magnus Group

International Conference and Expo on

APPLIED MICROBIOLOGY

17-18 JUNE 2022

VIRTUAL EVENT

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BOOK OF ABSTRACTS

INTERNATIONAL CONFERENCE AND EXPO ON

APPLIED MICROBIOLOGY

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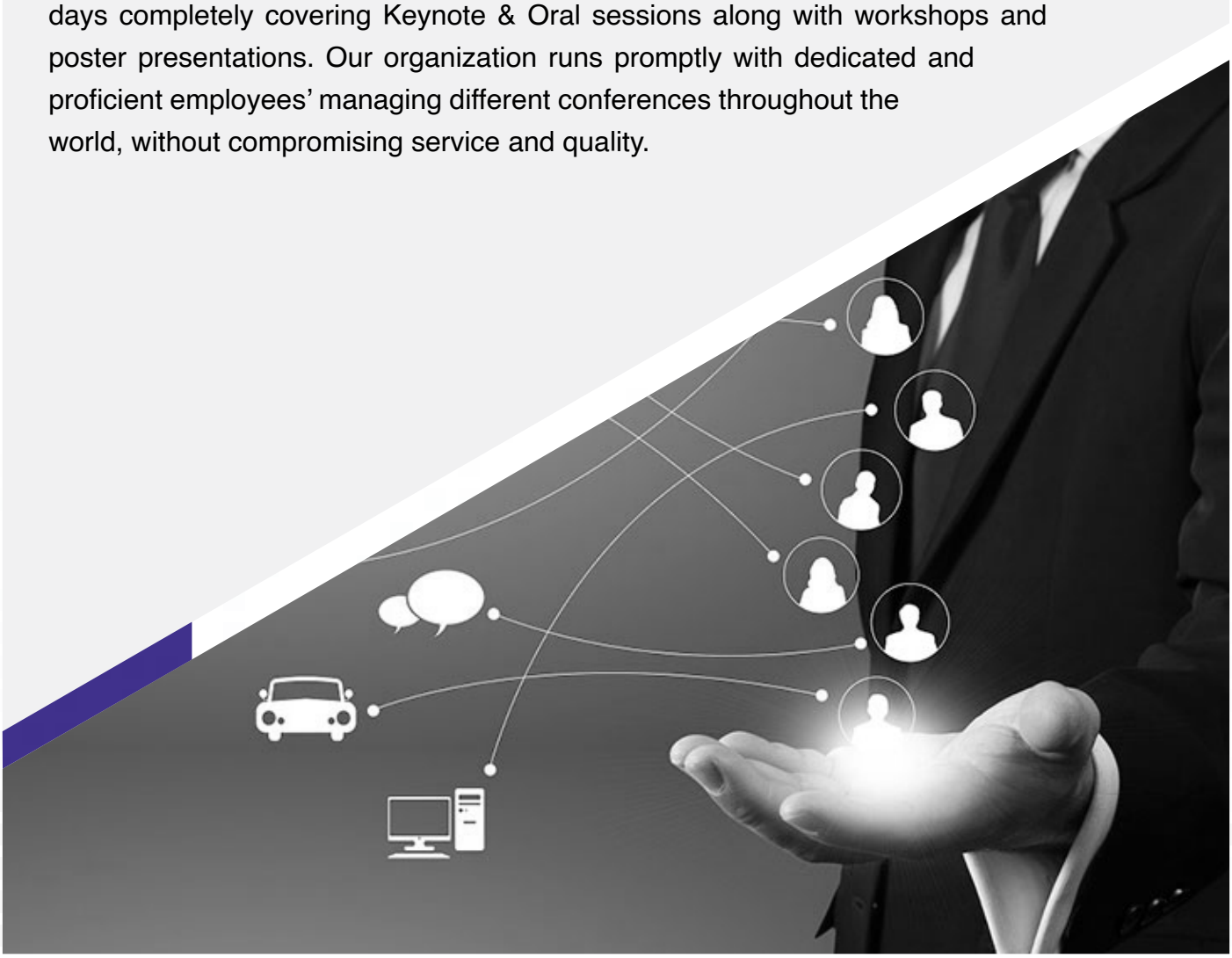
ABOUT MAGNUS GROUP

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 ICAM 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 Applied Microbiology “ICAM 2022” going to be held from June 17-18, 2022 to discuss on Microbiology and Public Health concerns with the theme “Microscopic View of Applied Microbiology in The Genomic Era”

ICAM 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 ICAM 2022.

KEYNOTE FORUM

DAY 01

INTERNATIONAL
CONFERENCE AND EXPO ON

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Satya P. Singh

Saurashtra University, India

Bacterial diversity and biocatalytic potential of sea water and related saline habitats : A perspective from the Gujarat coast, India

The microorganisms of the saline habitats require dual extremities of alkaline pH and high salt concentrations. For the last three decades, we have investigated bacteria, actinobacteria and archaea from the sea water and related saline habitats of coastal Gujarat, India. Our studies focused on the cultivation, distribution, diversity, biochemical and metabolic traits, enzyme secretion, characteristics and expression of key enzymes. The antibiotic resistance is an effective strategy for the microbial survival and dominance in different seasons.While the production of the hydrolytic enzymes and ability to utilize variety of hydrocarbons projects their biotechnological and bioremediation avenues. The diversity was assessed by the conventional, phylogenetic and other molecular approaches. The phenograms based on the morphological and metabolic traits and the 16S rRNA genes based phylograms were useful in identification of the organisms and assessment of the diversity.

The comparison of both approaches reflected significant seasonal variations of the actinobacterial communities, despite limited phylogenetic differences. The impact of the abiotic factors on the bacterial diversity was analysed by the Canonical Correspondence Analysis (CCA).The cultivable diversity was compared with the metagenomic-generated dynamics of the microbial population. The sequence and function-based metagenomics provided detailed account on the diversity, phylogeny and putative physiological functions in the saline habitats. The dominant phylum were Bacteroidetes, Proteobacteria and Gemmatimona. The actinobacterial genera identified through metagenomics were substantially greater than cultivable genera. The genetic diversity of protease genes was assessed from the metagenome and cultivable bacteria using degenerative primers. The phylogenetic analysis of the protease genes reflected the novelty of the proteases. Further, the factors affecting the heterologous gene expression were investigated for the induction and solubility of the expressed protease. Gene profiling, cloning and expression of potential enzymatic genes paved the way to elucidate the structure and function relationship and prospects of applications.

Keywords: Bacterial diversity; Phylogenetics; Haloalkaliphilic bacteria; CCA; Geographical distribution, Metagenomics; Saline habitats; 16S rRNA gene; Protease Gene Diversity

Audience Take Away:

- Diversity, Phylogeny&Biocatalytic potential of halophilic/haloalkaliphilic microorganisms from saline habitats: Approaches & Analysis.
- Cloning, expression and characterization of Recombinant enzymes from haloalkaliphilic bacteria.
- Metagenomics of Extreme Environment : Diversity and search of novel genes.

Biography

Currently UGC-BSR Professor with Biosciences, Saurashtra University, Rajkot, India. Earlier, Professor & Head (2003-2020) in the same Department. Masters from G. B. Pant University, India, and PhD from Griffith University, Australia. Visiting Scientist at National Food Research Institute, Tsukuba, Japan and Visiting Professor at Yangon University, Myanmar. Published 106 research papers, 25 book chapters and 1 edited book (Springer), with H-Index 31 and citations round 3000. Supervised 25 PhD, 23 MPhil and 105 MSc students;4 PhD and 4 Masters students currently working. Research collaborations with NFRI-Japan, Griffith University-Australia, IIT-Delhi, University of Delhi, Central University-Hyderabad and JNTU-Hyderabad. UGC, DBT, CSIR, MoES, DST, GSBTM, Saurashtra University and Government of Japan funded Research Projects.

Héctor Cervera, Alon Herschhorn*

University of Minnesota, USA

In-vivo evolution of a transmitted/founder HIV-1 strain that is highly resistant to broadly neutralizing antibodies

Envelope glycoproteins (Envs) of human immunodeficiency virus type I (HIV-1) mediate viral entry and are the sole target of neutralizing antibodies.Envs of most primary HIV-1 strains prefer to be in a closed conformation (State 1) and occasionally sample downstream conformational states (State 2 and State 3).Thus, current knowledge guides immunogen design towards mimicking the Env closed conformation as the preferred target for eliciting broadly neutralizing antibodies (bnAbs).Ideally, a vaccine for HIV-1 prevention should elicit bnAbs that can block the transmission of transmitted/founder (T/F) HIV-1 strains, which are a subset of HIV-1 strains that can cross the mucosal bottleneck and establish HIV-1 infection in vivo.

Methods: Here we studied different T/F strains that have been previously published and identified one T/F strain, CH040, that is highly resistant to bnAbs.We reconstructed the post-transmission evolutionary pathway of CH040 in vivo by building pseudoviruses based on consensus viral sequences at different time points during CH040 evolution in the infected individual. Consensus viral sequences were determined by analyzing available sequences from the HIV-1 database that span more than 4 years of viral evolution. We used reconstructed pseudoviruses to study the evolution of HIV-1 Env function and sensitivity to Env ligands.

Results: Evolved CH040 viruses were less sensitive than CH040 to cold and soluble HIV-1 receptor (CD4), and became resistant to the 19b antibody, which preferentially recognizes a more open Env conformations. All of which correlate with the evolution of a more closed Env state. These changes were associated with alterations in CH040 sensitivity to several bnAbs during viral evolution under the pressure of autologous antibody response in the infected individual.

Conclusion: Our results provide insights into HIV-1 evolution in vivo and evidence for the continuous range of Env conformational states. These findings can aid the development of new strategies to improve bnAb immunotherapy and Env-based immunogen design.

