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2nd Edition of Euro-Global Conference on

BIOTECHNOLOGY AND BIOENGINEERING

JUNE 2022

13-14

VIRTUAL EVENT

Contact us:
Ph: +1 (702) 988-2320
WhatsApp: +1 434 264 7183
Email: biotechnology@magnusconference.com
Website: https://biotechnology-conferences.magnusgroup.org/

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BOOK OF ABSTRACTS

2ND EDITION OF EURO-GLOBAL CONFERENCE ON

BIOTECHNOLOGY AND BIOENGINEERING

13-14 JUNE

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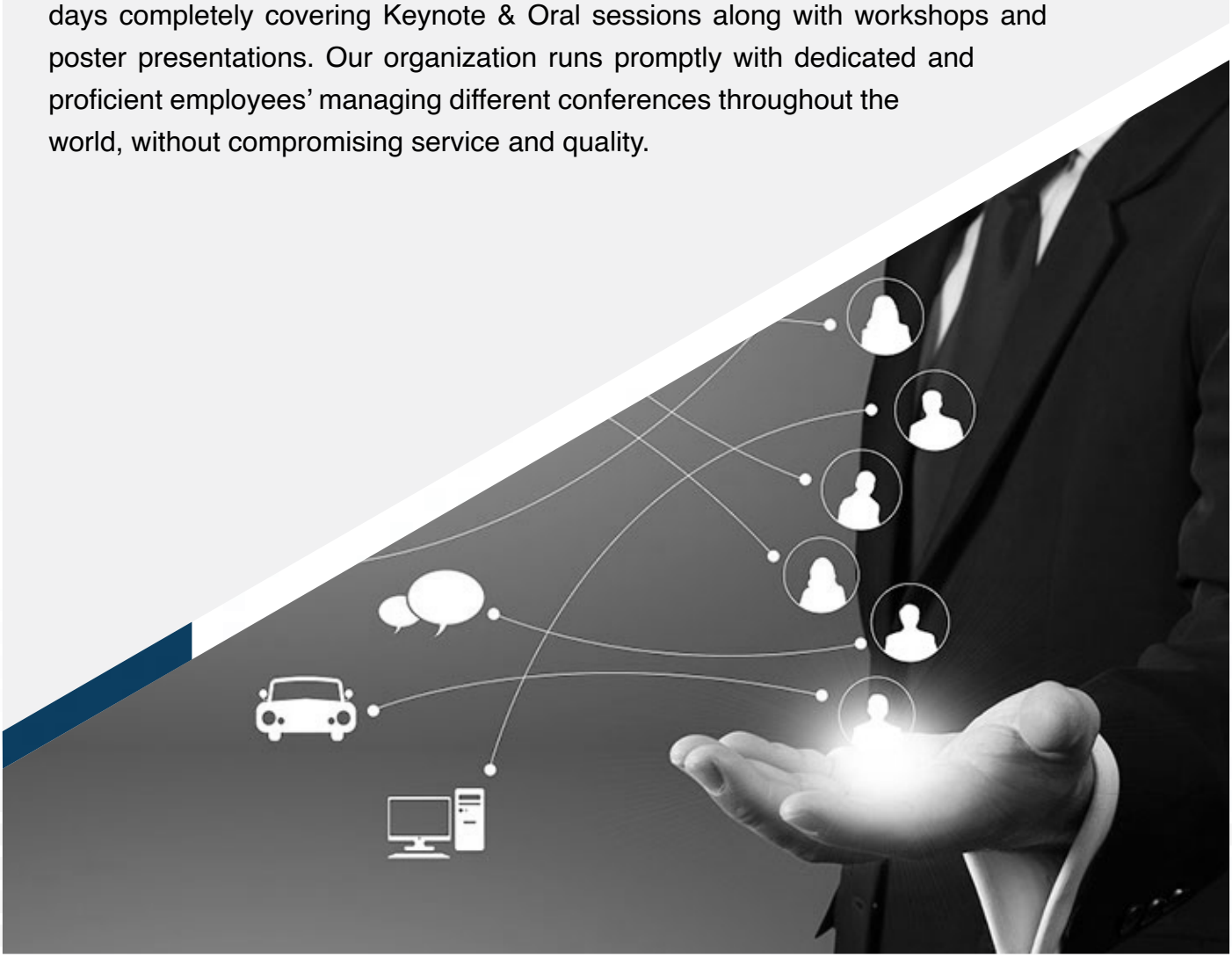
ABOUT MAGNUS GROUP

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 ECBB 2022

Magnus Group is glad to announce and extend a warm invitation to you to join its "2nd Edition of Euro-Global Conference on Biotechnology and Bioengineering" (ECBB 2022) which is going to be held Virtually during June 13-14, 2022.

The summit having the theme "Revealing and Transforming the Globe with Innovations in Biotechnology and Bioengineering" will once again unite researchers, scientists, biotechnologists, academicians, industry key players, policymakers and delegates from a wide range of disciplines to deliberate on the latest findings and trends across the bioengineering and biotechnology remit, providing a forum for the exchange of knowledge and forging of new ideas.

The diversity of issues that will be covered at this consortium reflects the fact that biotechnology and bioengineering are integral to many aspects of daily life and have the potential to address local and global challenges that we all confront. We try to adapt innovation in Industrial Biotechnology and bioscience to enable the bio-manufacturing of chemicals and functional products in a more sustainable method as the world faces crucial problems in establishing a more sustainable bioeconomy. Conference goers will get the opportunity to present their respective knowledge and experiences at the conference. You will also have the opportunity to meet people from all over the globe. The conference will be a valuable meeting for you to acquire new knowledge, engage in research discussion, establish new connections, and advance your plans for future research with the frontier topics of Bioengineering and Biotechnology covered in this two-day scientific gathering through parallel oral sessions, poster presentations, keynote session and panel discussions. The symposium will undoubtedly be a highlight for scholars and professionals working on this topic, which has a wide range of scientific applications. The event will feature a slew of illustrious speakers who will present their most recent findings on cutting-edge techniques that will transform the field of bioengineering and biotechnology in the future.

KEYNOTE FORUM

DAY 01

2ND EDITION OF EURO-GLOBAL CONFERENCE ON

BIOTECHNOLOGY AND BIOENGINEERING

13-14 JUNE

Dario Puppi

University of Pisa, Italy

Additive manufacturing of microbial polyesters for bone tissue engineering

Polyhydroxyalkanoates (PHA) s are a class of aliphatic polyesters synthesized by various bacteria, with well-assessed biodegradability and biocompatibility. Their potential for large-scale sustainable production through microbial fermentation, together with superior processing versatility and mechanical properties in comparison with other natural macromolecules, make PHAs unique polymer candidates for advanced research and development approaches. One of the key aspects of the ongoing fourth industrial revolution is the implementation of the aforementioned advantages of this class of materials. In particular, the integration of biopolymers and additive manufacturing (AM), also referred to as 3D-Printing, is leading to the next generation of commodity materials complying with the concept of sustainable development, as well as to biomedical devices for advanced applications. This lecture is aimed at presenting some recent research activities carried out in this context for the optimization of PHA-based scaffolds by AM for bone tissue engineering. The investigation of two different PHAs, i.e., poly (3-hydroxybutyrate-co-3-hydroxyexanoate) (PHBHHx) and poly (3-hydroxybutyrate-co-3-hydroxyvalerate) (PHBV) as scaffolding materials for bone regeneration will be presented. In particular, their processing by computer-aided wet-spinning (CAWS), an AM approach based on the extrusion of a polymeric solution/suspension directly into a coagulation bath, will be described as an effective approach to the fabrication of scaffolds with predefined external shape and hierarchical porous architecture. Indeed, CAWS is well-suited to endow PHA scaffolds with a microporosity integrated with a predefined macroporous network, by acting on phase inversion parameters governing polymer solidification. Blending PHAs with other aliphatic polyesters, e.g., poly (ε-caprolactone) (PCL) and poly (lactic-co-glycolic acid) (PLGA), as well as with osteoinductive ceramics (e.g., hydroxyapatite and β-tricalcium phosphate) is another effective strategy investigated to develop additive manufactured scaffolds tailored to bone tissue engineering. In this way, it is possible to tune scaffold's processing, physico-chemical, mechanical and bioactive properties by engineering material's composition. The employment of optimized PHA-based scaffold prototypes to support in vitro proliferation and differentiation of MC3T3-E1 murine preosteoblast cells will be finally described.

