosis and Pathogenesis of Chlamydia pneumonia in coronary artery disease patients and awarded PhD from BITS Pilani, Rajasthan. He then moved to University of Pennsylvania at Philadelphia for postdoctoral research where he joined Prof. Erle S Robertson group working on tumor viruses specifically EBV (Epstein bar Virus) and KSHV (Kaposi sarcoma associated Herpesvirus). He has been working on understanding role of EBV latent antigens in transformation of B-cells by regulation of Aurora Kinase B and Histone H2AX. He also involved in the study of epigenetics changes with virus infection in primary cells.

Further he moved to India at IIT Indore in July 2016 as Ramanujan Fellow. Subsequently join Assistant Professor in Feb 2017 and Head of the Department in Aug 2018 and promoted to Associate Professor in Feb 2022. His current research work comprises of how EBV co-infection with *Helicobacter* pylori leads to aggressive gastric carcinoma and drug resistance. What are the biological mechanisms behind this co-infected patient's higher mortality compared to other gastric cancer groups? Also, he is looking how this EBV is playing role in several neural diseases like Multiple Sclerosis and Alzheimer's diseases. He has published more than 80 research papers including PNAS, PloS Pathogens, mBio, Journal of Virology, etc. He is also members of Editorial and review board of several peer reviewed National and International journals. Last two years his research group actively working in SARS-CoV2 virus and exploring new avenues in these domains.

Houda Baati*[1], Siala[1], Chafai Azri[1], Emna Ammar[1], Christopher Dunlap[2], Mohamed Trigui[1]

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Heavy metal tolerance and adaptive strategies of halophilic archaea isolated from the highly contaminated Sfax solar saltern sediments (Tunisia)

Sfax solar saltern (Tunisia) is a thalassohaline environment significantly threatened, for more than 50 years, by industrial particulate fallouts highly enriched with heavy metals (Cd, Pb, Ni, Zn and Cu). The current study focuses on the met al tolerance of Halo bacterium salinarum isolated from the most contaminated superficial sediments of such solar, by using agar dilution methods in complex and minimal media. The results showed the least inhibitory metals in complex medium, based on Minimum Inhibitory Concentrations (MICs), were Pb (MIC=4.5 mM), Cd (MIC=4 mM), and Ni (MIC=2.5 mM). Their MICs were more inhibitory in the other tested media (< 2 mM). The archaeal strain revealed a high sensitivity for both Cu and Zn, with MICs below 0.5 mM. Growth kinetics in complex and minimal media showed a more sensitive strain to the all metals in liquid media than in solid one. The growth kinetic assays indicated the presence of selected heavy metals resulted in a lower growth rate and lower total cell mass relative to the control.

Despite that Cd and Pb are nonessential and have no nutrient value, they were the most tolerated metals by Halobacterium salinarum strain. In addition, pigment intensity in the strain was inhibited by the presence of the heavy metals relative to the control. The draft genome sequence was analyzed in order to reveal its adaptive strategies to live in heavy metal polluted hypersaline environments.The strain harbors many genes responsible for metal transport/resistance (copper-translocating P-type ATPases, ABC transporter, and cobalt-zinc-cadmium resistance protein), detoxification enzymes and secondary metabolites.

Keywords: Solarsaltern, Halobacteriumsalinarum, Heavymetals, Growthkinetics, Generationtime, Genomesequence.

Biography

Houda Baati Ph.D. is currently working as Assistant Professor at Preparatory Engineering Institute-Sfax “IPEIS”, University of Sfax, Sfax (Tunisia). She earned her degree thesis in the Research laboratory of “Environmental Sciences and Sustainable Development “LASED”, at IPEIS. Her thesis topic was on phylogenetic diversity of microbial community of the Sfax solar saltern. Her research interests deal mainly with the environmental microbiology, molecular microbiology, and geomicrobiology.

Dr. P. Hema Prakash Kumari
GITAM Deemed to be University, India

Applications of artificial intelligence in clinical microbiology diagnostic testing

Clinical laboratories have been playing a pivotal role in understanding biology, disease and molecular medicine. Approximately 70% of the decisions regarding a patient's diagnosis and treatment are based on laboratory results. Clinical Microbiology Laboratories have been relying on conventional diagnostic methods. Automation of clinical laboratories has transformed the departments of Biochemistry and Pathology in a significant way.Yet, Clinical Microbiology laboratories must have the technology to replace the existing conventional cultural methods.Clinical and microbiological diagnostics have made technological improvements, yet they are expensive to reach medium microbiology facilities. In the wake of Artificial Intelligence making a path into the diagnostics, as evidenced by the image-based diagnostics in Radiology and Pathology, Can Artificial intelligence provide solutions to clinical and microbiological laboratories? Clinical microbiology laboratories are the first line of defence in the fight against infectious illnesses and antibiotic resistance, particularly recently emerged. Although most clinical laboratories currently use traditional methods, technological advancements fueled by digital imaging and high-throughput sequencing will transform clinical diagnostics management for direct bacteria identification and rapid antibiotic susceptibility testing.Notably, such technical developments occur during the golden age of machine learning, when computers are no longer just passive data miners but can also assist clinicians in making diagnostic and treatment decisions once they have been adequately educated. This presentation will navigate through the applications of the Artificial intelligence and Machine learning in the Diagnostic Microbiology Laboratories and Discuss such technological advancements by providing practical instances of their use, as well as their limitations and potential challenges that their use in clinical microbiology laboratories could cause.

Audience Take Away:

- Audience will learn about Definitions of Artificial intelligence and Machine learning.
- Will be able to know the current advancements in the field of clinical microbiology diagnostic by incorporating Artificial intelligence and Machine learning.
- This knowledge will help them to take forward the implementation of artificial intelligence in the clinical diagnostics and also critically think about the limitations of the technology incorporation in routine diagnostics.
- They can form new solutions and come up with new technological solutions for diagnostic which can be economical.