Biography

Alon Herschhorn Ph.D. is an Assistant Professor in the Department of Medicine at the University of Minnesota. Prior to his current faculty appointment, Dr. Herschhorn held a faculty position as Instructor in Microbiology and Immunobiology at Dana-Farber Cancer Institute and Harvard Medical School, where he developed strong research program on virus entry and fate, with a specific focus on HIV-1. Dr. Herschhorn successfully obtained the prestigious Rothschild and amfAR fellowships as well as external funding, and developed productive collaborations with different research groups in USA and Canada. Dr. Herschhorn is leading a new research group in the Division of Infectious Diseases and International Medicine that will develop new tools to study, at the molecular and cellular levels, the mechanisms underlying virus-host interactions. His previous work provided new insights into the entry process of HIV-1, the conformational dynamics of the HIV-1 envelope glycoproteins, and the cellular processes that contribute to the fate of viral infection.

Xingmin Sun

University of South Florida, United States

The challenges and status of vaccine development for Clostridioides difficile infection

Clostridioides difficile is a Gram-positive, spore-forming and toxin-producing anaerobic bacterium. It is the most common cause of nosocomial antibiotic-associated diarrhea and the etiologic agent of life-threatening pseudomembranous colitis in the developed world. In the US, *C. difficile* infection (CDI) caused 223,900 estimated hospitalizations,12,800 deaths and $5 billion healthcare costs in 2017. A continual rise in severe CDI has been observed worldwide.*C. difficile* is intrinsically resistant to many antibiotics, limiting treatment options. Currently, very limited antibiotics are available for the treatment of CDI, and none of them is fully effective with a recurrence rate of 15-35%.Prevention and treatment of recurrence is one of the major challenges in the field. CDI symptoms range from diarrhea to intestinal inflammation/lesion and death, and are mainly caused by two exotoxins TcdA and TcdB. Active vaccination provides the attractive opportunity to prevent CDI and recurrence. No vaccine against CDI is currently licensed. Tremendous efforts have been devoted to developing vaccines targeting both toxins. However, ideally, vaccines should target both toxins and *C. difficile* cells / spores that transmit the disease and cause recurrence. Furthermore, *C. difficile* is an enteric pathogen,and mucosal/oral immunization would be particularly useful to protect the host against CDI considering that the gut is the main site of disease onset and progression. This talk will review current progress and remaining challenges in the field of *C. difficile* vaccines.

Audience Take Away:

- Pathogenesis of *C. difficile* infection.
- Why it is important to develop vaccines against CDI?
- The challenges to develop an effective vaccine against CDI.
- The current status of vaccine development for *C. difficile.*

Biography

Dr. Sun is an Associate Professor with tenure in the Department of Molecular Medicine, College of Medicine at the University of South Florida (USF). He holds courtesy appointments in the Department of Internal Medicine, Department of Cell Biology, Microbiology & Molecular Biology, Department of Chemistry at USF, and USF Genomics. He received his PhD in Natural Sciences from the University of Kiel, Germany, and his Master Degree in Veterinary Microbiology and Immunology from the Nanjing Agricultural University, China. He received his postdoctoral training in Molecular Microbiology and Biochemistry at Brown University, USA. The research in his laboratory is focused on the pathogenesis of Clostridioides difficile and the development of novel therapeutics including vaccines to prevent / treat C. difficile infection (CDI).

He was an NIH (National Institutes of Health) Career Development K01 Awardee. His laboratory has been continuously supported by the NIH. He has been actively serving NIH study section panels including chairing the NIH study section panel in 2020. He serves as an Associate Editor for “Molecular Medicine”, Associate topic editor for “Frontiers in Microbiology”, and editorial boards for “Infection and Immunity” and “Applied and Environmental Microbiology”. He received Tufts Institute for Innovation Inaugural Award in 2014. In 2018, he was awarded “Faculty Outstanding Research Achievement Award” at USF. In 2019, he was awarded “Excellence in Innovation Award” at USF. He chaired the Research Committee of College of Medicine at USF from 2019 to 2020. Currently, he serves as the Secretary for the USF Chapter, National Academy of Inventors, USA.

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SPEAKERS

DAY 01

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Eugene Boon Beng Ong*[1], Jee Whu Lee[1], Tee Gee Ong[1], Mohammed Razip Samian[1], Aik-Hong Teh[1], Nobumoto Watanabe[1,2], Hiroyuki Osada[1,2]

[1]Universiti Sains Malaysia, Malaysia
[2]RIKEN Centre for Sustainable Resource Science, Japan

Screening for proteins that extend chronological life span in yeast

Ageing is a biological process that occurs with gradual structural and functional changes in living organisms with the passing of time. There are two types of ageing which are organismal ageing and cellular ageing. At the organismal level, organisms such as humans for example become 'older' with external observational changes such as the appearance of wrinkles and grey hairs, while internally organs will also change albeit unseen. At the cellular level, cells such as epidermal, neuronal or muscle cells undergo ageing with the accumulation of cellular damage that causes the loss of cellular function and eventually cell death. There are two types of cellular ageing which are replicative ageing and chronological ageing. Replicative ageing occurs in replicating cells such as skin cells that can replicate to produce new cells, while chronological ageing occurs in non-replicating cells such as neuron and muscle cells that do not continue replicating.

Ageing-related proteins play distinct roles in cellular processes such as regulating stress response, apoptosis, ubiquitin-proteasome system, and signal transduction pathways amongst others. Many ageing-related proteins have been identified overtime, however the roles of most of these ageing-related proteins are still unknown. In this study, three ageing-related proteins, Ptc4, Zwf1 and Sme1 identified from a yeast chronological life span (CLS) screen were validated to extend yeast CLS. The CLS-extending proteins contributed to thermal and oxidative stress responses differently, suggesting different mechanisms of actions. Ptc4 and Zwf1 promoted cell proliferation during cell growth upon protein overexpression, suggesting their involvement in cell division or growth pathways. Interestingly, the Ptc4 deletion mutant still promoted cell proliferation. Additionally, investigations revealed that the overexpression or loss of type 2C protein phosphatases (PP2C) could promote cell proliferation, suggesting an adaptive cell division mechanism regulated by PP2Cs in yeast.

Audience Take Away:

- Semi-high throughput recombinant cloning and protein expression.
- Developing 96-well plate workflows.
- Protein characterisation with molecular biology techniques.

Biography

Dr Eugene Ong studied Molecular Biology at the Universiti Sains Malaysia (USM) and graduated as MSc in 2005. He then joined the research group of Dr Hiroyuki Osada at RIKEN, Japan in 2007 was awarded his PhD in 2011 in chemical biology. He was a postdoctoral fellow and is currently a Senior Lecturer at the Institute for Research in Molecular Medicine, USM. His group uses yeast as a model to study protein functions.

Samar Solyman*, Shymaa Kamal, Amro Hanora
Suez Canal University, Egypt

The effectiveness of B cell and T cell epitopes cocktail as a potential vaccine against Staphylococcus aureus in two murine models

Development of an effective vaccine against *Staphylococcus aureus* (*S. aureus*) is a key global health concern, especially in light of rising antibiotic resistance and the wide spread of methicillin resistant *Staphylococcus aureus* (MRSA) strains. Previous attempts for *S. aureus* vaccine development were unsuccessful. Inclusion of T cell immunity in *S. aureus* vaccine may be essential for the effectiveness of the vaccine. Previous work in our laboratory showed that Phosphatidylinositol phosphodiesterase (PIc) B cell & T cell peptides induced high protection in mice bacteremia model. In this study, Manganese transport protein C (MTC) B cell & T cell epitopes, Nickel ABC transported (NABC) B cell & T cell epitopes and PIc B cell & T cell epitopes were used as vaccine in two mice models; bacteremia and skin infection models.

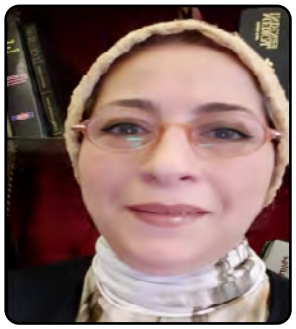
Results shown robust humoral immunity in both models that was correlated with high survival level in mice immunized with PIc and peptide mixture groups in bacteremia model.In skin infection model, mice immunized with peptide mixture and MTC peptide group showed the best skin lesion healing results. The protection level of both models was correlated with the highest level of INF γ and lowest levels of IL-2 which was shown in the peptide mixture group. The mixture group also showed the highest count of CD8 cells in both models. results demonstrated that inclusion of multiple genes B cell and T cells epitopes improved both the humoral and cellular immunity and resulted in the best outcome in both bacteremia and skin infection mice models.A more expanded in-vivo study is recommended for testing MTC and PI B cells and T cells peptides cocktail as promising *S. aureus* vaccine.

Audience Take Away:

- Current situation regarding Staphylococcus aureus vaccine.
- Role of the two arms of immunity in infection protection and vaccine efficiently.
- Peptide vaccines as a new approach in vaccinology.

Biography

Dr. Samar Solyman, associated professor of Microbiology & Immunology-Faculty of Pharmacy- Suez canal University- Egypt, earned her Bachelor and Master degree from the Faculty of Pharmacy, Suez Canal University. Doctoral degree was earned from the University of Tennessee, USA in 2012. Dr. Samar earned several research projects from the academy of science, Egypt in the fields of vaccinology and marine Microbiology. She published more than 20 international publications in the field of Microbiology & Immunology.



Amira Hegazy
BSU, Egypt

Development and validation of two robust simple chromatographic methods for estimation of tomatoes specific pesticides? residues for safety monitoring prior to food processing line and evaluation of local samples

Plant infestation by pets is one of the worst effects of bacteria and fungi on human food. Plants as a primary food resource are critical for human muscle building and mental health. Many farmers worldwide misuse the pesticides' mixtures to keep crops, fruits, and vegetables uninjured, fight grown bacteria and fungi or produce abundant high-quality issues the pesticides' mixtures to keep crops, fruits, and vegetables uninjured, fighting grown bacteria and fungi or to produce abundant high-quality agricultural products. Detecting and analyzing pesticide residual traces could be a crucial issue.Much instrumental weather coupled with Mass or not could be used for the process of estimation. Not only is the estimation of residual insecticides critical in labs of official institutions in the authority of citizen health but also in labs on exporting-importing boundaries between countries.