Audience Take Away:

- The audience will be updated on current progress in the field of application of Additive Manufacturing, referred to also as 3D-Printing, to microbial polyesters (i.e., polyhydroxyalkanoates, PHAs) for biomedical applications
- The talk will help professional audience in understanding critical aspects on PHAs processing and functional characterization tailored to tissue engineering strategies. Both academic researchers and industrial actors can benefit of the optimized experimental protocols presented in the talk, complying with the basic principles of sustainable development

Biography

Puppi studied Chemical Engineering at University of Pisa, Italy, and graduated as MS in 2005. She then joined the research group of Prof. Emo Chiellini at the Department of Chemistry and Industrial Chemistry, University of Pisa. He received his PhD degree in Biomaterials in 2009 at the same institution, where he currently works as Senior Research Fellow in Industrial Chemistry. He has published more than 50 research articles in SCI (E) journals, receiving more than 2300 citations (Scopus database).

Alexandra Peregrina*[1], Joao R. Pereira[2,3], Ana T. Rebocho[2,3], Filomena Freitas[2,3], Joao Martins-Lourenco[1], Maria A. M. Reis[2,3] and Cecília M. Arraiano[1]

[1]Control of Gene Expression Lab., Instituto de Tecnologia Quimica e Biologica Antonio Xavier, NOVA University of Lisbon, Oeiras, Portugal

[2]Associate Laboratory i4HB-Institute for Health and Bioeconomy, School of Science and Technology, NOVA University of Lisbon, Caparica, Portugal

[3]UCIBIO—Applied Molecular Biosciences Unit, Department of Chemistry, School of Science and Technology, NOVA University of Lisbon, Caparica, Portugal

Post-transcriptional control in the regulation of polyhydroxyalkanoates synthesis

The large production of non-degradable petrol-based plastics has become a major global issue due to its environmental pollution. Biopolymers produced by microorganisms such as polyhydroxyalkanoates (PHAs) are gaining potential as a sustainable alternative, but the high cost associated with their industrial production has been a limiting factor. Post-transcriptional regulation is a key step to control gene expression in changing environments and has been reported to play a major role in numerous cellular processes. It involves bacterial small non-coding RNAs (sRNAs) and important enzymes as ribonucleases (RNases), which are versatile and potent regulators. However, limited reports are available concerning the regulation of PHA accumulation in bacteria, and many essential regulatory factors still need to be identified. Some of these studies and a recent review on the topic, have informed that the synthesis of PHAs can be regulated at the post-transcriptional level, and analyze the RNA-mediated networks involved. The absence or truncation of some of those regulating-genes could result in the alteration of the total PHA cellular accumulation. In consequence, it suggests that those riboregulators would be interfering (direct-or indirectly) some PHAs synthesis pathways in very well recognized bacteria for their abilities to synthesize polyhydroxyalkanoates. Therefore, the discussion of the forthcoming research on riboregulation, synthetic, and metabolic engineering could lead to improved strategies for PHAs synthesis in industrial production, thereby reducing the costs currently associated with this procedure.

Audience Take Away:

- The audience will be able to apply what they learn to a wide range of topics: microbiology, polyhydroxyalkanoates, post-transcriptional regulation, riboregulation, and synthetic biology
- This talk would lead to improved strategies for PHAs synthesis in industrial production, what is a practical solution to a problem that is limiting the replacement of petroleum-based plastics with biodegradable plastics
- The talk connects the biopolymers industrial production with the synthetic biology area, which can be used for the design of tailor-made microorganism able to produce biopolymers that cover the specific requirement of the industry

Biography

Alexandra Peregrina Lavin received her PhD degree from the University of Granada (Spain) in 2017, and during her professional activities joined others research groups, such as the SYNMIKRO LOEWE Center in Marburg (Germany) and the ITQB NOVA Institute (Oeiras, Portugal). She has been co-author of 8 research articles of high impact, based in the areas of Natural Sciences and Engineering & Technology, with emphasis on Microbiology. In 2018 participated in the EmPowerPutida consortium in the frame of H2020, and in 2019 was awarded with the competitive individual fellowship of the Marie Sklodowska-Curie Actions for the production of bioplastics from microorganisms, as sustainable alternative to petrol-based plastics.

Cristiano Jose de Andrade

Federal University of Santa Catarian (UFSC), Brazil

Effect of hydrophobic inducers on the production of biosurfactants

Biosurfactants are amphipathic molecules that are synthesized by living cells with numerous potential applications in the areas of health and the environment, among others. However, the high production cost limits massive applications of biosurfactants. An interesting approach to reduce its production cost is the replacement of synthetic culture media by agro-industrial residues associated with hydrophobic inducers. Some of these studies and a recent review on the subject reported that biochemically, the productivity of the biosurfactant can be easily increased by adding inducers to the culture medium, which stimulates microbial growth and also triggers the metabolism of biosurfactant production. Biosurfactant inducers are mainly hydrophobic molecules (e.g. olive oil) that are composed of a pool of molecules (e.g. saturated and unsaturated fatty acids, proteins, and vitamins). However, there is little information about the effect of these specific molecules (e.g. oleic acid) on the production and chemical structure of biosurfactants. In this study, the use of hydrophobic inducers (palmitic acid) at different concentrations (1%, 2%, 5%, and 10%) in the production of surfactin by Bacillus subtilis ATTCC 6633 using cassava wastewater as a carbon source was investigated. Production was carried out at 30 °C, 150 rpm for 72 h. In the analysis of the results of all fermentations, the wastewater cassava was able to produce surfactin (37% (w surfactin/w crude surfactin)) when using the inducer palmitic acid (1%, 2%, 5%, and 10%) in addition to of increasing production (30%, 16%, 75% and 86% (w/w)), respectively, still indicated the formation of different surfactin homologues. There was no influence of the addition of inducers on pH and/or biomass. The surfactin produced was able to reduce the surface tension of water from 72.2 to 30-26 mN/m, using all concentrations of inducers respectively. This study confirms that the use of hydrophobic inducers can reflect on different chemical structures, providing a strong basis for exploring new structures and unknown bioactivities.

Biography

Andrade studied Food Engineering at Federal University of Lavras in 2008. He received his PhD degree in 2016 at UNICAMP. After two years postdoctoral fellowship supervised by Dr. Oller at Mass Spectrometry Laboratory/Dempster USP, he obtained the position of an Associate Professor at the Federal University of Santa Catarina (UFSC) also in Graduate Program in Chemical Engineering at UFSC (PósEnq). Dr. Andrade has plenty of experience on biotechnological processes, in particular fermentation, bacterial metabolism, bioproducts with high surfactant activity, purification processes (ultrafiltration), algae cultivation and green-based extraction methods, and identification of biomolecules by mass spectrometry. He has published 35 scientific articles, 14 book chapters, and 2 patent deposits.

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SPEAKERS

DAY 01

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13-14 JUNE

Beilei Wu*, Chenchen Liu, Rongqun Wang, Zhaoyan Tan, Xiliang Jiang

Chinese Academy of Agricultural Sciences, China

Exploration of mycoviruses from trichoderma spp. In China

The mycovirus is the research hot in recent years. Until now, seven isolates were explored from Inner Mongolia and Xinjiang provinces in China. They mediated the host (Trichoderma spp.) have the functions of enchancing the growth of plant and improving the capability of resistance to pathogens though the functions had the differences on different isolates of mycovirus. It indicated the complex interaction among mycovirus, Trichoderm, plant and pathogens.

Biography

Beilei Wu, born on 17th June, 1974. She, as an Associate Prof. in Institute of Plant Protection, Chinese Academy of Agricultural sciences (CAAS), She received her PhD degree in 2007 from the same institution. After two years, postdoctoral fellowship was supervised by Dr Xifeng Wang in the same institution, and then she worked in the Institute of Plant Protection, Chinese Academy of Agricultural sciences (CAAS). As the visit scholar, she worked in the Evolutionary Systems Virology Group, Institute de Biology Molecular y Celular de Plantas (CSIC-UPV), Valencia, Spain. 2014-2016. Until now, she has published more than 30 research articles in SCI (E) journals.)