Biography

Dr. P. Hema Prakash Kumari, Professor and Head, Department of Microbiology, GITAM Institute of Medical Sciences and Research, India is Medical graduate from Guntur Medical College in the year 2000. She Completed Post Graduation in M.D. Microbiology from the same Medical College. Later she completed Senior residency in Jawahar Institute of Post Graduate Education and Research, Puducherry . She worked in various medical colleges in Andhra Pradesh in the roles of Assistant professor , Associate Professor and Professor. She has a 27 total publications with 8 publications in Scopus and 6 in Pubmed central and one chapter to her credit.

Anindya Sundar Panja
Vidyasagar University, India

Extremophiles protein structural, functional and evolutionary adaptation driven by its structural plasticity is proven by different physicochemical factors

Several microorganisms can live in a variety of harsh conditions, including high temperatures, low pH, and high salt concentrations. Extremophile stability is offered by ensembles of multiple weak connections, which causes compactness-rigidity in proteins, limiting their flexibility and function. Understanding how microbial proteins change structurally under stress is crucial. A vast number of protein sequences and structures were systematically studied to understand protein stability and distinguish microbial extremophilic proteins from their non-extremophilic orthologs. The results demonstrated that environmental pressures influenced the method for packing the protein core through substitutive structural processes and improved ionic interaction. According to data analysis, there is a difference in the number and composition of amino acids among them. The lack of a functional relationship between most extremophile and non-extremophile proteins in microorganisms was shown by the negative correlation of pairwise sequence alignments and structure alignments. A significant number of salt bridges were detected on the surface of the extremostable proteins. A large number of tiny nonpolar amino acids and a modest number of charged amino acids, such as Arginine and Aspartic acid, have higher nonplanar Omega angles in their peptide bonds. In severe environments, microorganisms may predispose amino acid composition, including geometric variability, to molecular adaptation of extremostable proteins to atmospheric fluctuations and related alterations under natural selection pressure. Variation in amino acid content and structural diversification in microbial proteins play a key role in evolutionary adaptation in different climatic conditions.

Audience Take Away:

- This study will aid in the improvement of enzyme stability in general, including chemical usage, protein engineering, and immobilisation.
- The biophysical pleiotropy of extremostable proteins was also used to develop a global prediction model for assuming the effect of mutations on protein stability.
- How adaptative mechanisms of extremosable proteins will help to mitigate climatic changes throughout the evolutionary time scale.

Biography

Dr. Anindya Sundar Panja is affiliated to post graduate Department of Biotechnology, Oriental Institute of Science and Technology affiliated by Vidyasagar University, India. Dr. Anindya Sundar panja is currently working as Assistant Professor. Dr. Anindya Sundar panja is actively associated with various institute and University regarding Research and academic activities. Dr. Anindya Sundar panja is working last 11 years on protein Evolution against various environmental stresses, last few years Dr. Anindya is working on agriculture Biotechnology and medical bioinformatics, specifically on multi drug resistance mechanisms. He has published more than 18 research articles in SCI(E) journals.

Manisha Mandal
MGM Medical College, India

Studies on alteration of gut microbial composition with probiotics administration in health and disease using metagenomic analysis

Background and objectives: Functional foods, including probiotics, have attracted increased attention in many countries. Probiotics are live microorganisms that when ingested in sufficient quantities, confer health benefits. The gut microbiome, an immensely diverse and dynamic niche of the human body, is a critical determinant of human health and disease, and a key regulator of host physiology. But it is not clearly known to what extent the ingested probiotics effect the composition and functionality of the gut microbiota. Here, the study expands the understanding of probiotic food benefits by metagenomic analysis of 16S rRNA gene marker from human gut microbiome.

Methods: MiSeq single-end fastq sequences of 16S rRNA bacterial genes were fetched using SRA (https://www.ncbi.nlm.nih.gov/sra), pertaining to 25 gut samples (5 datasets) in health and disease including Type 2 diabetes melltitus (T2DM), Prader Willi Syndrome (PWS), and obesity. The sequences were imported to QIIME2 (https://qiime2.org) in Miniconda-3, and subjected to demultiplexing, quality control with Dada2 algorithm, phylogenetic analysis, and taxonomic classification using GREENGENES. The OTU abundance were attached with their corresponding taxonomy to generate the biom file. The downstream statistical analysis and data visualization were carried out using MicrobiomeAnalyst (https://www.microbiomeanalyst.ca). Community profiling was achieved with alpha-, beta diversity, and core microbiome analysis; clustering analysis with heatmap to compare abundance of different taxonomic levels, dendrogram,correlation analysis, pattern search; differential abundance analysis with univariate statistics, and marker-gene survey with metagenomeSeq. The PICRUSt was used for prediction of the functional potential and pathway analysis of the microbiota from 16S output (https://www.microbiomeanalyst.ca).

Results: Healthy omnivorous individuals exhibited greater level of alpha-diversity than healthy vegetarians, without probiotic supplementation. Probiotic intervention, in obesity exerted higher diversity compared to T2DM followed by PWS; OTU diversity in T2DM was greater than non-diabetics. Probiotic ingestion in healthy individuals was associated with lowest diversity. Species richness was more evenly distributed after probiotic administration in obesity, diabetes, and health. Beta diversity revealed similar variance in bacterial diversity with formation of three clusters consisting of healthy individuals without probiotic administration, obesity and PWS both with probiotic intervention.Firmicutes (46.0%), Bacteroidetes (45%), Proteobacteria (4%) and Actinobacteria (5%) were observed in all the samples. Univariate analysis indicated significant abundance of *Clostridiales* in T2DM with probiotic administration comprising two OTUs (2626509, 290018), and *Coriobacteriales* (OTU: 276120), among healthy vegeterians without probiotic consumption. The significantly expressed KEGG pathways were metabolism of carbohydrate, amino acids, energy, lipid, nucleotide, and xenobiotics; biosynthesis of secondary metabolites and glycan; xenobiotics biodegradation.