Fresh or processed tomatoes are the most common constituent in our dining tables. Combination of pesticides; acetamiprid, flutolanil and etofenprox are usually used for tomato fruits for protecting them against pest infection. Two specific simple sensitive chromatographic methods are developed for simultaneous estimation of the concerning pesticides' residues using simple economic steps of field sample preparation. The first method is HP- TLC method. Hexane : methanol : acetone : glacial acetic acid (8:2:0.5:0.1, by volume) is proposed as a developing system. The second one is RP- HPLC. Acetonitrile : Water (75:25, v/v) is proposed as a mobile phase. The recommended methods are completely validated regarding ICH guidelines. Their means percentages and standard deviations of accuracy range 100.32 ± 0.89 to 99.27 ± 0.9.The methods' repeatability and intermediate precision relative standard deviation percentages range 0.395–0.894.They are successfully applied for estimating the pesticides in pure and commercial forms and field samples.

Biography

Asso. Prof. Amira Hegazy studied pharmaceutical sciences and graduated with an MS at Cairo University, Egypt. She then joined the research group of Prof. Raimar Loebenberg (Director of the Drug Development and Innovation Center), School of Pharmacy, University of Alberta, Canada, after receiving a scholarship award from her country for her excellence. She obtained a postdoctoral clinical training program at Harvard Medical School. She has published many research articles in highly reputable and impacted journals.

Wesam S. Qayed*[1], Mostafa A. Hassan[1], Ahmed Megahed Abouwarda[2], Yasser Musa Ibrahim[2], Tarek Aboul-Fadl[1]

[1]AssuitUniversity, Egypt

[2]Formerly National Organization for Drug Control and Research (NODCAR), Egypt

Structure based design of novel azine linked hybrids of 2 - Indolinone - Thiazolodine scaffold as potential quorum sensing inhibitors for fighting antimicrobial resistance

Microbial multidrug resistance is becoming a global menace to humanity and finding alternative techniques to combat these "superbugs" is critical.Quorum sensing (QS) is a cell-to-cell communication mechanism in many bacterial strains uses to control the production of biofilm and virulence proteins to carry out their pathogenicity. Therefore, interfering with QS provides a viable alternative technique for combating a variety of diseases. Accordingly, the current work presented a potential QS inhibitors (QSIs) mediated by protein chromobacterium violaceum transcriptional regulator (CviR) against Chromobacterium violaceum to overcome bacterial multidrug resistance. Aided with virtual screening results of structural based designed hybrids of 2-indolinone- thiazolodine Scaffold on the CviR active pocket residues a panel of novel hybrids were synthesized. The ability of these molecules to inhibit the QS system were tested and a promising two candidates of the designed hybrids revealed promising antivirulence agents to disarm bacterial resistance in the tested bacteria. Moreover, biofilm formation, and motility were also impaired in treated cultures. Molecular docking of designed compounds was comparable with the native inhibitor Chlorolactone (CL) of CviR. The global chemical descriptors were calculated for native inhibitor CL and the promising compounds and found to be more reactive than the native inhibitor CL. *In silico* ADME prediction profiles of these lead compounds showed good ADME profiles.

Audience Take Away:

- Potential of Structure based drug design for drug discovery and development.
- How to improve the activities of the bioactive molecules.
- Searching for new leads to overcome of global disaster.
- Opening the windows for global scientific collaborations.
- Improvement of the accuracy of drug design and providing new information to assist in solving drug design problems.

Biography

Wesam S. Qayed received her B.Sc (Honors) in 2002 and MSc in 2005, both in Pharmaceutical Sciences from Faculty of Pharmacy, Assiut university, Egypt. In 2016, She obtained her PhD in Medicinal Chemistry from Faculty of pharmacy, Assiut university, Egypt. During (2012-2014) she was a visiting researcher at Chemistry Department at University of Louisville, KY, USA. she is ACS member. She has been working since 2017 in research projects related to anticancer, antiviral and anti TB research. Throughout this time, she helped in establishing "computer-aided drug design unit" which aims to train postgraduate students and academic using "Molecular Operating Environment" software and other computational programs. Further, it carries out research related to designing new druggable compounds against variable diseases. She has active interest in several areas of medicinal chemistry. In particular, her research lies at the interface of structure-based, ligand-based drug design and other computer aided design tools for discovery of candidate molecules against infectious diseases and cancer.

Pennisi Rosamaria*, Maria Pia Tamburello, Davide Barreca, Maria Teresa Sciortino, Giuseppina Mandalari
University of Messina, Italy

Anti-HSV-1 activity of natural raw and roasted unsalted pistachio kernels in human monocytic THP-1 and vero cells

In recent years, a great interest has been devoted to the search for alternative clinical treatment for HSV infections. To date, acyclovir and related nucleoside analogues are effective viral DNA polymerase inhibitors but their intensive use has led to the expansion of drug-resistant strains. Therefore, the search for novel sources to develop new antiherpetic agents have gained major priority to overcome the problem. Plants are a rich source of new antiviral, pharmacologically active agents which provide several advantages such as reduced side effects, less resistance, low toxicity and various mechanisms of action. Therefore, the purpose of the current study was to investigate the effects of natural raw (NRRE) and roasted unsalted (RURE) pistachio polyphenols-rich extracts in both human monocytic cells THP-1 and epithelial VERO cells on HSV-1 replication. Pistachio polyphenolic extracts were prepared following two different extraction methods, with or without *n*-hexane.The identification and quantification of phenolic compounds by RP-HPLC-DAD reported that the NRRE extracts are generally richer in polyphenolic compounds compared with RURE extracts. Besides, the cell viability was measured by monitoring over time the metabolic activity of cells following NRRE and RURE dose-dependent (0.2, 0.4, 0.8 mg/mL) treatment. A better profile of cellular tolerability was reported for the NRRE and RURE extracts obtained without using *n*-hexane in both cell lines. Moreover, non-toxic concentrations of NRRE and/or RURE (0.6, 0.4 and 0.3 mg/mL) were employed to verify the antiviral effect by plaque reduction assay. Cells and virus dilutions were pre-treated with both extracts for 1h and mixed to allow viral adsorption.

After 1 hour, any unabsorbed virus was aspirated and the monolayer covered with Dulbecco's Modified Eagle's Medium containing 0.8% methylcellulose in presence of both extracts, separately.We found that in Vero cells, NRRE and RURE exhibited a significant inhibitory activity at 0.6 mg/mL and in particular, the treatment with the mixture extracted with *n*-hexane determined a significant reduction of plaque numbers and size, as reported by change of morphology and by detection of microplaques. Based on this, NRRE and RURE *n*-hexane were used to treat cells and virus suspension and detect the viral DNA and genes. We report that NRRE significantly reduced viral DNA and genes, at 0.4 and 0.6 mg/mL and viral protein expression only at higher concentration. Otherwise, RURE affected not strongly the viral DNA but partially reduced viral transcripts and protein at 0.6 mg/mL. Besides, we measured the intracellular virus production in THP-1 cells pre-treated with NRRE and RURE *n*-hexane and infected with HSV-1 by plaque assay and showed a strong reduction at both concentrations which matches with the viral DNA reduction following treatment. These data report that human monocytic THP-1 cells treated with NRRE and RURE are less susceptible to HSV-1 infection, suggesting their potential use as antiherpetic agents.

Audience Take Away:

- There is no cure for HSV-1 infections, but antiviral drugs are commonly used to prevent and treat outbreaks. Antiviral resistance has begun to emerge, giving importance to the search for new and effective therapies for the prophylaxis and treatment of HSV outbreaks.
- The antiviral activity of polyphenol-rich extracts of pistachios may be useful for the formulation of adjuvant drug in anti-herpetic infection and against acyclovir-resistant HSV-1 strains.
- Biological properties of HSV are neuroinvasiveness, neurotoxicity, and latency. Therefore, the antiviral effect of pistachio kernels was investigated in human monocytic cells which interact with herpes simplex virus (HSV) and are of importance for the pathogenesis of HSV infections.

Biography

Dr. Pennisi studied Biology at the University of Messina, Italy and graduated as MS in 2014. She joined the research group of Prof. Sciortino at the University of Messina working in the field of Virology, analyzing the molecular pathways linked to immune evasion during HSV-1 infection. She received her PhD degree in 2018 at the same institution. She collaborated with foreign research groups such as IARC in Lyon, SIIBR in Shenzhen and University of Turku in Finland, as documented by the related scientific production which were carried out in collaboration with. After two- year postdoctoral fellowship supervised by Prof. Zhou Grace at the International Institute for Biomedical Research (SIIBR) Shenzhen, Guangdong, China, she obtained the academic position as a researcher in the chemical, biological, pharmaceutical and environmental department of the University of Messina.

Teresa Gervasi*[1], Giuseppina Mandalari[2], Giovanna Ginestra[2], Antonella Nostro[2], Iolanda Corrado[3], Seyedeh Fatemeh Mirpoor[3], C. Valeria L. Giosafatto[3], Cinzia Pezzella[3], Davide Barreca[2]

[1]University of Messina, Italy
[2]Università di Messina, Italy
[3]Università Federico II, Italy

Bioplastics functionalization with phloretin to enhance their antioxidant and antimicrobial properties against food born pathogens

The formulation of eco-friendly biodegradable packaging has received great attention during the last decades to replace traditional widespread petroleum-based food packaging. Biodegradable polymers may play a pivotal role as delivery system for bioactive compounds able to protect the packed foods against their oxidative damage and bacterial contamination. In recent years, a new generation of food packaging, in particular biopolymer matrices based on proteins and polysaccharides from agro-industrial wastes as well as on bio-composites based on microbial polyesters, the polyhydroxyalkanoates (PHA) are on the rise. The aim of the present study focuses on the formulation of innovative and active packaging materials from renewable sources represented by proteins from argan (*Argania spinosa*) (APC) seed oil cakes, and PHA produced by microbial fermentation of lignocellulosic biomasses. The produced materials were functionalized with phloretin. Phloretin is a dihydrochalcone, belonging to the class of flavonoids, which is the most abundant compound identified in apples and in apple-derived products as well as in the kumquat, characterized by the presence of the pharmacophore 2,6-dihydroxyacetophenone, that is responsible of its biological potential.