Simona Braccini*, G. Pecorini, F. Chiellini, D. Puppi
University of Pisa, Italy

Chitosan-based polyelectrolyte complex hydrogels by additive manufacturing for 3D in vitro cancer modeling

Polymeric hydrogels have been used over the past two decades as one of the most common types of tissue engineering scaffold thanks to their ability to maintain a distinct 3D structure in physiological environment, offer structural support for cells in the engineered tissues, and simulate the native extracellular matrix (ECM) functions. The high-water content absorbed by hydrogels can provide an ideal environment for cell survival mimicking that in many native tissues. One of the most common methods for hydrogel preparation is through physical crosslinking of hydrophilic macromolecular chains. Polyelectrolyte complexes (PEC) s are supramolecular self-assembled systems formed upon combination of oppositely charged compounds by means of electrostatic interactions. The possibility of directly mixing polyelectrolytes of natural origin with inherent biocompatibility, to obtain PECs with controlled water stability, biodegradability, and mechanical properties, has attracted great interest for various biomedical applications. In particular, additive manufacturing (AM) integration with naturally-derived PEC strategies is resulting into novel layered hydrogels designed for engineering human tissues. In this contribution different ratios of chitosan, the reference cationic polysaccharide, and either alginate or hyaluronic acid, polyions of natural origin with established biocompatibility, were used to fabricate 3D PEC hydrogels with a predefined porous structure by means of Computer-Aided Wet Spinning (CAWS). Indeed, this AM technique allows the fabrication of scaffolds with advanced control over external geometry, internal pore size and distribution, determined by the deposition path of a polymeric fibre in a coagulation bath. Experimental investigations showed that the designed chitosan-based PEC hydrogels were stable in physiological environment, demonstrating their suitability for long-term 3D cell culture applications. Moreover, biological characterization carried out with A2780 and A2780cis ovarian cancer cell lines highlighted interesting differences in cell adhesion and colonization among investigated hydrogels with different compositions that could be correlated to the influence of PEC composition on hydrogel's physical-chemical and mechanical properties. Ongoing experimental investigations are dedicated to evaluating in vitro chemotherapeutics response.

Audience Take Away:

The networks of physical hydrogels can be formed by chitosan complexation with an oppositely charged polyelectrolyte. The electrostatic attraction between the positively charged amino groups of chitosan and the negatively charged groups of another polyelectrolyte leads to the formation of a polyelectrolyte complex (PEC). The production of PECs is industrially advantageous due to the simple and safe preparation processes consisting in the direct mixing of two species with opposite charges in aqueous solution at controlled pH, without the addition of toxic additives or catalysts, which could compromise the biocompatibility of the developed systems. For these reasons, PECs are particularly suitable for the development and manufacturing of porous and biocompatible 3D scaffolds to simulate the functions performed by the extracellular matrix and support cell adhesion and proliferation in vitro or in vivo. Hydrogels have shown great potential in several biomedical applications due to their structural similarities to the extracellular matrix (ECM) of native living tissues. Due to their ability to absorb large amounts of water and their mechanical behavior as soft matter, they present physicochemical and mechanical properties comparable with those of many soft tissues. Moreover, PEC hydrogels hydrophilicity, swelling behavior, and mechanical properties can be tailored to the specific applications by changing the type of polycation and polyanion, as well as the ratio between them in the PEC formulation. 2D cell culture models are still the first option that scientists turn to due to its simplicity in order to obtain preliminary results. Nevertheless, 2D cultures may not sufficiently mimic the physiological conditions in a3D network where in vivo cells reside. Therefore, deceptive data from 2D cell culture model often leads to the irrelevant prediction of drug efficacy and toxicity and finally causes the failure in drug validation and approval processes. One advantage of cell culturing in a 3D manner over 2D cell culture is that it contributes

the expression of ECM components as well as the interactions between cell-cell and cell-matrix. The traditional 2D cell cultures result in a monolayer cell expanding on a flat surface of glass or commercial polystyrene plastic flasks for tissue culture. In contrast, 3D cells cultures promote cells to form 3D spheroids by utilizing an ECM material. Cell spheroid is the important characteristic that resembles in vivo cells for further replicating cell differentiation, proliferation, and function in vitro. Thus, 3D spheroid culture is considered an improved model for predictive in vitro cell-based assays and may deliver high physiological relevance for preclinical drug discovery, especially in cancer cell research

Biography

Simona Braccini received a Master degree in Pharmaceutical Chemistry and Technology in 2017 at the University of Pisa. After obtaining a two-year research fellowship on "Study of biofunctional characteristics of micro/nanostructured polymeric materials for biomedical applications, by cellular culture use", she has been attending the PhD course in Chemistry and Materials Sciences since 2019, under the supervision of Professor Chiellini and Dr Puppi. Her research interests concern the design, fabrication and characterization of hydrogel scaffolds obtained from naturally-derived polymeric materials, for the development of 3D in vitro modeling of tumor tissues. She is co-author of more than ten scientific articles in high impact international journals.

Francesco Secundo*[3], Sikandar Khan[1], Pengcheng Fu[2], Alessandro Di Fonzo[3], Irene Marasca[3]

[1]Department of Biotechnology, Shaheed Benazir Bhutto University, Sheringal, Khyber Pakhtunkhwa, Pakistan

[2]State Key Laboratory of Marine Resource Utilization in South China Sea, Hainan University, Haikou 570228, China

[3]Istituto di Scienze e Tecnologie Chimiche ''Giulio Natta'', Consiglio Nazionale delle Ricerche, Milano, Italy

Augmented whole-cell biotransformation of the toxic 3-chloropropiophenone into 1-phenyl-1-propanone by microalgae Chlorella emersonii immobilized in hydrogel

Dehalogenation of halogenated organic substrate (3-Chloropropiophenone, 3-CPP) is conducted using whole cells microalgae Chlorella emersonii (211.8b) as biocatalyst. C. emersonii cells were immobilized by entrapment (without any covalent bonds) in Aquasorb (an anionic polyacrylate received from SNF Italia able to absorb water up to 400 times the dry weight) and used to catalyse the biotransformation of the toxic 3-chloropropiophenone. The reaction produced 91% or 93.5% 1-phenyl-2-propenone (from a non-catalyzed reaction) and 9% or 6.5% 1-phenyl-1-propanone obtained thanks to the entrapped or the free (non-immobilized) whole microalgae cells, respectively. The number of entrapped cells was achieved in terms of colony-forming units (CFUs = 2.1 x 104) per hydrogel bead with a comparable growth pattern to that of free cells. The viability of C. emersonii in the presence of 3-CPP was monitored by analysing the fluorescence emitted by the chlorophyll of microalgae (Schulze et al. 2011). The decrease of fluorescence of the culture of microalgae in the presence of 3-CPP (and the derivatised products) indicates the destruction of chlorophyll and cell death (90% after 52 h with 5 mM of 3-CPP) after which the ratio between the two products (0.36 ± 0.02) remained unaltered, suggesting the inhibition of the biocatalysed reaction. Instead, in the same conditions, the hydrogel entrapped cells show viability in terms of chlorophyll fluorescence even after 52 h. Thus, it can be suggested that the higher biotransformation of 3-CPP to 1-phenyl-1-propanone with the entrapped cells depends on the higher cell viability. In conclusion, the results did not confirm that the biotransformation is due to dehalogenase or hydrogenase activity. However, the study indicates that the immobilization of microalgae in Aquasorb (and likely also in other types of hydrogels) can be a procedure for improving microalgal applications for biotransformation or bioremediation processes.

Audience Take Away:

- Use of whole cells microalgae for the biotransformation of organic halogenated compounds
- Immobilization of whole cells by entrapment in hydrogels can be a way to improve cell resistance against toxic molecules
- The study can inspire chemists for the synthesis and development of new hydrogels starting from natural polymers useful to entrap microalgae for environmental applications
- Expertise on materials for cell entrapment could be organized in a job as consultant to suggest and improve biotransformation and bioremediation processes

Biography

Beilei Wu, born on 17th June, 1974. She, as an Associate Prof. in Institute of Plant Protection, Chinese Academy of Agricultural sciences (CAAS), She received her PhD degree in 2007 from the same institution. After two years, postdoctoral fellowship was supervised by Dr Xifeng Wang in the same institution, and then she worked in the Institute of Plant Protection, Chinese Academy of Agricultural sciences (CAAS). As the visit scholar, she worked in the Evolutionary Systems Virology Group, Institute de Biology Molecular y Celular de Plantas (CSIC-UPV), Valencia, Spain. 2014-2016. Until now, she has published more than 30 research articles in SCI (E) journals.)