Conclusions: Post probiotic treatment among T2DM, PWS, and obese individuals expressed *Lachnospiraceae* as the dominant family known to be involved in the production of SCFAs compared to healthy individuals dominated with *Ruminococcaceae* known to be more abundant in a stable gut microbiota during probiotic treatment. Bacteroidetes, which is highly relevant in dysbiosis and disease, was significantly reduced with probiotic administration in T2DM, PWS, obese, and was eliminated from otherwise healthy individuals. *Enterobacteriaceae*, responsible for causing nosocomial and community-acquired infections, were completely removed from healthy individuals with probiotic intervention, while supression of *Enterobacteriaceae* was comparitively more effective in T2DM than PWS and obesity.There was an abundance of beneficial bacteria Bifidobacterium breve with probiotic intake more in PWS compared to healthy, T2DM and obese people.

Audience Take Away:

- The present study revealed the association of probiotic administration with gut microbiome effecting bacterial diversity, community structure, functional enrichment and metabolic potentiality specific in health and certain diseases.
- Modification of gut microbiota composition by probiotic administration might be a promising therapeutic approach to treat many disorders.

Biography

Dr. Manisha Mandal has her expertise in the field of molecular epidemiology of infectious diseases, data analysis using bioinformatics approaches towards drug development, disease modelling, next generation sequencing, bioremediation of pesticide using bacterial system, and pollution abatement. She has published more than 70 research articles in her research field in different journals, one book, and presented several papers in different conferences.

Mussarat Shaheen*[1] and Fariha Hasan[2]

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Prediction and annotation of lipase encoding genes and phylogenetic diversity of lipase producing bacteria from metagenomes of different glaciers of Pakistan

Microbes dwelling successfully in glaciers naturally produce various enzymes as a result of an adaptation to combat extreme cold conditions. Researchers are trying to exploit natural potential of microbial enzymes production for various industrial and biotechnological applications. Different cold environments have been investigated to find out microbial diversity, cold enzymes and their relevant enzyme encoding genes through different methods. However, glaciers in the northern regions of Gilgit, Baltistan, and Chitral (Pakistan), are yet untapped especially with respect to bioprospecting for microbial enzymes. These glaciers are condensed in one of the world's greatest mountain ranges of Hindu Kush, Karakoram and Himalayan (HKKH) region. Here, we report our first attempt to investigate sediments and surface ice samples collected from HKKH glaciers for bacterial lipases by applying metagenomics approach. Metagenomic DNA from HKKH samples was extracted and sequenced through Illumina technology.

Metagenomic assemblies were generated using CLC assembler and lipase genes were predicted by using online prediction tool (GeneMark.hmm). Total 323 cold lipase genes were annotated through both Swiss and TrEMBL (UniProt) databases. Phylogenetic similarities were analyzed through BLASTp. These cold lipase genes were present in following bacterial genera *Moraxella* and *Psychrobacter* and in *Janthinobacterium*. Lipase gene's conserved motifs (GXSXG) and (HGG) were visualized through multiple sequence alignment using Clustal Omega program. Current study would be considered a good effort in exploration of new habitats to exploit their natural potential for novel microbial communities and genes for microbial enzymes. This will also enhance the understanding of ecological and industrial importance of HKKH glaciers.

Audience Take Away:

- Bioprospecting for new cold microbial enzymes genes from unexplored cold habitat.
- Environmental microbiology and role of microbial communities in cold environment and advanced methods to explore un-culturable microbes.

Biography

Ms. Shaheen is working as lecturer at GCUF, Faisalabad, Pakistan and also submitted Ph.D thesis as a Ph.D student in Department of Microbiology at Quaid-e-Azam University, Islamabad, working on metagenomic detection of bacterial enzyme genes from glaciers samples collected from glaciers of Pakistan. During Ph.D, she visited Bristol Glaciology center (University of Bristol, UK) under 6 months research fellowship program. She is also teaching at Government College University. During her master degree her research work was about "Incidence of *Pseudomonas* sp isolated from different clinical samples", NIH, Islamabad. In M.Phil, she did her work related to "Studies on production, optimization, characterization and purification of hydrolytic enzymes produced by oil degrading *Bacillus subtili.*

Kishalay Paria*[1], Ananya Gantait[2], Susanta Kumar Chakraborty[3]

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Roles of microbes (fungi) in the bioremediation of heavy metals at estuarine of marine confluence of West Bengal, India

The benthic environment at an ecotone, at the confluence of an estuary, named Subarnarekha with the sea; Bay of Bengal in West Bengal, India (21°33′ to 23°32′ north latitude and 85°9′ to 87°27′ east longitude) supports the lives of an array of microbes along with other benthic fauna in several niches of intertidal zones. Deposition and accumulation of bio-recalcitrant heavy metals in this biologically sensitive but productive saline habitat disrupt normal ecological balances by disrupt prime objective to study the eco-biological potential of benthic fungi in the processes of bio-accumulation and bio-removal of a persistent toxic substances such as heavy metals i.e. lead (Pb-II), cadmium (Cd-II), and mercury (Hg-II). One species Aspergillus penicillioides (F12), after being identified by the ITS genetic system (gene bank deposition with the number, MN210327) was found to exhibit the highest heavy metal tolerance activity. By exhibiting resistance against Hg (II) up to 200 ppm where such resistances were recorded as up to 1000 ppm. for Pb (II) and Cd (II) .The heavy metal binding regions of fungus were determined by FTIR, SEM, and EDEX analysis. The studied fungal strain A. penicillioides was observed to release higher quantity of exopolysaccharide (EPS), which helps absorb heavy metals in maximum amount.