Recently, our group has shown the broad spectrum of beneficial properties of phloretin for human health, such as antiinflammatory, antimicrobial, anti-hypertensive, antioxidant and anti-cancer activity. Starting from this evidence we have manufactured and technologically and biologically characterized APC- and PHA-based bioplastics added with phloretin. In addition, the evaluation of the active molecule released from the functionalized materials was performed by reverse-phase HPLC-DAD detection. The assessment of their antimicrobial properties has been carried out against Gram-positive bacteria (*Listeria* monocytogenes ATCC 13932 and Staphylococcus aureus ATCC 6538) and Gram-negative bacteria (*Escherichia coli* ATCC 10536 and Salmonella enterica serovar Typhimurium ATCC 13311). The results revealed an increase of the antioxidant properties of the phloretin containing films when compared with the neat material. PHA-based functionalized polymers also caused a decrease of the growth of food-born pathogens (such as Listeria. monocytogenes ATCC 13932). The results described, for the first time, the possibility to exploit phloretin as a functionalizing agent for bioplastic formulation, especially as far as food packaging is concerned.

Audience Take Away:

- This research can be of great interest for the audience because
- Nowadays the bioeconomy plays a central role, this work is perfectly in line with the demand, from the European Community, for a transition to a more circular economic model offering many environmental, social and financial benefits.
- The impact of this study could be important as the research provides considerable insights into various fields, promoting a reduction of fossil carbon use and an increase in the use of biodegradable plastics; encouraging the processing of by-products and waste into high value-added products; maximizing the use of food waste, thus reducing the amount of waste in landfills.
- Theproductionofnewbioplasticscouldhelptocreatenewprofessionalfigures.

This study addresses the green chemistry principles and circular economy, as it promotes the following benefits:

- The pivotal role of bioeconomy;
- Processes inspired by the green chemistry principles;

- Waste valorization which will contribute to the implementation of European Bioeconomy Strategy (IEA Bioenergy Task 42 report 2011).
- Transition toward a circular and sustainable bioeconomy, which has the potential to contribute to all dimensions and objectives of the European Green Deal.

Biography

Dr. Teresa Gervasi is Assistant Professor of "Fermentations Chemistry" of the University of Messina. She studied at the University of Messina, Italy and graduated cum laude in Biology.Being a PhD student in "Chemistry and Food Safety", she joined the research group of Prof. Arjan Narbad at the Institute of Food Research (Norwich, UK). In April 2013 she obtained the title of "Doctor Europaeus". Since 2014 she has been "Cultore della materia" for "Fermentation chemistry" teaching at the University of Messina and she has been awarded several scholarships. She has published more than 40 research articles in SCI(E) journals.

Latika Bhatia
Atal Bihari Vajpayee University, India

Lignocellulose derived functional oligosaccharides : Production, properties, and health benefits

Lignocellulosic biomass (LB) is the renewable feedstock for the production of fuel/energy, feed/ food, chemicals, and materials. LB could also be the versatile source of the functional oligosaccharides, which are non-digestible food ingredients having numerous applications in food, cosmetics, pharmaceutical industries, and others. The burgeoning functional food demand is expected to be more than US$440 billion in 2022. Because of higher stability at low pH and high temperature, oligosaccharides stimulate the growth of prebiotic bifidobacteria and lactic acid bacteria. Xylooligosaccharides (XOS) are major constituents of oligosaccharides consisting of 2–7 xylose monomeric units linked via b-(1,4)-linkages. XOS can be obtained from various agro-residues by thermochemical pretreatment, enzymatic or chemoenzymatic methods. While thermochemical methods are fast, reproducible, enzymatic methods are substrate specific, costly, and produce minimum side products. Enzymatic methods are preferred for the production of food grade and pharmaceutically important oligosaccharides. XOS are potent prebiotics having antioxidant properties and enhance the bio-adsorption of calcium and improving bowel functions, etc. LB can cater to the increasing demand of oligosaccharides because of their foreseeable amount and the advancements in technology to recover oligosaccharides. This paper summarizes the methods for oligosaccharides production from LB,classification, and benefits of oligosaccharides on human health.

Biography

Dr. Latika Bhatia is an assistant professor in department of Microbiology and Bioinformatics in Atal Bihari Vajpayee Vishwavidyalaya, Bilaspur, C.G., India. She did her Ph.D. from ITM University, Gwalior, on Biofuel Technology. She has awards and honors in her credit. She has published more than 30 research articles in peer-reviewed journals of an international repute, 10 book chapters and 03 monographs, 05 books, with citation index more than 400. Her primary research interest is to develop the sustainable process for bioconversion of lignocellulosics into renewable energy and biochemicals.

Bashir Akhlaq Akhoon
University of Jammu, India

Using cutting-edge computational genomic methods to deconstruct major pathogenic fungi : A case study of monilinia

Several *in silico* technologies will be described throughout the talk in order to bring fresh genetic insights into fungal diseases. The lecture will highlight how computer algorithms may assist us in assessing the completeness of genome assemblies, generating repeat libraries, and discovering new genes from drafted genomes. The presentation will demonstrate the *in silico* examination of the secretome which consists of genes that encode effector proteins and aid fungus in invading their hosts. Secondary metabolites (SMs) are compounds produced by fungi that help in adaption and reproduction in a variety of settings, as well as in competition with other microbes. The potential *in silico* strategy for identifying these SMs will be discussed. The lecture will explain how to identify pathogenicity genes that are experiencing positive selection and implicated in the local adaptation of host genotypes or environmental pressures in fungal infections. The talk will also reveal a viable method for investigating the impact of evolution on the secretome architecture of pathogenic fungus. A possible approach for investigating the effect of evolution on the secretome architecture of pathogenic fungus in order to determine if there is secretome expansion or contraction will also be discussed.The discovery of pathways that are overrepresented during pathogen-host interactions and help in the successful colonisation of fungi will also be addressed.The session will cover functional annotation methodologies that can aid in the identification of a large catalogue of genes involved in cellulolysis, pectinolysis, and proteolysis in annotated genomes.The presentation will also address RNA-Seq analysis to better understand the expression of numerous virulence-promoting genes. The applicability of *in silico* techniques to understanding the mechanism of fungal disease will be examined using the pathogenic fungus *Monilinia* as an example.

Audience Take Away:

- The widespread use of next-generation sequencing holds immense promise for improving our understanding of microbial etiology. The comparative and functional genomic techniques provide an integrated future for microbiology that blends the capabilities of classical microbiology with the promise of emerging sequencing technology. The approaches discussed in the presentation will let the audience conduct genome-wide structural, functional, and transcriptomic analysis to add depth and context to the mechanism of microbial pathogenesis. Understanding which genes are expressed in microbes and when, as well as the backdrop of putative pathways and evolutionary biology, can provide insights into how they function. More importantly, all of the computational tools utilised for the investigation are open source and hence accessible to any researcher.The methods outlined in the presentation will be a realistic option for any microbiologist to address the genomic aspects of fungal pathology.

Biography

Dr. Akhoon received his PhD degree in life sciences at the Jawaharlal Nehru University, New Delhi, India in 2017. He has gained research experience from both international and national institutes including International School for Advanced Studies, Italy; CSIR- IITR, CSIR-IIIM, IISC Bangalore, and University of Jammu, India where he is currently a faculty member in the School of Biotechnology. Dr. Akhoon has several prestigious fellowships to his credit including the UGC Kothari Postdoctoral Fellowship, SERB - NPDF, and CSIR-SRF. He has published several peer reviewed research articles and is also serving as a reviewer in many international journals.

Julliany Pereira Silva* , Jugpreet Singh, Katchen, Marc Fuchs, Awais Khan

Cornell University, USA

Potential role of weather, soil and plant microbial communities in rapid decline of apple trees

An unusual decline and collapse of young established trees known as “rapid apple decline” (RAD) has become a major concern for apple growers, particularly in the northeastern United States. his decline is characterized by stunted growth, pale yellow to reddish leaves, and tree collapse within weeks after onset of symptoms. We studied declining apple trees to identify potential involvement of abiotic and biotic stresses. We used 16S and ITS to profile bacterial and fungal communities in the soil, rhizosphere, roots, and shoots and tested for the presence of six viruses in scions and rootstocks of symptomatic and asymptomatic trees. The viruses detected were not associated with RAD symptoms. Bacterial and fungal populations were highly variable in plant tissue, soil and rhizosphere samples, with bacteroidetes, firmicutes, protobacteria, acidobacteria, and actinobacteria the predominant bacterial classes in various samples. ‘Alphaproteobacteria-rickettsiales’,a bacterial class usually reduced in water-limiting soils, had significantly low abundance in root samples of symptomatic trees.

Basidiomycota and Ascomycota fungal classes were the most common fungal classes observed, but neither showed differential enrichment between symptomatic and asymptomatic trees. Analyzing weather data showed an extremely cold winter followed by drought in 2015–2016, which likely weakened the trees to make them more susceptible to varied stresses. In addition, similar physical and nutritional soil composition from symptomatic and asymptomatic trees rules out the role of nutritional stress in RAD. Necrotic lesions and wood decay symptoms dispersing from bark or vascular cambium towards the heartwood were observed primarily below the graft union of declining apple trees, suggesting that the rootstock is the originating point of RAD. We speculate that differences in abiotic factors such as moisture levels in declining roots in combination with extreme weather profiles might cause RAD but cannot clearly rule out the involvement of other factors.

Audience Take Away:

- Get to know the Rapid apple decline (RAD) syndrome affecting young, dwarf apple trees with no known cause to date.
- Acquire knowledge on bacterial and fungal communities in the soil, rhizosphere, roots, and shoots, and their influence on RAD.
- Think outside the box: how abiotic factors could be associated to plant health and how we can investigate a similar unusual sudden collapse of other trees.