Biyue Zhu*, Jing Yang, Chongzhao Ran
Massachusetts General Hospital and Harvard Medical School, Boston

Differentiating Aβ40 and Aβ42 in amyloid plaques with a small molecule fluorescence probe

Differentiating amyloid beta (Aβ) subspecies Aβ40 and Aβ42 has long been considered an impossible mission with small-molecule probes. In this report, based on recently published structures of Aβ fibrils, we designed iminocoumarin–thiazole (ICT) fluorescence probes to differentiate Aβ40 and Aβ42, among which Aβ42 has much higher neurotoxicity. We demonstrated that ICTAD-1 robustly responds to Aβ fibrils, evidenced by turn-on fluorescence intensity and red-shifting of emission peaks. Remarkably, ICTAD-1 showed different spectra towards Aβ40 and Aβ42 fibrils. In vitro results demonstrated that ICTAD-1 could be used to differentiate Aβ40/42 in solutions. Moreover, our data revealed that ICTAD-1 could be used to separate Aβ40/42 components in plaques of AD mouse brain slides. In addition, two-photon imaging suggested that ICTAD-1 was able to cross the BBB and label plaques in vivo. Interestingly, we observed that ICTAD-1 was specific toward plaques, but not cerebral amyloid angiopathy (CAA) on brain blood vessels. Given Aβ40 and Aβ42 species have significant differences of neurotoxicity, we believe that ICTAD-1 can be used as an important tool for basic studies and has the potential to provide a better diagnosis in the future.

Biography

Zhu received her Ph.D degree in pharmaceutics at Sichuan University. She works as an exchange student at massachusetts general hospital/harvard medical school during her Ph.D study. Currently, she works as a postdoc at massachusetts general hospital/harvard medical school. Her research field is related with the imaging probe, therapeutics, and drug screening platform of Alzheimer's disease.

Belen Cortes Llanos*[1,2], N.L. Allbritton[1], D.M. Murdoch[2]

[1]Department of Bioengineering, University of Washington, Seattle, Washington, USA

[2]Department of Medicine, Duke University, Durham, North Carolina, USA

Embedded-microstructures arrays for single-cell sorting and collecting of lymphocytes following HIV latency reactivation

The study of single cells has recently accelerated in many fields, oncology, neuroscience, virology, and immunology, among others.1, 2 Bulk studies provided excellent knowledge, but much information was lost when collecting data from cell populations. Different cell-separation platforms have been developed to comprehend single-cell heterogeneity. Microwell-based devices are among the most outstanding technologies for single-cell analysis due to their simplicity.3 We describe a new approach to manufacture microarrays. Depending on the deposition parameters, materials, and topography, embedded- microstructures arrays (EMA) were fabricated. These arrays possess optically transparent microwells with collectible magnetic microcarriers upon which the cells are cultured and screened using standard imaging techniques. EMA enables time-resolved imaging of cells combined with efficient isolation of target cells. Cultured cells can be identified by many selection criteria, including fluorescence intensity that changes over time. An individual carrier containing a target cell can be efficiently released and collected for genomic analysis using magnetic collections. In the current work, time-resolved assays will be carried out in order to evaluate the dynamics of HIV latency. HIV-infected CD4+ T cells comprise a latent viral reservoir that can be reactivated using latency reversal agents (LRAs)4. Since HIV reactivation is not uniform across an entire population of latent cells, approaches to track reactivation within a single cell are critical to develop new strategies to eradicate HIV reservoirs. Our microarray platform was used to understand gene expression in newly reactivated HIV-infected cells compared to uninfected cells. The arrays used in this work are composed of 19,600 microcarriers with dimensions of 100 x 100 μm (W x L), 60 μm depth, and 50 μm spacing between the microrafts. We tracked mCherry and GFP expression of latently infected cells following exposure to three latency reversing agents (LRAs), prostratin, vorinostat, and iBET151. After single-cell analysis, reactivated latent cells were released to study transcriptional heterogeneity by performing single-cell RNA-sequencing. These results will advance our conceptual understanding of HIV reactivation dynamics.

Audience Take Away:

- A new microarray-based technology development. The design and microfabrication to the application for image-based live cell sorting following HIV latency activation
- See new trend in biotechnology about image-based live cell sorting technologies
- New single-cell platform for live imaging, sorting, and collecting for further analysis. Insights into the HIV latency reactivation kinetics under latency reversal agents

Biography

Belen Cortes-Llanos received her Ph.D. in Physics at the Complutense University of Madrid (Spain) in 2018. She worked on multidisciplinary projects between UCM, IMDEA Nanoscience (Spain), and the International School for Advanced Studies (Italy). She joined Nancy Allbritton's laboratory in the bioengineering department at the University of North Carolina (Chapel Hill, USA) and the University of Washington (USA) for her postdoctoral studies. She is now on a multidisciplinary project with Duke University using microarrays-based technology to follow single-cell latent HIV reactivation. She joined the Murdoch laboratory at Duke University (Medicine department) to apply developed microarray tools for single-cell RNA-sequencing.

Daniel Felipe Bohorquez Vargas*, Luis Mauricio Agudelo Otalora, Henry Humberto Leon Ariza

University of La Sabana, Colombia

Portable system for the acquisition and processing of electrocardiographic signals to obtain different metrics of heart rate variability

Heart rate variability (HRV) is defined as the temporary variation between heartbeats or RR intervals (distance between R waves in an electrocardiographic signal). This distance is currently a recognized biomarker. With the analysis of the distance, it is possible to assess the sympathetic and parasympathetic nervous systems. These systems are responsible for the regulation of the cardiac muscle. The analysis allows health specialists and researchers to diagnose various pathologies based on this variation. For the acquisition and analysis of HRV taken from a cardiac electrical signal, electronic equipment and analysis software that work independently are currently used. This complicates and delays the process of interpretation and diagnosis. With this delay, the health condition of patients can be put at greater risk. This can lead to an untimely treatment. This document presents a single portable device capable of acquiring electrocardiographic signals and calculating a total of 19 HRV metrics. This reduces the time required, resulting in a timelier intervention. The device has an electrocardiographic signal acquisition card attached to a microcontroller capable of transmitting wirelessly the cardiac signal to a mobile device. In addition, a mobile application was designed to analyse the cardiac waveform, the device calculates the RR and different metrics. The application allows a user to visualize in real time the cardiac signal and the 19 metrics. The information is exported to a cloud database for remote analysis. The study was performed under controlled conditions in the simulated hospital at the University of La Sabana, Colombia. A total of 60 signals were acquired and analysed. The device was compared against two reference systems. The results show a strong level of correlation ($r > 0.95$, $p < 0.05$) between the 19 metrics compared. Therefore, the use of the portable system evaluated in clinical scenarios controlled by medical specialists and researchers is recommended for the evaluation of the condition of the cardiac system.

Audience Take Away:

- The use of the evaluated system reduces the possibility of human errors in the transference of the information from an acquisition system to an analysis system, and the real-time processing facilitates decision-making for specialists
- The device allows the medical community to develop research projects that seek to relate metrics of heart rate variability with different pathologies
- From the field of medical bioengineering, new research can be generated associated with the improvement of the implemented system, by adding new features, such as the development of a predictive model of pathologies or the performance improvement for prolonged acquisition sessions

Biography

Graduated in electronic engineering in 2020 from the Central University of Colombia, with a degree project focused on the integration of hardware and software for the development of electronic devices for research, currently in the last semester of the master's degree in Design and Process Management at the University of La Sabana. He currently serves as a graduate assistant and part-time professor at the same university. He has additionally developed different electronic devices (in patent process) with an IOT focus in the field of bioengineering.

Poonam Kumari*[1], B. Yutika Nath[1], C. Sanjay K Banerjee[1] D. Upadhyayula Surayanaryana Murty[1] D. Velayutham Ravichandiran[2] and Utpal Mohan[2]

[1]Department of Biotechnology, National Institute of Pharmaceutical Education & Research (NIPER), Guwahati-781101, India.

[2]Department of Medicinal Chemistry, National Institute of Pharmaceutical Education & Research (NIPER), Kolkata-700054, India

Surfaces modification with antimicrobial peptides using sortase A enzyme

Bacterial growth and biofilm formation on the medical devices may cause serious infection in hospitalized patients. Infection related to implants leads to ~50 % of all hospital acquired infection. Even with continuous and rigorous improvement in these devices design and material, there is surge in the medical devices related infections. To tackle these obstacles, we need new molecules and strategies to coat medical devices to make its anti-microbial. Antimicrobial coatings are emerging as a potential approach to manage medical devices related infection. In the following study, we have used antimicrobial peptides as a coating molecule. We have successfully coated the antimicrobial peptides onto the surface using Sortase A mediated enzymatic labelling. Peptides coated surfaces was shown 50 % decrease in the microbial growth on these surfaces. The current approach has an immense potential as AMP promising bioactive molecules which are highly biocompatibility and have less chances of causing bacterial infections.