In such context, EPS and biomass of fungal strain can be treated as biologically potential ingredients for the effective bioremediation of heavy metals from the soil-water interphase. This study also emphasizes the optimization of processes of different physicochemical parameters [pH, time (hours) and temperature (0C)] by employing Box-Behnken Design (BBD) of experiments with the prime objective of understanding the bio-absorption capability of an important heavy metal [lead (Pb II)] from Subarnarekha river estuary by EPS of Aspergillus penicillioids (MN210327). From statistical analysis (ANOVA) has revealed that the optimized bio-absorption (72.76%) of Pb (II) by EPS occurred at pH of 11 and temperature of 37.57 0 C, for a period of 8 hours. Based on the research findings, it has been hypothesized that benthic fungi by virtue of their sensitiveness and power of tolerances against ecological perturbations can play both as bio-remediator as well as bio-indicator organisms in the changing of ecological conditions which impose serious threats not only on larger aquatic floral and faunal components but on other such eco-potential microbes, necessitating to undertake sustainable eco-management of the entire aquatic ecosystem.

Keywords: Heavy metals, Bioremediation, Bio-indicators, Box-Behnken Design, Transboundary River.

Audience Take Away:

- The audience learns about the heavy metal bioremediation activity of marine microbes.
- Fungi act as bio-indicator species of heavy metal contaminated site. So, several researchers can detect the bio-indicator species of different field of research. Beside that heavy metal resistance microbes have huge industrial importance.
- Although several researchers are involved these types of research. Future researches about the development of effective heavy metal removal technology, such as fungal EPS based bio-remediation. In addition, the present research studies have recognized the prospective multidimensional application of benthic fungi for the reduction pollutants load, further investigations are required to find out more multi toxic metal tolerant fungi from the natural ecosystems in the waste management processes.
- One advantage of this technology is the ability of the EPS to adsorb heavy metals (evenin low concentrations). This is important to meet the permissible standard for drinking water or the quality of effluents to be discharged into the surface water. Bioremediation has emerged as an efficient treatment option for water purification, yet numerous challenges and constrains with regard to its practical applications on a large commercial scale still prevail. . Besides, several modified biological approaches such as bioleaching, bioreduction, and bioflotation should also be evaluated with an assessment of their potential for metal recovery from industrial wastewater.

- Heavy metal pollution in the environment and associated toxicity in living beings is of serious eco-environmental concern. The feasibility of bioremediation as a cost-effective and efficient technique should be explored.
- Recombinant DNA technology of metal-accumulating fungi and associated bacteria or algae with required traits could be a very valuable approach for the improved bioremediation, but associated risks should also be considered before field trial.
- The association of fungi and algae (mycorrhiza) could be an economically viable approach for bio-fertilizer production and thus, their use under strict monitoring can be recommended for agricultural applications with bioremediation.
- Bio-energy (hydrogen) production from wastewater bioremediation is a unique approach that not only reduces the pollution but also leads the generation of eco- friendly fuel. This technology must be further explored with the aim of achieving possible commercialization.
- The use of fungal derived nano-biocomposites may become an effective approach for the removal of toxic pollutants from aqueous solution.

Biography

Dr. Kishalay Paria completed the Ph.D. degree from Vidyasagar University, India. Now He join as Assistant Professor of Biotechnology ,OIST, Vidyasagar University. He has published some research papers and few book chapters in reputed international journal. Recently he selected as Bentham Ambassador. He is life member of Biotech Research Society, India. He serve as reviewer for scholarly journals such as: Phytotherapy Research (Wiley) ,Heliyon (Elsevier),Recent Patents on nanotechnology (Bentham Science) ,Sustainability, Agriculture, Food and Environmental Research, International Journal of Optics and Photonic Engineering, VIBGYOR. He serves as Editorial board member of SCIREA Journal of Environment.

Muktadir Hossain*[1], M. Mahtab Hossain[1], Bijoyeeta Roy[1], Tangerul A. Jepu[1], Nusrat U. A. Saleh[1], Kabirul Bashar[2]

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Isolation of a mosquito larvicidal strain of Providencia vermicola

Mosquito-borne diseases are a serious concern for many countries in Africa and Asia. As alternatives to environment polluting chemical insecticides biocontrol agents like entomopathogenic (insect killing) organisms like bacteria (EPB) are needed to be isolated to control mosquito population. Here, we used the larvae of the lepidopteran insect, *Bombyx mori* (commonly called silkworm) as a bait to isolate entomopathogenic nematodes (EPNs) from soil samples collected from various regions of Bangladesh. These EPNs harbor EPB in their gut that can kill host insects after being infected by the nematodes. We buried *Bombyx* larvae with soil samples and monitored appearance of nematodes on the dead larvae.The isolated nematodes were sequenced and found to be entomopathogenic (*Heterorhabditis indica* and *Oscheius chongmingensis*).To isolate bacteria from the EPNs, the abdominal legs of silkworm larvae infected with the nematodes were excised to collect hemolymph (blood) which was cultured in NBTA agar medium that is selective for isolation of EPB.The isolated bacteria were sequenced and among the bacteria identified, we performed mosquito larvicidal bioassay using *Providencia vermicola* due a previous report by another group that this bacterium can kill mosquito larvae. The P. vermicola strain isolated in this study killed larvae of Aedes aegypti or wild-collected larvae obtained from local drainage systems with ~50% efficiency in bioassays conduced in laboratory conditions. These results indicate that the *P. vermicola* strain isolated in this study can be used directly a biocontrol agent or as a component of an integrated pest management strategy to control mosquito population.

Audience Take Away:

- The study is important to emphasize the importance of using entomopathogenic bacteria as a pest management strategy.
- This study will facilitate other researchers to design integrated pest management strategies to control mosquito population.

Biography

Muktadir S. Hossain completed his graduation on Biochemistry and Molecular Biology from the University of Dhaka in 2000.He completed his Ph.D. from the University of Tokyo, Japan in 2004.He joined NCI, NIH, USA with a Fogarty Cancer Research Training Award as post-doctoral fellow.He worked as a Senior Research Fellow in Shanghai Institutes for Biological Sciences, China.He was serving as a Research Professor in the Jeonbuk National University, South Korea before joining North South University as an Associate Professor.