Biography

Dr. Silva studied Agronomy at the Federal Rural University of the Semi-arid Region, received her M.Sc. degree in Plant Sciences from the University of Viçosa in Brazil, and her PhD in Horticultural Sciences from the University of Florida, USA. She then joined Dr. JD Swanson´s team at Salve Reginal University and later Dr. Awais Khan´s program at Cornell University, where he gained extensive experience with molecular mechanisms of disease resistance, high-throughput phenotyping, and genotyping. Currently, Dr. Silva is a Technology Implementation Specialist LATAM at Syngenta Seeds.

Christina Isber*[1] and Ziad Daoud[2]

[1]University of Balamand, North Lebanon

[2]Central Michigan University, United States of America

Quadruple checkerboard : A modification of the three dimensional checkerboard for studying drugs combinations

Since the discovery of antimicrobial agents, their use had increased in the medical field and expanded to other fields. This caused the development of the "shadow epidemic" .Antimicrobial resistance caused by the misuse and overuse of antimicrobial drugs resulted in a crisis that needs to be solved. Drug combination is one of the solutions that can help in decreasing and controlling the development of resistance.The concept of combining drugs as a treatment for several diseases showed good results and promising control for the misuse of these drugs. Drugs acting synergistically in a combination given as treatment showed positive results and can be explained by several principles (collateral sensitivity) Several methods were developed and used to test for drug combination options, however, none of the methods was declared to be the gold standard. The methods used can test for all possible combinations obtained by combining 2 drugs (checkerboard, combined E-test, Time Kill Curve assay) and by combining 3 drugs (three dimensional checkerboard and Time kill curve assay).Only the Time kill curve assay can test for the combination of 4 drugs.However, this method is time consuming and requires a lot of labor work to conduct it.Thus, Quadruple checkerboard also called Q-checkerboard was developed.

This new modified technique can study all possible combinations that can be obtained by combining 4 drugs in one single experiment. It is time saving and requires less labor work. The experimental steps will be discussed highlighting the crucial steps needed to perform this technique.In addition to the experimental protocol, an FIC sheet will be also discussed which was developed using excel in order to visualize easily the results with a minimum amount of work.The FIC criteria used to assess synergy, antagonism and indifference is not standard where we can see in literature the difference in the values used for synergy and antagonism.For the Q-checkerboard, several modifications were taken into consideration regarding the FIC value and how to obtain it.These modifications will be discussed in the presentation explaining the idea behind doing such changes.

Audience Take Away:

- Learning such technique, will give researchers a deeper idea about it which will be useful if they want to engage such technique in their research experiments.
- Discussing this technique will open doors to further discussions about FIC interpretation that should be highlighted regarding the big dilemma about the interpretation values.
- As for the technical part of this technique, it opens door for biomedical testing companies and other companies to manufacture a better suiting plates and other equipment according to the developed experimental conditions.

Biography

Christina Isber studied Bachelor's degree in Biology at the University of Balamand, Lebanon, Faculty of Arts and Sciences. She then pursued her MS degree from the same University under the supervision of Prof. Ziad Daoud and graduated in 2020 holding a degree in Biomedical Sciences from the Faculty of Medicine and Medical Sciences, department of Biomedical Sciences. She published her masters project recently in Jove Journal entitled: Quadruple Checkerboard: a modification of the three dimensional checkerboard for studying drugs combinations.

Jasna Novak*, Andreja Leboš Pavunc, Martina Banić, Katarina Butorac, Nina Čuljak, Blaženka Kos

University of Zagreb, Croatia

Postbiotics of beneficial bacteria as microbial based therapies to modulate intestinal microbiome

Disturbance of the intestinal microbiome composition is associated with gastrointestinal as well as extraintestinal disorders. Growing knowledge suggests that microbial-based therapies through activities of biomodulators may restore a healthy intestinal microbiome. Biomodulators, besides the use of probiotics and prebiotics, also include novel approaches based on the application of postbiotics, live biotherapeutics and faecal microbiota transplantation. Althought probiotic strains have been extensively investigated, the mechanistic basis of their health-promoting effects remains unclear. It is the surface-exposed or secreted cellular compounds that are the key to interface bacteria to the environment. Therefore, the goal is to present specific probiotic trigger molecules that have the potential as postbiotics.

In particular,case studies related to the structural and/or functional characterization together with challenges in their discovery bacteriocins,S-layer proteins and exopolysaccharides will be presented.Also, enzyme activities encompassed within the proteolytic system responsible for the accumulation of biopeptides in casein-rich sources will be discussed. At first, the approaches in the screening and identification of novel lactic acid bacteria as probiotics and their target trigger biomolecules will be shown as well as evaluation of their importance in cell-to-cell or cell-to-host interactions.This implies their biological role in the functional properties of probiotic strains, particularly protective roles after exposure to stress, immunomodulatory activity,antimicrobial activity and adhesion capacity. A metagenomics approach was applied to assess the potential biomodulators of the intestinal microbiome in vivo. Expanding knowledge on probiotics and trigger molecules thereof will induce further research related to both the improvement of bioprocess and new applications of probiotics as promising living drugs.

Biography

Professor Jasna Novak holds a PhD degree from the Faculty of Food Technology and Biotechnology, University of Zagreb, where she has been employed since 2003. Several times she was visiting scientist at eminent institutions: PhD fellow at INRA (2006), a postdoc at Univ. of Helsinki (2011), and researcher at Univ. of Belgrade (2011) and Univ. of Ljubljana (2014). She is visiting as an Erasmus teacher at the University of Insubria. Her research interests include applied aspects of lactic acid bacteria.

A significant part of research activities is devoted to the characterization of the molecular factors of the probiotic mode of action and their potential for modulation of the intestinal microbiota. She regularly acts as a reviewer for a wide variety of journals. In 2005 and 2007 she was awarded the Biotechnical Foundation Award. She co-authored the 2 technological achievements awarded by the First Prize of Poland's Innovation Union (2007) and by a Silver medal at the 5th International Exhibition of Inventions ARCA 2017. In 2011, she was the recipient of the Young Scientist "Vera Johanides" Award. She is a member of the Croatian Society of Biotechnology, Croatian Microbiological Society and EBTNA Association.

Bhanu Priya Ganesh*, Tushar Das, Maria Pilar Blasco, Janelle Korf

University of Texas, USA

The gut-brain axis in neurodegenerative diseases

Amyloid plaques in Alzheimer's disease (AD) are associated with inflammation. Recent studies have demonstrated the involvement of gut in central amyloid-beta (Aβ) pathogenesis; still the mechanisms are not well understood. Dysregulation in gut pathophysiology due to imbalanced microbiota may be involved in promoting chronic inflammation. Using Tg2576 AD mice we tested the hypothesis that gut bears the Aβ burden prior to brain. We used presymptomatic 6-months old and symptomatic 15-months old Tg2576 compared to their age-matched littermate WT control mice. We study human AD patients gastrointestinal microbiome profiling. We identified that dysfunction of intestinal epithelial barrier (IEB), dysregulation of absorption, and vascular Aβ deposition in the IEB occur before central Aβ aggregation is detectible. The intestinal dysfunction observed before brain pathology was associated with elevated inflammatory and angiogenic plasma cytokines like IL-9, VEGF, and IP-10. When we measure human oral microbiota profiling we see a distinct separation of bacterial composition from AD patients compared to control subjects. Our novel data provide evidence that gut dysfunction in association with dysbiotic gut microbiota occurs in AD and may contribute to its etiology.

Audience Take Away:

- Audience will learn that neurology diseases does not always originate from brain. Peripheral components plays a major role in central disease progression.
- Audience will understand the importance of a healthy microbiome and how much they can impact the health of an individual with age.

Biography

Dr. Ganesh received her Ph.D. under the supervision of Dr.Michael Blaut from the German Institute of Human Nutrition-Potsdam Rehbruecke (DIfE), Leibniz institute, Germany from 2010 to 2014. Shortly thereafter, she relocated to Houston, TX for her post-doctoral training where she was trained by Dr. James Versalovic in the Department of Pathology and Immunology at Baylor College of Medicine from 2014 to 2017. She in-between held a visiting scientist position at Massachusetts Institute of Technology (MIT), Cambridge from 2014-2016 where she was trained by Dr. James Fox. After post-doctoral training at Baylor, she joined the department of Neurology (BRAINS lab) led by Dr. Louise McCullough at University of Texas Health Science Center Houston (UTHSC) as a senior postdoctoral fellow, Texas, USA from 2017 to 2018. In 2018, she was promoted as an Assistant Professor in the department of Neurology. Currently, her primary interest lies on investigating signaling mechanisms involved in gut- brain axis interactions in aging-associated cerebrovascular diseases especially, stroke, Alzheimer's disease, Cerebral Amyloid Angiopathy, Neonatal Hypoxic encephalopathy at UTHSC.

Bushra Muneer
Government College University, Pakistan

Cloning, expression and characterization of pullulanase enzyme from locally isolated klebsiella Pneumoniae

Pullulanase is a potential candidate for bioremediation. It has found potential applications in medical, dental, pharmaceutical, food, baking, dishwashing, laundry and textile industry. Pullulanase act on α-1,6 glycosidic bonds and produce maltotriose as a major product. The recombinant *Klebsiella pneumoniae* IIB *Pullulanase E* shows similarity with *Klebsiella pneumoniae* strain 1864 Pullulanase. The pullulanase from *Klebsiella Pneumoniae* was amplified using *PulE* primers, cloned into *E. coli* with pJET1.2 as a cloning vector, expressed into BL21 with pET21a (+) as an expression vector, purified using NH4(SO)4 precipitation 60% and dialysis, CM-Sepharose fast flow, Sephadex G-150. ~1.5Kb was the size of the amplified product. 1.49Kb was the confirmed size of the gene by gene sequencing and multiple alignments. The total protein content of the crude enzyme solution was 54mg while the total protein content of purified protein was 2.24mg with 420.98U total enzyme activity, specific activity of 187.93U/mg having purification factor of 2.87fold with 11.91% enzyme recovery. 45ºC was the optimum temperature for *PulE* and it was stable up to 40ºC. It has an optimum pH of 6.5 with pH stability ranging from 6-7.5. It is a demanding candidate for potential industrial applications due to its features.