Biography

Poonam Kumari completed here Master in technology and currently pursuing her PhD from NIPER Guwahati, India. Her Ph.D. work is on "Sortase based biomolecular engineering". During the last one year, she was able to develop a method for the generation of novel protein coding gene libraries, for which an Indian Patent application has been filed. She has screened the surface of S. aureus for evolving novel peptides that bind its surface with high affinity. Apart from her expertise in molecular biology tools set, she also has learned solid phase peptide synthesis, which is an asset for a Biology student. She has synthesized her peptides and analysed them for antibacterial activity. Her work has generated enough results, on which we are about to file a patent and communicate a manuscript from her last one-year work. She has published one research paper also from her thesis work and few are in communication.

Sayan Bhattacharyya*, Atul Raj, Amit Banik, UK Chattopadhyay

AIIH&PH, India

Evaluation of 3 different disinfectants to decontaminate face masks

Introduction: Masks need to be worn in pandemics, like the current COVID-19 pandemic. They have gained popularity and importance among people now. Face masks protect the non-exposed or susceptible persons from acquiring COVID-19, and also stop spread of the virus-laden aerosols from infected or convalescent individuals. However, these masks tend to get contaminated with microbes, with use, which can transmit infections to others. So there is need of disinfectants for removing germs on mask surfaces, without disturbing the filtration efficacy and leaving no chemical residues on surfaces.

Materials and methods: Here 50 masks of each type (cloth /N95 /Surgical, 3 types) were selected. Hence total number of samples was 150. Place of study was laboratory of Department of Microbiology, of our institute. The 3 disinfectants that were tested on mask surfaces were: (a) 76% Ethyl alcohol, (b) A mixture of 1 gram of shredded Betel leaf (Piper longum) (sweet variety) and 1 Gram of torn curry leaves (Murraya koenigii) in 100 ml boiled water, and (c) A mixture of 1 gram crushed Ajwain seeds and 1 gram common lemon (Citrus limon) extract in 100 ml boiled deionized water. Two swabs were taken from the masks, before and 5 minutes after spray with the 3 disinfectants. Each set of disinfectant was tested on each type of mask, although worn by different persons. A spray bottle was used for spraying disinfectant solutions. CLED (Cystine Lactose Electrolyte Deficient) and SDA (Sabouraud's Dextrose agar) plates were used for culturing swabs before and after spraying. After inoculation, plates were incubated at 37 ^{0}C overnight. Next day, colonies were observed for reduction in colony count. Bacteria or fungi isolated were identified using standard tests.

Results: Number of colonies of bacteria like Staphylococcus aureus, other Staphylococci and Micrococcus spp. were reduced significantly (p value<0.05, Z test of significance). Mixture of betel leaf and curry leaves was most effective against bacteria, among these 3 disinfectants. However, these disinfectants did not have much inhibitory effect on Gram negative bacilli, non-fermenters like Burkholderia spp., and fungi.

Discussion: Many chemical agents and others have been used so far for cleaning or disinfecting masks. Our study can help in establishing these 3 different novel types of disinfectants for decontamination of various face masks. There is ample scope for commercialization also in this.

Conclusion: New chemical and herbal disinfectants can effectively reduce microbial count on mask surfaces and thus stop spread of infection from used masks.

Audience Take Away:

- The audience will learn new techniques for disinfecting masks and other forms of PPE
- It will also indirectly help in their job as they can learn and train others new skills

Biography

Sayan Bhattacharyya studied MBBS at Calcutta Medical College, Kolkata and completed MD (Microbiology) in 2008 from PGIMER, Chandigarh, India. He worked as Faculty in many Government Institutes and is now working as Associate Professor, Microbiology in All India Institute of Hygiene and Public Health (AIIH&PH) Kolkata, India. Dr Sayan has won best essayist award on One Health and Rabies (2021), and second best oral paper in STMIDI TROPICON, 2018, Kolkata, and has published 77 research articles in peer-reviewed indexed Medical journals. He is also the editorial board member of many medical journals. His career interests are AMR and Mycology.

Shyamapada Mandal
University of Gour Banga, India

In silico studies support the anti-scrub typhus activity of the bioactive phytocompounds andrographolide and withanolide D

An obligate intracellular bacterium Orientia tsutsugamushi is the causative agent of a febrile disease, scrub typhus, which is endemic to Southeast Asia, including India, wherein there is a recent report on increased emergence of the disease in West Bengal state. The antibiotic treatment failure of scrub typhus prompted us to search for non-antibiotic plant-based therapeutics. Herein we have performed in silico molecular docking of two bioactive phytochemicals, andrographolide (from Andrographis paniculate; Family: Acanthaceae) and withanolide D (from Withania somnifera; Family: Solanaceae) along with a standard treatment, tetracycline against OtDUB (Orientia tsutsugamushi deubiquitylase) protein associated with Orientia tsutsugamushi infection and pathogenesis of scrub typhus. The compound withanolide D (binding energy: -10.2 kcal/mole) had higher affinity to OtDUB compared to tetracycline (binding energy: -9.1 kcal/mole) and andrographolide (binding energy: -8.4 kcal/mole). Both the phytocompounds, andrographolide and withanolide D obeyed Lipinski's rule of without any violation, and both exhibited high GI absorption and no BBB permeation. The current study results signify the effectiveness and importance of the phytocompounds as non-antibiotic therapy for scrub typhus.

Biography

Shyamapada Mandal is Professor and Head of the Department of Zoology, and Dean (Science), University of Gour Banga, India. He is interested on infectious diseases, probiotics, and genomics and bioinformatics research. He did pre-PhD, PhD, and post-PhD research under the guidance of Professor Nishith Kumar Pal at Calcutta School of Tropical Medicine, India. He has published 118 articles with eight book chapters. He is life member of IAMM and IASR, India, and fellow member of SASS, India. Eight national academic and research awards have been conferred to him. He has guided 52 post graduate students; supervised three MPhil and three PhD students, and supervising 7 PhD and one MPhil students. Professor Mandal is among the world's top 2% scientists as per the survey of the Stanford University, published in PLOS (Public Library of Science) Biology (October, 2020). He is featured in the top 2% world scientists list for second consecutive time as published by the Stanford University-Elsevier BV (October, 2021).

Deepak Kumar*[1], Sakshi Behal[2], Rajasri Bhattacharyya[1], Dibyajyoti Banerjee[1]

[1]Department of Experimental Medicine and Biotechnology, Postgraduate Institute of Medical Education and Research, Chandigarh (PGIMER), India 160012.

[2]Department Obstetrics and Gynaecology, PGIMER, Chandigarh, India 160012.

Pseudoesterase activity of human serum albumin

Albumin is a plasma protein that maintains the oncotic pressure of the blood. It also acts as a carrier of lipophilic biomolecules like bilirubin. Recent research highlights that serum albumin exhibits various enzymatic functions apart from the aforementioned properties. Namely, albumin possesses RNA hydrolyzing activity, enolase activity, acrylamidase activity, beta-lactamase activity, peroxidase activity, acetoacetate decarboxylase activity. There is considerable current interest regarding the pseudoesterase activity of human serum albumin, particularly in albumin estimation. However, very little is discussed in the scientific literature regarding the physiological relevance of the albumin's pseudoesterase activity (and the other enzymatic activities). In my talk, I shall focus on the issue mentioned above and discuss the role of the enzymatic function of albumin in health and diseases.

Audience Take Away:

- Pseudoesterase activity of HSA
- How to detect such activity
- How to innovate a method for microalbuminuria detection

Biography

Deepak Kumar has done his PhD degree working under the supervision of Prof Dibyajyoti Banerjee in 2021 from PGIMER, Chandigarh, India. The title of his PhD work is "Development of a novel strategy for rapid detection of human serum albumin pseudoesterase activity – A step towards a novel point of care screening for microalbuminuria". He is currently working as Junior Demonstrator in the Department of Experimental Medicine and Biotechnology, PGIMER, Chandigarh and teaching postgraduate students. Besides, he is also working to understand the effect of post-translational modification of the enzymatic activity of HAS and other relevant enzymes.