Deepesh Kumar Neelam*[1], Akhil Agrawal[2] and Pawan K. Dadheech[3]

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Calcium-independent extracellular α-amylase production by moderately thermophilic bacillus sp. 4s isolated from Sand Dune, Bikaner, India

Currently, starch industries are extremely demanding the calcium-independent and thermostable α-amylase for starch saccharification. Characterization of extremophiles has received a great attention owing to a valuable source of novel enzymes. In the present will be focused on production of extracellular thermostable and thermo active Ca^{2+} independent alpha-amylase by moderately thermophilic *Bacillus sp*. 4S, which was selected from a set of 10 bacterial strains isolated from sand dune sample of Bikaner, India. On bases of morphology, physiology, biochemical characters and 16S rRNA gene analysis strain 4S belongs to genus *Bacillus*. The media was optimized for α-amylase production by physical and nutritional factors using one factor-at-a time-approach (OFAT) though submerged fermentation. The optimum pH and temperature for amylase activity was found 7.0, 60 °C respectively. A combination of beef extract, yeast extract and jaggery gave maximum 25 U/ml^{-1} alpha amylase production after optimization of all parameters. The molecular weight of alpha-amylase was estimated to be 60 kDa by polyacrylamide gel electrophoresis (SDS–PAGE). The enzyme activity and production were Ca^{2+} independent. Among of all tested additives and detergents; glycerol, Tween 40-80 and polyethylene glycol 8000 stabilized the enzyme activity, on the other hand glycine, SDS, dextran and Triton X-100 decreased the stability. The production of α-amylase enzyme has been reported from diversified thermophilic bacterial species. *Bacillus* sp., is widely known for production of α-amylase and fulfills the industrial needs but calcium-independent species are less. So, this study could be more useful for starch industry.

Audience Take Away:

- This study useful for understands about thermophiles because at present, only a minor fraction of the heterotrophic bacteria inhabiting extreme conditions have been exploited.
- Students, faculty members and PhD scholars are more will get more knowledge about amylase enzyme because nowadays enzyme industries trying to replace chemical with naturally occurring more stable and affective enzyme. This research work useful for teachers to explore their students about use of extremophiles more interesting than mesophiles. Amylases are starch degrading enzymes that have potential application in baking, detergent, and textile industries.

Biography

Dr. Deepesh Kumar Neelam is an assistant Professor, Department of Microbiology, JECRC University, India. He has been achieved his PhD. from Central University of Rajasthan, Ajmer, India. He completed his post graduation in Industrial Microbiology from Amity University and graduation in Biotechnology from Rajasthan University, India. Right now he is supervising two PhD. scholars for their research work. He has been published more than 10 research articles in repudiated journals. He was awarded by IMRF Best Scientists Award in 2020. Currently, he is working on plastic degrading bacteria and extremophiles.

Hamed Aboelkhair*[1], Pedro Diaz[2], and Attila Attia[3]

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[3]The British University in Egypt, Egypt

Comparative study of biosurfactants production and optimization using bacillus subtilis and *bacillus licheniformis*, and environmental aspects

Microorganisms provide a unique opportunity to make hydrocarbon production economically and environmentally considerate in a technique known as microbial enhanced oil recovery. Three main limitations affect the robustness of the synthetic surfactant flooding in oil reservoirs, which are environmental impacts, synthetic surfactant cost, and oil price. Increasing ecological concerns, biotechnology development, and the rise of more rigorous environmental laws have encouraged biosurfactants to be a potent alternative to synthetic surfactants existing in the market due to their biodegradability, low toxicity, and cost-effectiveness. This study was conducted to investigate the potential of the biosurfactants produced by indigenous bacteria isolated from the Egyptian oil fields, optimize their surface and emulsification activity to maximize the oil recovery, and analyse their environmental aspects for microbial enhanced oil recovery. The selected bacterial strains *Bacillus licheniformis* and *Bacillus subtilis* were grown in the new proposed nutrient medium H to optimize the surface activity of the produced biosurfactant. Comparative stability studies were performed for the produced biosurfactants under different conditions (temperature, salinity, and pH). The core flooding experiments were conducted to investigate the effect of produced biosurfactants in improving oil recovery. Finally, the environmental risk assessment of any possible threats of producing biosurfactants by the selected bacteria was performed.

Results showed that the selected bacterial strains *Bacillus licheniformis* and *Bacillus subtilis* show their ability to produce effective biosurfactants that gave the maximum surface activity within 24 hours of incubation in the new proposed nutrient medium H, where the surface tension of water reduced from 71.8 mN/m to 27.13 mN/m and 25.74 mN/m, and similarly the interfacial tension of water against kerosene reduced from 48.4 mN/m to 1.27 mN/m and 0.38 mN/m, at Critical Micelle Concentration of 0.06 g/l and 0.04 g/l, Respectively. No significant change in the surface and emulsification activity of produced biosurfactants over a wide range of temperatures. The surface activity of produced biosurfactants was marginally affected by increasing the salt concentration up to 20% (w/v) NaCl, and pH values range 5-12. The emulsification activity of biosurfactants produced by Bacillus licheniformis and Bacillus subtilis showed a significant increase against long-chain hydrocarbons such as crude oil, which are 50.2% and 63.7%, respectively. The *Bacillus licheniformis* and *Bacillus subtilis* biosurfactants yield was found to be 2.47 g/l and 2.85 g/l, respectively. The core flooding tests show the potential of biosurfactants produced by *Bacillus licheniformis* and *Bacillus subtilis* to recover 31.41% and 39.35% of additional oil over the water flooding residual oil saturation under simulated reservoir conditions, respectively. This study reveals the potential of the selected indigenous bacterial strains *Bacillus licheniformis* and *Bacillus subtilis* to grow in the new proposed medium H and produce effective biosurfactants that could significantly improve oil recovery and retain more than 60% of their surface and emulsification activity under harsh reservoirs conditions. Besides the beneficial effects of the selected indigenous bacteria in producing effective biosurfactants, the performed environmental risk assessment reveals that it could be an outstanding tool to be used in enhanced oil recovery schemes and could lead to promoting environmental sustainability.