Biography

Dr. Bushra Muneer working as Associate Professor in Institute of Industrial Biotechnology, Government College University, Lahore. She completed her Master of Sciences in 1995 and Master of Philosophy in 1999 from Department of Zoology,University of the Punjab Lahore. In 2006, She completed her Doctor of Philosophy. She is working on the production of industrially important enzymes and on the removal of heavy metal contaminants from the industrial wastewater with the help of microorganisms. She have cloned reductase, oxidase as well as laccases from different microorganisms and have used it for the removal of heavy metals from industrial wastewater. She have published 38 research Publications and 2 books in HEC recognized journals holding 42 impact factor.She have completed 9 research projects and 1 HEC research Project Named as “Cloning, Characterization and Improvement of xylose isomerase from thermophiles”.

Mario Meza-Segura*[1,2], James R. Birtley[3], Ana Maldonado-Contreras[1,2], Christian Mueller[4], Karl J. Simin[5], Lawrence J. Stern[3], Beth McCormick[1,2]

[1]University of Massachusetts Chan Medical School, USA

Alpha-1-antitripsin, a key target to understand *shigella* pathogenesis in humans

Shigella spp. are highly adapted pathogens that cause bacillary dysentery in human and non-human primates. An unusual feature of *Shigella* pathogenesis is that this organism invades and subsequently colonizes the colonic epithelia from the basolateral pole. Therefore, *Shigella* has evolved the ability to disrupt the intestinal epithelial barrier to reach the submucosa and invade epithelial cells. Our lab has previously described that the secreted Serine Protease A (SepA), which belongs to the family of Serine Protease Autotransporters of Enterobacteriaceae, is responsible for the initial destabilization of the intestinal epithelial barrier that facilitates Shigella invasion. However, the mechanisms used by SepA to regulate this process remain unknown. Therefore, to investigate the protein targets cleaved by SepA in the gut, we incubated a sample of homogenized human colon with purified SepA or with a catalytically inactive mutant of this protease. The results revealed that SepA targets an array of 18 different proteins, including α-1-antitrypsin (AAT), a major circulating serine proteinase inhibitor in humans. In contrast to other serine proteases, SepA cleaved AAT without forming an inhibitory complex. Instead, SepA's enzymatic activity significantly increased in the presence of high concentrations of AAT (1:5 and 1:10 in a molar ratio). We determined that SepA hydrolyzes the Met-358-Ser-359 bond of AAT, which results in the release of a 4.2 kDa peptide previously described to behave as a neutrophil chemoattractant.Furthermore, we demonstrated that the products of the AAT-SepA reaction induce a mild but significant increase in neutrophil transepithelial migration *in vitro*. Moreover, the presence of AAT during Shigella infection stimulated an increase in neutrophil transmigration and dramatically enhanced the number of bacteria invading enterocytes in a SepA-dependent manner.We conclude that by cleaving AAT, SepA releases a chemoattractant that promotes neutrophil migration, which in turn disrupts the intestinal epithelial barrier to enable *Shigella* invasion. We posit that the activation of SepA by an excess of AAT could be physiologically relevant during the earlier stages of *Shigella* infection when the amount of synthesized SepA would be very low compared to the concentration of AAT in the intestinal lumen. Altogether, our results could be critical to explain the high infectivity of *Shigella* in vivo despite the requirement of first reaching the basolateral side to invade and colonize the colonic epithelium.

Audience Take Away:

- The audience will learn how Shigella, a human enteric pathogen, has evolved to hijack the immune system to facilitate the colonization of the colon. This knowledge will be relevant for the design of new in vivo models to study Shigella infection, which ultimately could be used for the development of new vaccines or therapies to treat this disease.

Biography

Dr. Mario studied Biochemistry at the National Polytechnic Institute (IPN), Mexico. In 2013 he graduated as MS in Genetics and Molecular Biology from the Center for Research and Advanced Studies (CINVESTAV) of the IPN, Mexico. He then joined the group of Dr. Teresa Estrada-Garcia at the same institution and received his PhD degree in Molecular Biomedicine in 2017. Currently, Mario works as a postdoctoral associate in the group of Prof. Beth McCormick at the University of Massachusetts Chan Medical School. During his career, Mario has collaborated with different renowned research groups and published multiple research articles in SCIE journals.

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POSTERS

DAY 01

INTERNATIONAL CONFERENCE AND EXPO ON

APPLIED MICROBIOLOGY

17-18 JUNE

Timothy Ting Leung Ng*[1], Hiuyin Lao[1], Wui-Wang Lui[2], Amy Wing-Sze Leung[2], Henry Chi-Ming Leung[2], Chloe Toi Mei Chan[1], Stephanie Hoi Ching Jim[1], Kingsley King-Gee Tam[3], Kenneth Siu-Sing Leung[3], Ketema Tafess[1], Rahim Rajwani[1], Wing Cheong Yam[3], Ruibang Luo[2], Gilman Kit-Hang Siu[1]

[1]The Hong Kong Polytechnic University, China
[2]The University of Hong Kong, China
[3]The University of Hong Kong, China

The journey to rapid antibiotic resistance detection in mycobacterium tuberculosis with direct sequencing of sputum samples : The benefits, the precautions, and the solution

Direct sequencing of clinical specimens is now a trending approach for antibiotic resistance detection in Mycobacterium tuberculosis (MTB). Comparing with the golden standard phenotypic drug susceptibility test (pDST) and targeted sequencing with clinical isolates that requires 14-day Mycobacteria Growth Indicator Tube (MGIT) culture, it can greatly reduce the time to report from weeks to a few working days. This is crucial for the choice of correct antibiotics during medical prescription, especially for patients carrying resistant MTB or intolerant of certain side effects of antibiotics. It also helps to understand the antimicrobial resistance (AMR) profile within the community and take action to control the spread. Unlike target sequencing with pure clinical isolates, variant calling from sequencing data of clinical specimens was susceptible to different source of contamination and background nasal/oral flora interference.

These potential risks should be highlighted and should be addressed before putting direct sequencing into clinical service. In this study, a new target sequencing workflow was developed, including a set of multiplex PCR primers and a bioinformatics pipeline. The sequencing panel allowed the rapid direct sequencing of clinical specimens. With the synergistic power of MegaPath (a software was designed for detecting low similarity to the reference genome) and Clair-ensemble (one benchmarking deep neural network based variant caller achieves high precision, recall and speed in variant calling for NGS, PacBio, and ONT sequencing data), minimized background nasal/oral flora interference and accurate variant calling were achieved. In short, this study was not only about how a targeted sequencing workflow for antibiotic resistance detection was developed, but it also revealed the advantages and the challenges of direct sequencing of clinical specimens that could be a reference for future direct sequencing development in infectious diseases.

Audience Take Away:

- An updated strategy for using direct sequencing can be used for detecting antimicrobial resistance in sputum samples.
- The potential source of contamination and the precautions in using sequencing technologies will be covered.
- A strategy is proposed to minimize the potential background nasal/oral flora interference that will potentially cause false positive or negative results in antimicrobial resistance detection.
- Multiple quality control steps should be considered in sequencing analysis for both clinical research and basic research inmicrobiology.

Biography

Timothy obtained his bachelor's degree in science in Biochemistry at Hong Kong University of Science and Technology in Year 2004. Then he received a master's degree in science in Biotechnology at the same university in 2006. After thirteen years of working experience in the commercial field, he continued his academic journey, as a Ph.D. student under Dr. Gilman Siu's guidance and supervision, in Year 2019.

Agnieszka Zylicz-Stachula*[1], Kamil Myszczyński[2], Magdalena Koczkowska[3], Anna Kostecka[3], Monika Horbacz[3], Arkadiusz Piotrowski[3], Ireneusz Sobolewski[1], Piotr M. Skowron[1]

[1]University of Gdansk, Poland
[2]University of Gdansk Medical University of Gdansk, Poland
[3]Medical University of Gdansk, Poland

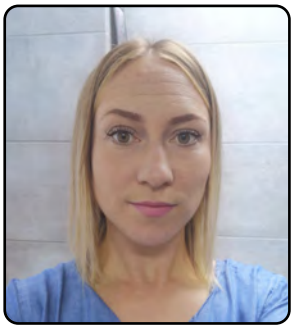
Comparative genomics of geobacillus species sensitive to TP-84 bacteriophage: Identification of the bacterial defense systems

Defense systems are an essential weapon for prokaryotic microorganisms to resist heterologous DNA. Such weapons help them survive the persistent invasion of bacteriophages. Additionally, microbes use various defense systems to filter, control or degrade mobile genetic elements. However, functional defense systems are also a serious obstacle in the genetic engineering of biotechnologically relevant bacterial species, such as *Geobacillus stearothermophilus*. Due to its unique properties, *G. stearothermophilus* is a perfect candidate for the construction of a new procaryotic expression system for the production of thermostable recombinant proteins, as well as a bacterial host for a novel phage display system based on thermophilic TP-84 bacteriophage.

Unfortunately, *Geobacillus stearothermophilus* could not be efficiently transformed using recombinant plasmid DNA vectors. To solve this problem, we selected five *Geobacillus* and *Parageobacillus* strains sensitive to TP-84 bacteriophage. We isolated genomic DNA from the selected strains and subjected it to DNA sequencing, using three next generation sequencing (NGS) platforms: Oxford Nanopore, Pacific Bioscience, and Illumina. We performed a detailed bioinformatic analysis of the resulting NGS data, compared the obtained complete genome sequences, identified the defense islands, and established patterns of DNA methylation.The identified defense genes will be used as molecular targets for the design and construction of recombinant *Geobacillus* strains with increased transformation efficiency.This work was financially supported by the National Center for Research and Development (Poland) grant TECHMATSTRATEG2/410747/11/NCBR/2019.