Magdalena Hryhorowicz*[1], Daniel Lipinski[1], Agnieszka Nowak- Terpilowska[1], Jacek Jura[2], Wojciech Juzwa[3], Ryszard Slomski[4], Natalia Mazurkiewicz[5], Barbara Gawronska[1], Joanna Zeyland[1]

[1]Department of Biochemistry and Biotechnology, Poznan University of Life Sciences, Poznan, Poland
[2]Department of Animal Reproduction, National Research Institute of Animal Production, Balice, Poland
[3]Department of Biotechnology and Food Microbiology, Poznan University of Life Sciences, Poznan, Poland
[4]Institute of Human Genetics, Polish Academy of Sciences, Poznan, Poland
[5]Institute of Human Biology and Evolution, Adam Mickiewicz University in Poznan, Poznan, Poland

CRISPR/Cas9 system in the generation of genetically modified pigs for purpose of xenotransplantation

CRISPR/Cas (clustered regularly interspaced short palindromic repeats, CRISPR; CRISPR-associated proteins, Cas) system has revolutionized of genetic engineering research and animal biotechnology. Introducing precise modifications in a specific site of the genome is possible due to cellular processes of repairing double strand DNA breaks induced by Cas9 nuclease. The CRISPR/Cas9 technique, thanks to its high specificity, easy construct design and the ability to introduce several of genes, is one of the most promising methods for obtaining multitransgenic animals. The application of the CRISPR/Cas9 technology in pig-to-human xenotransplantation research has enabled enormous development in this field of science. Xenotransplantation is the use of genetically modified animals as a source of cells, tissues, and organs for transplantation into human recipients and pig (Sus scrofa domestica) is the most suitable species for organ donor. Thanks to CRISPR/Cas9 system, pigs with multi-modifications can be obtained, enabling the reduction immune response to a porcine xenograft and inhibiting the processes leading to xenotransplant rejection.

Audience Take Away:

- Audience will have basic knowledge of CRISPR/Cas9 technology in the scope of genome editing
- Audience will have basic knowledge of application of genetically engineered pigs in xenotransplantation
- Students will know typical steps in design and preparation genetic construct using CRISPR/Cas9 system
- Audience will know how to detect and characterize transgenic organisms

Biography

Magdalena Hryhorowicz studied Biotechnology at the Poznan University of Life Sciences, Poland and graduated as MS in 2010. She then worked at the Institute of Human Genetics, Polish Academy of Sciences for two years. After that she joined the research group of Prof. Słomski at the Poznan University of Life Sciences and she received her PhD degree in 2016 at the same institution. The most important achievement of her PhD was the generation and comprehensive characterization of transgenic pigs for purpose of xenotransplantation. Moreover, during her doctorate, she completed an internship at The National Centre for Biotechnology in Madrid (Spain) in the research group of Prof. Lluís Montoliu concerning "CRISPR/Cas9 system- for genetic engineering of large animal models". In 2016 she obtained the position of an Associate Professor at the Poznan University of Life Sciences, Poland. She has published more than 30 research articles in SCI journals/chapters in the books.

Borja G. Leon
Imperial College London, UK

Towards automated decision-making through reinforcement learning

Artificial intelligence (AI) holds considerable promise to tackle challenging decision-making problems such as automated health testing and drug discovery. Among the different AI paradigms, reinforcement learning (RL), a technique that concerns autonomous agents interacting with their environment in the hope to maximise the expectation of a reward signal, has achieved considerable milestones in real-world problems, leading to multiple state-of-the-art solutions. Yet, modelling problems in a fashion where RL is applicable may be non-trivial and require of careful thinking, e.g., if we are building an agent that learns to detect Alzheimer from brain scans, how do we design the problem so that this agent can "take actions" on the given images? and how do we reward such actions so that the agent learns to tell whether there is Alzheimer? Moreover, different families of RL algorithms hold diverse strengths and biases, meaning that evaluating which kind of algorithms is best suited for our problem may be key to success. We will go through all these aspects within RL and continue by providing evidence of how brittle RL solutions can be if we do not take the necessary steps towards robustness and generalisation. Last, for those interested in basic research, we will see some comparisons between RL agents and animal cognition and will review basic tools to test RL solutions before bringing them to costly real-world environments.

Biography

Borja is a third-year PhD candidate in the Department of Computing at Imperial College London. His research focuses on finding new artificial neural network architectures that enable situated agents to fulfil complex human instructions in unseen scenarios. He is also an external thesis advisor at Valencian International University (VIU) on the topic of deep reinforcement learning. Previously, he worked on various applied research projects including autonomous driving and satellite imagery. His contributions to the field of artificial intelligence have motivated his inclusion in the 35 under 35 2021 List of Future Leaders by Santander–CIDOB.

Annie Frelet-Barrand
Institute FEMTO, France

Lactococcus lactis, a promising cell factory to functionally express membrane proteins

Membrane proteins (MPs) play key roles in most crucial cellular processes ranging from cell to cell communication to signaling processes. Despite recent improvements, the expression of functionally folded membrane proteins in sufficient amounts for their functional and structural characterization remains a challenge. Indeed, it is still difficult to predict whether a protein can be overproduced in a functional state in some expression system(s). Prokaryotic expression systems present several advantages over eukaryotic ones. Among them, Lactococcus lactis (L. lactis) has emerged in the last two decades as a good alternative expression system to E. coli. The purpose of this presentation is to describe L. lactis and its tightly inducible system, NICE, for the effective expression of membrane proteins from both prokaryotic and eukaryotic origins.

Audience Take Away:

My presentation on L. lactis and its use for expression of MPs for their functional and structural characterization will help people facing problems of expression of proteins of interest in classical expression systems, either prokaryotic or eukaryotic. It will give practical information while facing troubles/problems of protein expression but also of protein characterization and opens new collaborations

Biography

Annie FRELET-BARRAND studied biochemistry at the University of Franche-Comte (France) and was graduated as MS in 1998. In 2006, she received her PhD degree on MPs characterization at the Institute of Plant Biology, Zurich. During her postdoctoral fellowship (CEA Grenoble, France), she developed L. lactis system for functional characterization of MPs. In 2009, she became CNRS Researcher at CEA Saclay, studying MPs involved in liver detoxification. In 2015, she integrated the Institute FEMTO-ST and is now studying on biochemical and biophysical ways to study proteins and other biological elements. She published 19 research articles and 4 book chapters (h=14).

KEYNOTE FORUM

DAY 02

2ND EDITION OF EURO-GLOBAL CONFERENCE ON

BIOTECHNOLOGY AND BIOENGINEERING

13-14 JUNE

Giovanni Vozzi*[1,2], Francesco Biagini[1,2], Costanza Daddi[2], Carmelo De Maria[1,2], Marco Calvigioni[3], Emilia Ghelardi[3]

[1]Research Center "E. Piaggio" - University of Pisa, Largo Lucio Lazzarino 1, 55122, Pisa, Italy

[2]Department of Information Engineering - University of Pisa, Via G. Caruso 16, 56122, Pisa, Italy

[3]Department of Translational Research and New Technologies in Medicine and Surgery - University of Pisa, Via San Zeno 37, 56127 Pisa, Italy

3D dynamic in vitro model of the human gut microbiota

The word "microbiota" refers to all the microorganisms that reside within human body. Several types of microbiota are associated with different district in our body and, in each of them; the mutualist interaction between the microorganisms and the host plays a critical role in health and disease. For example, an alteration of the human gut microbiota composition, which is the most studied microbial population in our body, seems to have one of the leading roles in the development of several systemic diseases ranging from dementia to autism, from renal (e.g. Pyelonephritis) to hepatic diseases (Non-alcoholic fatty liver disease). Here, we present a dynamic in vitro model for culturing the microorganisms from the human gut microbiota with the principal goal to maintain the complexity of the microbial profile over time and to connect this dynamic module to different cells compartments for studying the interactions between the microorganisms and the host. The entire platform was composed by a gelatin electrospun structure (e.g. a scaffold where the microorganisms were cultured), and the culture chamber which is housed in an anaerobic box (i.e. the anaerobiosis was generated through commercial filters). In particular, we analysed the adhesion and the microbial profile through quantitative RT-PCR. The results showed a batter increase in the adhesion and in the number of microorganisms in the dynamic culture chamber respect to a static control. Also, the chamber was modified to monitor different environmental parameters (e.g. dissolved oxygen and pH) using sensor spots. Finally, to develop a complete dynamic model of the cross-relation between bacteria and human cell in different diseases, the presented platform could be adapted for a co-culture. In particular, a dialyzer-based system has been implemented to physically and chemically isolate the microorganism culture to reduce the mortality of human cells. Results and final data of this work will be further presented at the conference. Here, indirect (i.e. using conditioned media from bacteria culture) co-culture system will be taken in account.