Audience Take Away:

- This study was conducted to investigate the potential of the biosurfactants produced by indigenous bacteria isolated from the Egyptian oil fields.
- This study was conducted to optimize the surface and emulsification activity of the produced biosurfactants to maximize the oil recovery.
- This study was conducted to analyse the environmental aspects of the selected biosurfactants producing bacterial strains for microbial enhanced oil recovery.

Biography

Dr. Hamed Aboelkhair studied Petroleum and Gas Technology Engineering at the British University in Egypt, Egypt and graduated with a BS in 2011. Then studied renewable energy engineering at the British University in Egypt, and graduated as MS in 2018. The PhD degree will be received in 2022 at London South Bank University, UK. He has published a research article in one of the top-rated journals of Elsevier (Journal Of Petroleum Science And Engineering). He has also reviewed a journal article for one of Springer's journals Biomass Conversion And Bio refinery.

Rolee Sharma*[1], Tarun K Upadhyay[2] and Firoz Ahmad[3]

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Particulate glucan from yeast : Novel application as delivery vehicles

A biocompatible, biodegradable β-1,3-D-glucan based macrophage targeting delivery system has been developed in our lab as 1–4 μm spherical, hollow shells extracted from the cell wall of *Saccharomyces cerevisiae* (Baker's yeast). Macrophage are the first line of defense against infections, as they phagocytose any bacilli or foreign particles they encounter. Yeast derived particulate 1,3-*β*-glucan thus provides for receptor-mediated uptake by phagocytic cells expressing *β*-glucan receptors, making GPs an ideal drug delivery vehicle to target phagocytic cells in the immune system. These also act as "natural polysaccharide immunomodulators," and activate the immune system. We report here, the preparation of *β*-glucan particles (GP) from yeast cells, their characterization and demonstration of their rapid phagocytic uptake by the macrophage. The beta glucan structure of particles was validated by fourier transform infrared spectroscopy (FTIR), and NMR. The particles were loaded with an anti-tuberculosis drug, Rifabutin and sealed with alginate. Electron microscopy revealed the porous nature of these particles with drug nano-precipitates. The drug entrapment and drug loading was seen up to 81.46 ± 4.9 % and ~40.5 ± 1.9 %, respectively. These results indicate that these yeast derived glucan particles have the potential to be used as an effective agent for delivery of Rifabutin and targeting to macrophage. Additionally, these particles have been seen to induce phagosomal maturation and autophagy induction within *M.tb*. infected macrophage. The particles thus not only act as effective delivery vehicles but also activate anti-microbial defence mechanism within host cells. Thus, the intracellular drug delivery supplements the innate response in *M. tuberculosis* infected macrophage, thereby accounting for the enhanced efficacy observed for this delivery system and holding promise for their use as formulations against TB.

Audience Take Away:

- The audience shall learn about the various applications of this delivery system.
- The audience shall learn about the preparation of these particles from yeast cells.
- The audience shall come to understand that these particles can be applied for the delivery of a diverse array of small molecules including prophylactics and therapeutics.
- The presentation shall explain the benefits of using this delivery system against intracellular infections, particularly M.tb.

Biography

Dr. Rolee Sharma received M.Sc. degree in Biochemistry from Lucknow University, Lucknow. She then joined the research group of Dr Amit Misra at the Central Drug Research Institute, Lucknow, India and earned her doctoral degree from the same Institute in 2006. Thereafter, she joined the Department of Biosciences, Integral University, Lucknow, and is currently working as Professor at the School of Life Sciences and Biotechnology, C.S.J.M. University, Kanpur. Her research interests lie in area of targeted drug delivery, innate responses and host defence. She has around 50 publications of National and International repute and has five international patents.

Rebecca Pratiti*, Parul Sud
McLaren Health Care, USA

Universal epidemic outbreak questionnaire

Epidemic outbreaks are a part of population and public health. The epidemiological triad of host, agent and environment are changing in their interaction with each other in recent years. Urbanization and deforestation cause closer contact with animal host, insect vectors and higher contaminations possibility. More localized epidemics are being observed around the world caused by a wide variety of organisms and chemicals. Some known viruses are being established in new geographical areas and new viruses are being discovered. Newer biological and chemical agents are continually being added to our environment with potential for acute or subacute epidemics. Acute chemical effects are found early, though most are subacute presentation and hence establishing causality takes time. As health care professionals lack training and time to assess risk factors of epidemic, important information about epidemic source identification (ESI) is missed. ESI is important to decrease disease burden. Irrespective of the logistics in epidemic detection, there is an immense contribution by reporting delays on population health. The reporting delay could be medical, administrative or socioeconomic. A good surveillance system is timely, sensitive, specific with readily interpretable output. These factors should motivate us to draft and implement an accessible universal epidemic outbreak questionnaire (UEOQ) with a good online database for ESI. We have tried to formulate UEOQ that may be used by providers if they suspect unusual occurrence of cluster of cases. Some of the questions have been adapted from the previous 'Food- and waterborne disease outbreak investigation questionnaire tool repository with European Centre for Disease Prevention and Control' with approval and attribution.