Biography

Biotechnologist and molecular biologist with extensive industrial experience. M.Sc. in biotechnology, Intercollegiate Faculty of Biotechnology of the University of Gdansk and Medical University of Gdansk, Poland. Ph.D. in biological sciences in the field of biochemistry, Institute of Biochemistryand Biophysics, Polish Academy of Sciences, Warsaw. Habilitation in the field of microbiology, Faculty of Biology of the University of Gdansk (UG), Poland. 1999-2006 - employed in biotechnology industry; 2007-2012 employed as assistant professor in the Department of Theoretical Physical Chemistry, Faculty of Chemistry,UG. Since 2012 associate professor in the Laboratory of Genetic Engineering, Department of Molecular Biotechnology, Faculty of Chemistry, UG. Co-author of 35 scientific publications and 4 patents.



Żebrowska Joanna*, Krefft Daria, Prusinowski Maciej, Mucha Piotr, Skowron Piotr

University of Gdansk, Poland

Biointeraction with nanoparticles - microscopic observations

Recently, nanotechnology is a very dynamically developing field of science. Scientists are trying to miniaturize materials in virtually every field. Nanotechnology has found application in such aspects of science as: drug and medical supplies, materials and manufacturing, environment, electronics, alternative energy sources, mechanical industry.Nanoparticles are gaining more and more attention from all medical departments for their ability to deliver drugs in the optimal dosage range, often resulting in increased therapeutic efficacy of drugs.The attenuation of side effects and the improvement in the susceptibility of the therapeutic proteins are recorded. Recently, in addition to metal particles or their oxides, nanoparticles and sugar nanoparticles have become very popular. Nanocellulose is a very stiff, light material and has eight times the tensile strength compared to steel. Moreover, it was found that the nanocellulose crystal is impermeable to gases, and when used as a base for foams and aerogels, it is highly absorbent and, above all, non-toxic for eukaryotic cells.

As for the potential application of nanocellulose in medicine, it is used as a biomaterial for the construction of tissue restorations, extensive research is conducted on the use of nanocellulose in the fields of tissue regeneration, tissue repair, replacement implants, biosensing, drug delivery, as hemodialysis membranes, in absorbable hemostats, biocatalysts and finally as an antibacterial compound. Our team focused on discovering the field of drug delivery of a new generation, i.e. polyepitope proteins with therapeutic and regenerative properties. In order to investigate the functionality of the interaction of obtaining cellulose microparticles with properly prepared therapeutic proteins, we decided to explore the world of electron microscopy for this purpose. TEM and SEM analysis are great tools for the registration of such microcellulose-protein biocells, which we will show in the images on the presented poster.

Audience Take Away:

- Studies of intermolecular interactions, the interaction of microcellulose with therapeutic proteins, the use of TEM and SEM microscopy for the analysis of intermolecular interactions, an innovative approach to the observation of intermolecular interactions and the release of therapeutic proteins from carriers, an innovative method of drug delivery.

Biography

Joanna Żebrowska Ph.D. from the Faculty of Chemistry, University of Gdansk, graduated LiSMIDoS at the Faculty of Biotechnology University of Gdansk-Medical University of Gdansk. Assistant Professor at the Department of Molecular Biotechnology, Faculty of Chemistry at the University of Gdansk. Manager of the 5 academic grants “Research of Young Scientists” cloning and analysing thermostable restriction endonuclease belonging to Thermus family enzymes. Research area : Purification of polyepitopic proteins with therapeutic and regenerative proteins, design and cloning synthetic genes, bacteriophage proteins, chemical synthesis cofactor analogues for Thermus family enzymes, engineering DNA-recognition specificity of enzymes, biochemical and physico-chemical properties of the enzymes. Co-author of 13 publications (IF = 38, H-index = 3) and 32 conference presentations.

She has experience in 4 Biotechnology Companies, co-author of 3 patents application. Project task manager NCN: Bacteriophage proteins 2019/03/X/NZ1/01903;557T041225192M(acronymMINIATURA)(20192020).ProjectcontractorNCBiR:newpoliepitopicregenerativeproteinsSTRATEGMED1/235077/9/NCBR/2014 (acronym REGENNOVA) (2015-2017), new anti-cancer therapy STRATEGMED3/306853/9/NCBR/2017 (acronym TARGETTELO) (2017-2019). Project task manager NCBiR nanobiomaterials – next-generation delivery system TECHMATSTRATEG2/410747/11/NCBR/2019 (acronym BIONANOVA) (2019-2022).

Ireneusz Sobolewski*, Katarzyna Adamowicz, Beata Łubkowska, Piotr M. Skowron

University of Gdansk, Poland

Emerging thermophilic bacteriophage model: Deciphering TP-84 proteomics

Thermophilic bacteriophages are a rare research objects, nevertheless they are highly interesting because of their often atypical biology and practical potential applications in molecular biology and biotechnology.Resistance to a wide temperature range makes them potentially a useful tool for scientists in areas not available for standard mesophilic model organisms. Our research focuses on unique thermophilic bacteriophage, TP-84 originally isolated in 1952 from greenhouse soil using *Geobacillus stearothermophilus* as a host. Previously we have sequenced TP-84 genome and bioinformatics analysis of its 47.7-kbp double-stranded DNA revealed the presence of 81 coding sequences (CDSs) coding for polypeptides of 4 kDa or larger (PLoS ONE 2018;13(4): e0195449). Because the genome sequence shown essentially no similarity to any previously characterized bacteriophage, TP-84 was classified as a new genus *tp84virus* within the *Siphoviridae* family. Based on a homology search, a hypothetical function could be assigned to 31 CDSs. The previous bioinformatics analysis was partially verified by confirmation of 33 TP-84 proteins, which included: a) cloning of a selected CDS in *Escherichia coli*, coding for a DNA single-stranded binding protein (SSB; gene TP84_63), b) purification and functional assays of the recombinant TP-84 SSB, which has been shown to improve PCR reactions, c) mass spectrometric (MS) analysis of TP-84 bacteriophage capsid proteins, d) purification of TP-84 endolysin activity, e) MS analysis of the host cells from infection time course.

To continue deciphering TP-84 proteomics and verify biosynthesized proteins have taken a novel approach - using commercial *Escherichia coli*-based cell-free protein synthesis (CFPS), *in vitro* alternative to the heterologous *in vivo* expression of proteins. Using a coupled transcription/translation system designed to synthesize proteins encoded by a cloned or PCR amplified DNA template under the control of a T7 RNA polymerase promoter in different mode than developed by the manufactures we synthesized bacteriophage proteins *in vitro*. The modification included omitting addition of T7 RNA polymerase and utilizing residual Escherichia coli RNA polymerase, as we have found out that it has affinity for TP-84 promoters. LCMS analysis confirmed the presence of 62 bacteriophage proteins, including 16 proteins not yet confirmed by proteomic analysis. Together with an independent biochemical approach, in our laboratory we have totally confirmed 71 TP-84 proteins.

What will audience learn from your presentation?

- How to aid in the decoding of proteomics in organisms using cell-free protein synthesis a powerful and versatile alternative to the heterologous *in vivo* expression of proteins.

Biography

Chemist and molecular biologist. Assistant professor at the University of Gdansk, Faculty of Chemistry, Department of Biotechnology. Developing his interests related to the chemistry of nucleic acids, he received his PhD in 2016 in chemical sciences in the field of biochemistry. 20 years of experience in the biotechnology industry (1999 - 2019) as a chemist, head of the isotope and DNA sequencing laboratory, general manager of the production of reagents used in molecular biology.

He developed a new product line - over 20 specialized kits designed to isolate RNA, DNA and proteins from various sources. Significant participation in genetic engineering projects involving cloning of bacterial and viral genes. Recently targeted at bacteriophages and their use as nanobiomaterials in a next-generation drug delivery system.

Daria Krefft*, Joanna Żebrowska, Maciej Prusinowski, Piotr Skowron

University of GdansK, Poland

Fusion proteins containing a binding domain as potential delivery systems for therapeutic proteins

Fusion proteins consist of at least two domains encoded by separate genes. These genes, when combined, are transcribed and then translated to form a single polypeptide. The use of biotechnological methods by using the fusion of the cloned foreign gene with the recipient's gene allows for obtaining fusion proteins, i.e. new proteins with different or improved properties. Currently, gene fusion techniques allow the production of recombinant proteins with traits that are a combination of those exhibited by the parent molecules. As a result, they have been used in many scientific fields, where they are used, inter alia, as gene expression reporters, as markers facilitating the purification of proteins or increasing their solubility, histochemical markers enabling the tracking of the location of proteins in cells, and as biopharmaceuticals. In the latter case, they mainly help by improving the pharmacokinetics and biodistribution of drugs.

The carbohydrate binding modules (CBM) are proteins that are great partners for fusion proteins. The most famous of these are the abundant cellulose binding domains. However, there are many other CBMs recognizing, inter alia, chitin, xylan, mannan, galactan, starch or glycans found on the surface of cells. Many of them are non-toxic to eucaryotic cells, so when combined with proteins with healing or pro-regenerative properties, they can be an excellent source of new generation drugs.We designed the appropriate vectors carrying the binding domain gene, which we used for cloning in the suitable places of genes encoding proteins with therapeutic effect. Thus, the obtained new plasmid constructs were used for gene expression in the *Escherichia coli* system. The fusion proteins were biosynthesized and then purified using the NiNTA resin. The interaction between fusion proteins and the selected carbohydrate were investigated using the BLItz analyzer.

Biography

Chemist and biotechnologist, She received her M.Sc. degree in biological chemistry (2011) and Ph.D. degree in biochemistry (2018) at the Faculty of Chemistry, University of Gdansk, Poland. From 2017 employed at the same institution, from 2020 as an Assistant Professor. Research area: genetic engineering and protein biochemistry, purification of 'artificial' polyepitopic proteins with therapeutic and regenerative properties, design and cloning of synthetic genes, bacteriophage protein fusion, novel protein expression strategies, engineering DNA-recognition specificity of enzymes, enzymes' biochemical and physico-chemical properties. Co-author of 11 publications and 2 patents, fellowships in 2 biotechnology companies.