Audience Take Away:

- The audience will learn the importance to study the human gut microbiota and why in vitro system could be the key in this field
- The modularity of our platform, which could be connected to other different bioreactors, could help other researchers to create more complex in vitro model shedding light to the interconnection between the microorganisms and human host in health and disease
- The design process of our platform (which also involved finite element analysis) could be used in other prototype

Biography

Giovanni Vozzi is Full Professor in Bioengineering and director of the degree in biomedical engineering at the University of Pisa, Italy. His research interests include biofabrication, mechanical characterization of biological materials and systems biology. He has published more than 100 papers, 11 book chapters, and holds 21 patents. He is part of Directory board of the International Society for Biofabrication, member of IEEE and of the Italian National Group of Bioengineering.

Vladimir G. Chigrinov

Hong Kong University of Science and Technology, Hong Kong

Liquid crystal photoaligned by azodye nano layers: Physics and applications in displays and photonics

Photoalignment and photopatterning has been proposed and studied for a long time. Light is responsible for the delivery of energy as well as phase and polarization information to materials systems. It was shown that photoalignment liquid crystals by azodye nanolayers could provide high quality alignment of molecules in a liquid crystal (LC) cell. Over the past years, a lot of improvements and variations of the photoalignment and photopatterning technology has been made for photonics applications. In particular, the application of this technology to active optical elements in optical signal processing and communications is currently a hot topic in photonics research. Sensors of external electric field, pressure and water and air velocity based on liquid crystal photonics devices can be very helpful for the indicators of the climate change. We will demonstrate a physical model of photoalignment and photopatterning based on rotational diffusion in solid azodye nanolayers. We will also highlight the new applications of photoalignment and photopatterning in display and photonics such as: (i) fast high resolution LC display devices, such as field sequential color ferroelectric LCD; (ii) LC sensors; (iii) LC lenses; (iv) LC E-paper devices, including electrically and optically rewritable LC E-paper; (v) photo induced semiconductor quantum rods alignment for new LC display applications; (vi)100% polarizers based on photoalignment; (vii) LC smart windows based on photopatterned diffraction structures; (vii) LC antenna elements with a voltage controllable frequency.

Biography

Vladimir G. Chigrinov is Professor of Hong Kong University of Science and Technology since 1999. He is an Expert in Flat Panel Technology in Russia, recognized by the World Technology Evaluation Centre, 1994, and SID Fellow since 2008. He is an author of 6 books, 31 reviews and book chapters, about 317 journal papers, more than 668 Conference presentations, and 121 patents and patent applications including 36 US patents in the field of liquid crystals since 1974. He got Excellent Research Award of HKUST School of Engineering in 2012. He obtained Gold Medal and The Best Award in the Invention & Innovation Awards 2014 held at the Malaysia Technology Expo (MTE) 2014, which was hosted in Kuala Lumpur, Malaysia, on 20-22 Feb 2014. He is a Member of EU Academy of Sciences (EUAS) since July 2017. He got A Slottow Owaki Prize of SID in 2018 http://www.ee.ust.hk/ece.php/enews/detail/660. He is 2019 Distinguished Fellow of IETI (International Engineering and Technology Institute). http://www.ieti.net/news/detail.aspx?id=184 http://www.ieti.net/memberships/Fellows.aspx. Since 2018 he works as Professor in the School of Physics and Optoelectronics Engineering in Foshan University, Foshan, China. 2020-2024 Vice President of Fellow of Institute of Data Science and Artificial Intelligence (IDSAI) Since 2021 distinguished Fellow of Institute of Data Science and Artificial Intelligence

Amy L. Thompson

Austin Peay State University, USA

Brown recluse spider venom holds promise in killing breast cancer cells

Brown recluse spiders, also known as Loxosceles reclusa, are endemic to the Southcentral United States. These spiders are known for their reclusive behavior and necrotic venom. Brown recluse bites can occasionally develop into dry wounds containing dead tissue or cause systemic symptoms. Brown recluse venom is comprised of a mixture of enzymes including lipases, nucleases, and phosphatases, among others with sphingomyelinase D being the most studied enzyme. Because of the nature of this necrotic venom, it can damage cell membranes and holds the potential to kill human cancer cells. Breast cancer is the second most common type of cancer in women and the second leading cause of cancer death behind lung cancer. Certain types of breast cancer cells, such as MDA-MB-231 breast cancer cells, can be especially invasive. MDA-MB-231 cells are triple negative meaning that they lack receptors for progesterone and estrogen and do not have the human epidermal growth factor receptor 2. When cells in this line are exposed to brown recluse venom, they exhibit cell features that are seen in cellular death processes. Some of these changes include condensed and fragmented DNA and cellular blebbing. Venom induced changes also seem to impact sodium channels, which are suggested to impart some of the invasive nature of cancer cells. These studies suggest that brown recluse venom holds promise as a biomedical agent capable of killing cancerous cells and may have therapeutic potential.

Audience Take Away:

- This presentation will provide an overview of the brown recluse spider (Loxosceles reclusa), which has only been identified as being in the Southcentral United States and is one of only three venomous spiders in the U.S
- This talk will help audience members to see that compound, such as venom, initially thought of as toxic, can hold therapeutic potential
- This may encourage researchers to look to their own areas of the world for biological agents that they might study for medicinal properties
- This research focuses on the impact of the venom at the molecular and cellular level only. Faculty may use what they learn to study their own venom or biological agent of interest and may wish to expand this type of research into an animal model
- This type of research can be discussed in the classroom to emphasize the impact that enzymes can have on cell membrane components. Additionally, students often enjoy learning about these spiders and find the use of its venom as a potential cancer treatment interesting

Biography

Amy L. Thompson is a Professor and Chair in the Department of Biology at Austin Peay State University. She earned her Ph.D. from the University of Kentucky in the Department of Molecular and Biomedical Pharmacology and her Bachelors of Science degree from Austin Peay State University in Medical Technology (Clinical Laboratory Science). She teaches Cellular & Molecular Biology, Anatomy & Physiology, Genetics, and Microbiology. Her current research focuses on brown recluse spider venom as a potential treatment for breast cancer and the antimicrobial properties of essential oils. She has published and presented on topics related to brown recluse spider venom, medicinal properties of plants and other biological agents, using popular culture in teaching, and the CDC and WHO response to disease. She is active in the Tennessee Academy of Science and served as the 2021 President. She was named one of the American Society for Clinical Pathology's 40 under 40 and holds Board of Registry Certification in Medical Technology.

magnus Group

SPEAKERS

DAY 02

2ND EDITION OF EURO-GLOBAL CONFERENCE ON

BIOTECHNOLOGY AND BIOENGINEERING

13-14 JUNE

Cornelia Braicu*, Ancuta Jurj, Oana Zanoaga, Ioana Berindan-Neagoe

Iuliu Hatieganu University of Medicine and Pharmacy, Romania

mir-29b inhibits proliferation and induces apoptosis in triple negative breast cancer cells

Triple negative breast cancer (TNBC) is a particular breast cancer subtype, with the worse prognostic, characterised by the lack of expression of progesterone, estrogen and Her2 protein. Alterations of condign and non-coding genes were observed; a particular attention received short non-coding RNAs transcripts, also called microRNAs (miRNAs). Among this class, captured attention a transcript overexpressed in TNBC and correlated with the overall survival rates, as revealed TCGA data. The aim of our study was to investigate the mechanistic role of miR-29b in TNBC, by using a miRNA inhibitor for this transcript, followed by evaluation the cellular and molecular effects on TNBC cells. A model for TNBC was selected BT549 and MDA-MB-231 cells, overexpressing miR-29b. In the case of transient inhibition of this transcript, on selected cell lines was observed a decreased cell proliferation rate and colony number. The fluorescence microscopy tests revealed activation of apoptosis and autophagy. Additional to this functional test, important alterations were observed at transcriptomic level, microarray evaluation revealed 8 upregulated and 11 downregulated miRNAs in BT549 cells, and 33 upregulated and 10 downregulated miRNAs in MDA-MB-231 cells in the group transfected with miR-29b versus negative control group. Additional validation by qRT-PCR of the main target genes revealed overexpression of two important genes that promote the resistance to therapy (MCL1 and BCL2). miR-29b-3p inhibited proliferation and induced apoptosis and autophagy, the molecular mechanism being complex; our data emphasis the activation of the mechanisms responsible for resistance to therapy. Acknowledgement: This study was financed by PCE grant “Testing small molecule targeting mitogen activated protein kinases: Successes, challenges and opportunities in triple negative breast cancer systems- ORIENT”.