This tool helps us to locate the source for food and water borne diseases. We have tried to improvise this tool to identify epidemics caused by air and dermal exposures. An optimal UEOQ should include detailed food, water, air, dermal exposure evaluation with chemical and work exposure. These factors are especially important if the disease-causing agent is unknown. Additionally, a short consent may be added for sample banking. Limitation for UEOQ is the time spent in form completion. An ideal form should be worded at fifth grade reading level with minimal necessary medical language to facilitate form completion by a patient solely or with some assistance from health care personnel. Validation of these questions is crucial. A pre-drafted Google forms database has been created for UEOQ to automatically translate to systematic data for effortless and timely data analysis. Patient identifier section is removed for possible data sharing. UEOQ could be retained as a part of patient's medical records and the database entry is optional. The Google form database version could be obtained by writing to the corresponding author. Thus, health professionals and insurance companies could improve in-built surveillance system to alert epidemic outbreaks with immediate access to data, knowledge sharing and expert advice in epidemiology in a Health Insurance Portability and Accountability Act (HIPAA) compliant way to prevent epidemic related disease burden. In summary, UEOQ may act as an adjunct tool for early ESI for mitigating its effect on public health.

Audience Take Away:

- The audience would learn about epidemics with its types, causes, barriers to identification.
- The audience if suspect cluster of cases, unusual cases could use the universal epidemic questionnaire (available at no cost through PubMed) to get detailed exposure history.This cold be retained with patient records. And could be analyzed further if needed with an online google form-based database.
- This would lead to possibly earlier epidemic source identification with decrease disease burden.

Biography

Rebecca Pratiti works as a faculty physician with McLaren Health Care. She had completed her Master of Public Health. She is interested in epidemiology and occupational health. She is involved in studies about harms of hookah smoking, biomass cookstove related air pollution health effects, developing epidemic outbreak questionnaire and disaster mitigation science.

Sofia S. Mendes*[1], Tanja Schneider[2], Heike Brötz-Oesterhelt[3], Carlos C. Romão[1], and Lígia M. Saraiva[1]

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Mechanism of action of clotrimazole-linked co-releasing molecules

Antibiotic resistance is one of the major causes of death worldwide increasing the demand for novel type of antibiotics. In the last years, the class of metal-based carbon monoxide releasing molecules (CORMs), that are active CO donors, have been described as bactericidal compounds. More recently, CORM conjugated with azoles were found to be effective antimicrobials against several microbes. To study the parameters that modulate its antimicrobial action, CORM-clotrimazole conjugates we produced several with various metals and ligands and tested their effect on Gram-positive and Gram-negative bacteria. Data showed that the bactericidal activity of the CORM-clotrimazole conjugates depend on the ligand but not on the metal. Of relevance, these conjugates were found to be more than the sum of its parts : while the CORM scaffold has no antibacterial activity and clotrimazole shows only moderate minimal inhibitory concentrations,the potency of the conjugates is one order of magnitude higher than that of clotrimazole. Treatment of *Staphylococcus aureus* with the most powerful compound of the studied series, namely ReBpyCtz, affects cellular energy functions, interferes with the membrane topology, and inhibits peptidoglycan biosynthesis. Exposure of *S. aureus* to ReBpyCtz triggers a sequence of events that is initiated by membrane insertion, followed by membrane disorganization, inhibition of peptidoglycan synthesis, release of CO, and breaking down of the membrane potential. Therefore, the conjugation of CORMs with known antimicrobial drugs has the potential to generate compounds that due to synergistic effects are more potent than the drug alone.

Audience Take Away:

- Carbon monoxide-releasing molecules (CORMs) conjugated with antibiotics can have an increased antimicrobial activity.
- The ligands of the CORMs modulate the antimicrobial activity.
- CORM conjugates are internalized and perturb the membranes of Gram-positive bacteria.

Biography

Sofia studied Cellular and Molecular Biology at NOVA School of Science and Technology and graduated in 2016. She then proceeded to a Master's in Biochemistry for Health at Instituto de Tecnologia Química e Biológica António Xavier NOVA where she received her diploma in 2018. During her master's Sofia joined Prof. Lígia Saraiva's research group where she continued for a PhD degree. Currently she is in her fourth year of the PhD.

Marcus Vinícius Dias-Souza

Integrated Pharmacology and Drug Interactions Research Group, Brazil

Interactions of antimicrobial drugs and natural products : A solution or even more trouble concerning bacterial resistance?

Bacterial infectious diseases are each time more difficult to treat. The limited options of antimicrobial drugs and the multidrug resistance profile of pathogenic strains are the main explanations for this context. Several works have provided evidence of the antimicrobial potential of different plant extracts and phytomolecules such as polyphenols and alkaloids, suggesting that they can be explored isolated or combined to antimicrobial drugs to overcome bacterial resistance. However, effective combinations of phytomolecules and antimicrobials are poorly predictable, and require experimental evidence to be confirmed.A complex scenario, therefore, develops in this context: potentially bioactive compounds can be found not only in industrially-manufactured or artisanally prepared phytotherapics, but also in nutritional supplements, food, juices and teas.As food intake is generally more recurrent than medication intake, drug-herbal interactions (DHI) are expected to be more frequent than drug-drug interactions (DDI).Nevertheless, DHI are often ignored and are not as investigated as DDI. Regarding antimicrobial drugs, negative (antagonistic) DHI may lead to increased bacterial resistance, in spite of their potential antimicrobial activity. In this talk, recent works on DHI related to antimicrobial drugs will be discussed, considering synergistic and antagonistic interactions, as well as perspectives on pharmaceutical development of formulations.

Audience Take Away:

- Molecular aspects of bacterial resistance to antimicrobial drugs.
- Pharmacology of natural products concerning antimicrobial potential.
- Technical aspects of analytical methods using GC-MS and UPLC for natural products.
- DHI that may be explored to treat bacterial infectious diseases.

Biography

Dr. Marcus Vinícius Dias-Souza obtained his PharmD in 2009 from University Center of Eastern Minas Gerais (Brazil), studying pharmaceutical care. In 2013 he obtained his Master of Science in Immunopathology from University Vale do Rio Doce (Brazil), and received his PhD in 2017 at the Federal University of Minas Gerais. Since 2013 he leads investigations on DHI focused in antimicrobial drugs. He has published more than 40 papers in peer-reviewed journals and eight book chapters. He is head of GPqFAR (Integrated pharmacology and drug interactions research group) and Editor-in-Chief of JAPHAC (Journal of Applied Pharmaceutical Sciences – ISSN 2358-3495).