Joanna Stec*, Urszula Kosikowska, Sylwia Andrzejczuk
Medical University of Lublin, Lublin, Poland

Detection of topoisomerase IV encoding *parc* gene in recreational water isolates of *aeromonas veronii*

Quinolones are frequently used drugs owing to their characteristics of easy to use, broad-spectrum activity, and high efficiency. Their presence in the environment can pose a threat to the ecosystem and to human health. Those antibiotics can enter water bacteria through e.g. humans and aquaculture. As a consequence, they cause selection and stimulate bacterial resistance. The aim of this study was to determine the prevalence of specific quinolone *parC* resistance genes in *Aeromonas veronii* isolated from natural water reservoir in the south-eastern Poland. This enzyme is involved with the decatenation of the interlinked daughter chromosomes. Quinolone resistance is essentialy due to chromosomal mutations. Sixty-seven *A. veronii* isolates obtained from freshwater reservoir were identified on the basis of their protein profile. Antimicrobial resistance was determined by the automatic method with Vitek 2 Compact System. The *parC* genes was investigated by PCR. All of the *A. veronii* isolates were phenotypically sensitive to levofloxacin and ciprofloxacin on the basis of MIC (Minimal Inhibitory Concentration) values. The presence of *parC* gene was found in 55.2% (37/67) of tested isolates. Our study confirms the presence of quinolone resistance gene - parC in the environmental *A. veronii* isolates derived from the recreational water reservoir. This may facilitate fluoroquinolone resistance, and increase the risk of *Aeromonas* spp. infections, and potentially serve as reservoirs for the dissemination of *parC* genes to other aquatic microbes.

Audience Take Away:

- The information helps to understand the possible risk of infections by the use of recreational waters by people (especially by those immunocompromised) as *Aeromonas veronii* cause for example skin and soft-tissue infections, wound infections, urinary tract infections.
- The presence of quinolones in the environment can pose a threat to the ecosystem and to human health. Those antibiotics can enter water bacteria through e.g. humans and aquaculture.As a consequence, they cause selection and stimulate bacterial resistance. This work increase the knowledge on prevalence of the quinolones resistance-gene *parC* in recreational waters microbes;
- Published data pay attention to potential reservoirs for the dissemination of *parC* genes to other aquatic microbes. Such information can contribute to design of other scientific studies and provide additive information to complete other research.

Biography

Joanna Stec studied Biotechnology at the University of Agriculture in Cracov and graduated as Master of Science in 2015. Then, in 2017, she graduated from postgraduate studies in Medical Analyst obtaining the professional title of laboratory diagnostician. In 2018 she joined the Chair and Department of Pharmaceutical Microbiology in the Medical University of Lublin to start her PhD.

Tori Langill*, Sofie Thijs, Jaco Vangronsveld
Hasselt University, Belgium

Seed endophytes against abiotic stress : An efficient solution to grow energy crops on marginal land?

Bioenergy and bioethanol crops are an efficient form of energy production and a step towards a greener future, but they use up our precious agricultural land which is better suited towards growing food in this era of booming population. Therefore, we explore a novel way to grow bioenergy crops on polluted and marginal land, using the seed microbiome of *Noccaea caerulescens*, to combat the abiotic stresses associated with term. *N. caerulescens* is a hyperaccumulator of zinc, often found growing on soils with high lead/ cadmium/ zinc pollution that are often dry and nutrient poor. To test to which extent the seed endophytes of *N. caerulescens* (can assist in minimizing stress to crop species, the microbiome was enhanced with selective media before being applied to seeds, prior to sowing. Results indicate that the seed microbiome of *N. caerulescens* can increase biomass size significantly ($p>0.005$) when the seed is enhanced with endophytes that have been subjected to metal stress. Seeds of Medicago sativa and Arabidopsis thaliana germinated more successfully under stress, when the seed was enhanced with the endophytic microbes of *N. caerulescens* prior to sowing on marginal soil. It is our strong belief that seed endophytes not only hold the key to more successful germination of crop species under stressful conditions, but also to enhancing plant health.

Audience Take Away:

- How to successfully transplant endophytic bacteria from seeds of interest onto crop seeds.
- Insight into the seed microbiome of Noccaea caerulescens which is a hyper accumulator.
- How the seed microbiome is integral to successful germination and how to optimize this.
- Ideas for marginal land use.

Biography

Tori Langill obtained her Bachelor's degree in science at Thompson Rivers University, Canada, specializing in cell, micro, and molecular biology. She then received her Masters from Hasselt University, Belgium, with a major in Biomedical science : Environmental health. She has also studied and been awarded a diploma in applied biology from the University of the Highlands and Islands in Scotland. Currently she is working on her doctoral thesis in the research group of prof. Dr. Jaco Vangronsveld at Hasselt University, Belgium.

Sarishna Singh*, Christoffel Opperman
National Health Laboratory Service, South Africa

A laboratory audit of successful line probe assays

The HAIN GenoType®MTBDR*plus* (first line) and GenoType MTBDRsl (second line) line probe assays are nucleic acid amplification tests that work with PCR technology. The GenoType MTBDRsl line probe assay (LPA) is recommended by WHO as a replacement test instead of culture based drug susceptibility testing of fluroquinones & second line injectables regardless of smear status. However, the laboratory staff noticed poor performance of this assay when done directly from smear negative sputum samples.

Objective: This audit aimed to determine the percentage of successful line probe assays in patients with smear negative and smear positive MTB.

Method: The investigators determined the number of LPAs performed over a three-month period. They then determined the number of successful LPAs (first line and second line) and correlated them with smear status.

Results: A total of 319 LPAs were performed. One hundred and eighty-four were first line LPAs and 135 were second line LPAs. All of the first line LPAs yielded successful results; 104/184 (56.52 %) were smear positive whereas 80/184 (43.48%) were smear negative. Seventy-three out of the 135 second line LPAs were successful and smear positive. The remaining 62 were smear negative, of these 27 (27/62; 43.55%) were successful the remaining 35/62 (56.45%) were unsuccessful and needed repeat LPAs from the cultured isolate. Conclusion: Due to rising reagent costs it is recommended that laboratories check the percentage of successful second line LPAs and investigate other methods to determine second line resistance in smear negative samples such as the Xpert® MTB/XDR.

Biography

Dr S Singh qualified as a medical doctor in 2010 from the University of Pretoria, South Africa. She completed her internship and community service and practiced in rural ARV clinics in South Africa. Thereafter she worked at The Desmond Tutu HIV Foundation. She then joined the postgraduate training program at The Division of Medical Microbiology and Immunology,National Health Laboratory Service (NHLS) Tygerberg Hospital and University of Stellenbosch. She completed her Masters of Medicine in Microbiology Pathology and was admitted as a Pathologist Clinical Microbiologist to the College of Medicine South Africa in 2021. She continues to work for the NHLS as a Consultant Microbiologist with a special interest in Tuberculosis.

Aubrey Frantz*, Perla Rivera, Ysidro Motta, Gustavo Gomez, Muhammed Yousufuddin

University of North Texas at Dallas, USA

Development of antimicrobial resistance to quaternary ammonium compounds in the human skin microbiota

The use of disinfectants and sanitizers are a common practice in homes, workplaces, industries and hospitals. Quaternary ammonium compounds (QACs) are positively charged polyatomic ions with broad-spectrum antimicrobial activity that are frequently used as the active ingredient in many antimicrobial products. Considering the abundant use of these products, QACs are perpetually in contact with the skin. While the human skin functions as a physical barrier between the external environment and the body proper, it is also colonized by a diverse microbiota that actively influence health and disease. To investigate the impact of QACs on the human skin microbiome, common skin bacterial species were exposed to purified benzalkonium chloride (BAC) and cetyltrimethylammonium bromide (CTAB) QACs with various alkyl chain lengths in short-term and long-term cultures.

Minimum inhibitory concentrations (MIC) and minimum bactericidal concentrations (MBC) were determined. While alkyl chain length directly affected the antimicrobial activity of the QAC, sensitivity to QAC inhibition was observed to be species specific. We found that the standard test organism used for antimicrobial effectiveness testing, Staphylococcus aureus, was 10-100 times more sensitive to QAC inhibition than other opportunistic and commensal skin bacterial species. Repeated exposure to sublethal QAC concentrations significantly reduced bacterial susceptibility to QAC inhibition. These results suggest that prolonged exposure to sublethal doses of QACs can lead to the development of QAC tolerance that may render these QAC disinfectants and biocides ineffective at the directed use concentrations.

These results

- Provide insights into the potential impact of widespread use of QACs on human health.
- Guide the selection and use of QAC-containing products.
- Identify potential concerns in the evaluation of QAC effectiveness.
- Establish a foundation to assess antibiotic co-resistance in QAC-tolerant bacteria.

Biography

Aubrey Frantz received her BA in Chemistry and Biology at the University of Kentucky in 2007. In 2012, she earned her PhD in Microbiology, Immunology and Molecular Genetics from the University of Kentucky, where she studied in the laboratory of Dr. Charlotte Kaetzel. Dr. Frantz is currently an Assistant Professor of Biology at the University of North Texas at Dallas and has numerous publications in various high impact journals, including PNAS, Pathogens, Mucosal Immunology, Immunological Investigations and Gut Microbes. Dr. Frantz and her UNTD undergraduate research students investigate the effects of environmental factors on the human microbiome.

KEYNOTE FORUM

DAY 02

INTERNATIONAL
CONFERENCE AND EXPO ON

APPLIED 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.

SPEAKERS

DAY 02

INTERNATIONAL
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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]

[1]Indian Institute of Technology Indore, India

[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.

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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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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]

[1]Universidade Nova de Lisboa, Portugal
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[3]University of Tuebingen, Germany

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).

Anfal M. Alkandari*[1], Yasser M. Alsayed [2], Atallah M. El-Hanbaly[3]

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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..

Miguel Vazquez-Moreno*[1], Cruz Miguel*[1], Chiara-Maria Homann[2,3], Daniel Locia-Morales[1,4], Fernando Suarez-Sanchez[1], David Meyre[5,6,7], Jennifer C. Stearns[2,3]

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[5]McMaster University, Canada
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[7]University Hospital Centre of Nancy, France

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.

Participants List

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