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Biodistribution and targeting specificity of liposomal agents encapsulated radiopharmaceutical 99mTc-tetrofosmin

Drug transportation to and retention within mitochondria (negative membrane potential) requires the passage of drugs through tissue, plasma membranes, and mitochondrial membranes. However, at equilibrium, cationic drug-delivery liposomes are sequestered within mitochondria and fixed intracellularly as long as the cell membrane integrity is maintained and the flow of nutrients through the blood persists. Thus, drug-delivery liposomes can preferentially locate tissues with mitochondrial dysfunction in the heart or brain, which is beneficial in perfusion imaging. Since 99mTc tetrofosmin is lipophilic, after intravenous injection, it diffuses passively through the cell membrane and is actively retained due to the presence of intact mitochondria, reflecting the presence of viable cells. In nuclear medicine, 99mTc-tetrofosmin is used to assess myocardial perfusion in ischemia and infarction. However, one of the main pitfalls associated with its use is extracardiac activity, which can lead to misleading by obscuring the targeted organ. Due to their enhanced permeability and retention (EPR), liposomal nano-vesicles, when used as a novel drug deliverysystem, offer the benefit of accumulating in the myocardium and cancerous tissues. Furthermore, liposomes are of different sizes, so they can target red blood cells to provide exact and pure cardiac quantification.

This test aimed to reduce the toxicity as well as enhance the targeted organ or tissue uptake. A preclinical toxicity test was conducted using rat myocardium (H9C2) cells, the SRB assay. A gamma camera scanning was also used to trace the radiopharmaceutical biodistribution.It was observed that by encapsulating the radiotracer within the liposomes, the toxicity effect was reduced at higher doses and made negligible at the regularly used dose.Audience will be able to understand the factors that affect the radiopharmaceutical encapsulation, uptake and the biodistribution that enhance image quality with better target-to-non target-ratio in nuclear medicine. Also they will be able to distinguish the effectiveness of delivery of drugs via liposomes in diagnostics or therapeutics.

Biography

Anfal M. Alkandari from Kuwait has dual bachelor degrees in nuclear medicine, from Kuwait university, and the second major in medical biophysics, then completed her master degree at the age of 32 from Helwan university-Alkasr Alaini in Egypt. She is a PhD candidate from Mansoura university in Egypt..

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Gut microbiome is associated with obesity, fasting plasma insulin and serum enzymatic activity of amylase in Mexican children

Background: The last national survey of health and nutrition in Mexico (2020) reported a prevalence of obesity of 18.6% and 17.0% in children and adolescents, respectively. Although recently, we evidenced a negative association of serum enzymatic activity of salivary (AMY1) and pancreatic (AMY2) amylase with obesity risk in children eating medium/high amount of starch,little is known about the relationship between obesity, serum AMY1 and AMY2 enzymatic activity, and gut microbiota.

Objective: We analyzed the association between obesity, serum AMY1/AMY2 enzymatic activity and gut microbiota in up to 92 and 78 Mexican children with normal weight (NW) and with obesity (OB).

Methods: Anthropometric data and serum AMY1/AMY2 measurements were analyzed. Composition of microbial communities was determined by high-throughput sequencing of the V3-V4 regions of bacterial 16S rRNA genes.

Results: The gut microbial community structure was associated with obesity and fasting plasma insulin (FPI) (P_{OB}=0.012, P_{FPI}=0.0003). Gut microbiata was also associated with serum enzymatic activity of AMY2 in children with NW (P_{NW}= 0.003) and OB (P_{OB}= 0.027) by separate. While obesity was positively associated with *Fusicatenibacter* (p= 0.017) and *Romboutsia* (p= 0.017), FPI was negatively associated with *Blautia* (p= 0.013). Additionally, a significant interaction was found between AMY2 and obesity status (p<0.05). There is a positive association between the highest tertile of AMY2 enzyme activity and alpha diversity (observed richness, Shannon diversity and Inverse Simpson index) in children with obesity (p<0.05). In children with NW and OB, tertiles of AMY2 were positively associated with one *Akkermansia* ASV ($p \leq 1.2x10^{-7}$) and one *Ruminococcaceae*_UCG-014 ASV ($p \leq 5.8x10^{-9}$).

Conclusion: Our results confirm that gut microbial community is associated with childhood obesity and FPI. For our knowledge, this is the first report regard the serum AMY2 enzymatic activity is associated with the relative abundance of Akkermansia and Ruminococcaceae_UCG-014 (oligosaccharide-fermenting and SCFA-producing bacteria).

Audience Take Away:

- Our results show an epidemiologic case of association between gut microbiota, obesity and serum enzymatic activity of amylase.
- The main objective of the global project is to accumulate evidence to support the use of serum enzymatic activity of amylase as a potential biomarker of obesity and its metabolic complications.
- In the future, we expect that serum enzymatic activity of amylase play an important role into the treatment and/or prevention of obesity and its metabolic complications, through the design of personalized prescriptions of diets.

Biography

PhD. Miguel Vázquez-Moreno. A National Investigator Level 1 and Posdoctoral Fellow in the Unidad de Investigación Médica en Bioquímica of the Instituto Mexicano del Seguro Social, in Mexico. PhD. Graduated with honors from the Universidad Naiconal Autónoma de México in 2020.Author of 11 journal articles with 74 citations. In the biomedical science, he has graduated 1 master and 2 medical specialty students. His scientist interest is on the Genetic bases of obesity and type 2 diabetes through the : 1) Creation of new study cohorts of children and adults, and 2) genetic identification and its biologic, ethnic and environment interactions.

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