Audience Take Away:

- The description of study design, selection of relevant models for study the inhibition of miR-29b, selection of optimal doses, followed by the evaluation of cellular and molecular effect
- Evaluation of miRNA pattern, emphasis the important role of the of some specific mutation in selected cell lines
- Discussion related to the activation of mechanisms responsible for the resistance to therapy, limitation of miR-29b inhibition as treatment strategy

Biography

Cornelia Braicu is a researched at Research Center for Functional Genomics, Biomedicine and Translational Medicine, “Iuliu Haţieganu” University of Medicine and Pharmacy. Dr. Braicu has a background in biotechnology, the major field of interest being functional genomics and she has over 110 ISI papers, of which 35 as first author, h-index (web of science): 32.

Thomas J. Webster
Interstellar Therapeutics, USA

Global warming due to biomaterials?

Biomaterials are composed of some of the same materials as those used in non-medical applications (such as automobile, aerospace, consumer goods, etc.). While these other fields have moved away from using materials that are not environmentally friendly (such as those which contribute to greenhouse gases, are not environmentally degradable, have a large carbon footprint, etc.), the medical device community continues to use non-environmentally friendly plastics, metals, and other materials throughout medicine. This is despite the fact that numerous agencies have found that medical devices contribute to a large component of waste causing greenhouse gases. This is also despite the fact that plastics have been predicted to contribute 2.8 gigatons of CO2 emissions by 2050, up from 850 million metric tons of greenhouse gases in 2019 with only 16% of plastics are currently being recycled. This presentation will highlight the current failures of the medical device industry in promoting the environmentally safe production as well as the use of products that can decrease greenhouse emissions. It will also highlight recent research on the use of natural as well as biodegradable materials for a wide range of medical applications. Most importantly, it will highlight that we need a paradigm shift in all fields, not just non-medical fields but most importantly in medical fields, to reduce greenhouse emissions to reduce global warming.

Audience Take Away:

- How biomaterials have contributed to global warming
- How future biomaterials are being fabricated to reduce global warming and effectively increase tissue growth
- How nanotechnology is being used to promote tissue growth, fight infection, reduce inflammation, and treat COVID-19

Biography

Thomas J. Webster's (H index: 108; Google Scholar) degrees are in chemical engineering from the University of Pittsburgh (B.S., 1995; USA) and in biomedical engineering from RPI (Ph.D., 2000; USA). He has served as a professor at Purdue (2000-2005), Brown (2005-2012), and Northeastern (2012-2021; serving as Chemical Engineering Department Chair from 2012 - 2019) Universities and has formed over a dozen companies who have numerous FDA approved medical products currently improving human health. Dr. Webster has numerous awards including: 2020, World Top 2% Scientist by Citations (PLOS); 2020, SCOPUS Highly Cited Research (Top 1% Materials Science and Mixed Fields); 2021, Clarivate Top 0.1% Most Influential Researchers (Pharmacology and Toxicology); and is a fellow of over 8 societies.

Debabrata Das*[1], Prakriti Das[2], Aranya Das[3] and Santa Ana Das[4]

[1]ICAR-CIFRI, India

[2]Department of Biotechnology, Amity University, New Town, Kolkata 700157, W Bengal, India

[3]Department of CSE, Chandigargh University, Mohali, Chandigarh, India

[4]AIMA Academy in Modern Ayurvedics, North Ghugia, Chakdaha, Nadia 741222. W Bengal, India

The ecotechnlogy of modern ayurveda can effectively spoil all the evils, virions, microbes which are mere foreign-proteins can easily gets denaturated with plants' acids (PH < 6.5) Or plants' alkaloids (PH > 8.0) For mankind

Ecotechnlogy with modern Ayurveda can effectively spoil virions, microbes, mere foreign-proteins, unlike multi-cellular can easily get denatured with plants acids (ph < 6.5) or with plants alkaloids (ph > 8.0) study found in fisheries and mankind The very well fact to mankind is that pathogenic or foreign-proteins, namely virus and bacteria can be denatured with mild Ayuyrvedic acids or Alkaloids. Ground-truth microbial counts and digital parameters of ecology can find relations viz. machine learning techniques, of departing hydrophilic viruses, microbes with hydrophobicity of hydrocarbons or else reactive Isoprene.. In earlier studies author found that hydrocarbon Isoprene the smallest unit of essential Authors are running Ayurveda gardens with fascinating plant specieses namely Justasia spp and Citrus plants those are releasing plants acids, Isoprene etc can protect and prevent any viruses with Isoprene instant proofs. May be gene editing of of all evil viruses with Isoprene remains be pre historic and established since Ayurvedic era Modern digital-research of Chromatography, Distillations or digital electronics can find that Isoprene and few others when emitted by plants or algae can prevent viruses and with a fact that oldest prescription of Ayurveda may be the worthiest to the mankind. Also naturally gene-editing possible with Ayurveda science since pre-historic era and re-invented. Today Ayurveda science may be as advanced and authentic with perspective to gene editing or gene-therapy. In recent years we find whole world is full panicked with every word-goes starting with viruses, their all kind of mutants etc. However once we take very worthy Isoprene to Terpenoids from plants and Fatty bio-molecules etc. This may be God gifted bio-molecules that prevent and cure virus attack or even its mutants by damaging their genetic traits. Modern Ayurveda says any anomaly in mankind caused by viruses or its mutants can be cured with natural gene-editing plants i.e. Justicia spp, with stated Ayurveda science containing Isoprene, acting gene-editing enzyme, non conventional and non protein bio-molecule by forming isoprene phosphate reversibly, along with all the precursors of desiring genetic-base materials such as Purine and Pyrimidine obtainable from very popular Alkaloid biomolecules namely Vasicine, Vascineone and Quinazoline, respectively sourced from Justacia spp, or else simply fed them with Citrus spp or Switenia mahagony leaves all this containing Isoprene and hence animals fed gets escaped from any kind of virus diseases. All this Ayurvedic plants since pre-historic era and proven true Ultra natural all the mentioned biomolecules also obtainable at their respective temperature of vapour point (vp) from individual plant extracts. Whereas examples are given with aquatic data of fisheries environments.

Biography

Debabrata Das experienced Senior Scientist skilled in Molecular Biology, Life Sciences, Data analytics science, and Statistics modellings. Strong research professional with a Doctor of Philosophy (Ph.D.) focused in Bio-Statistical and Eco-technological modelling from School of Biotechnology (BHU), Indian Agricultural Statistics Reserach Institute (IARI).

Manisha Mandal
MGM Medical College, India

Circulation of sars-cov-2 genetic clades in wastewater

Background and objectives: Recent studies have witnessed the emergence end reemergence of SARS-CoV-2 variants leading to a succession of epidemic waves worldwide. The monitoring of SARS-CoV-2 variants in sewage is important for understanding the epidemic evolution and spread of COVID-19 in the environment alongside evaluating the efficiency of its control measures. Thus, the present study was carried out to monitor the presence and evolution of SARS-CoV-2 variants in sewage water.

Methods: The DNA sequences extracted from waste water samples and submitted to GISAID (https://www.gisaid.org/) were retrieved and the nucleotide as well as the translated protein sequences were subjected to pairwise alignment against the reference strain SARS-CoV-2 Wuhan-Hu-1/2019 (genbank: MN908947) using modified algorithm of Smith-Waterman with affine gap-cost. Three genomic nomenclature systems i.e., Nextstrain (https://clades.nextstrain.org/), GISAID (https://www.gisaid.org/), and Pango (https://cov-lineages.org/) were applied to the submitted sequences. The alignment process consisted of indexing the reference genome using the Burrows Wheeler Aligner (BWA) and aligning the reads to the reference genome using the BWA-MEM algorithm. Samtools were used for the downstream analyses of the alignment file. Nucleotide substitution, deletion, and insertion variants were called using freebayes tool and related statistics were extracted using BCFtools. Phylogenetic analysis was carried out using distance metrics method between the query sequence and reference node, followed by clades assignment (https://clades.nextstrain.org/). Heatmaps were done in Rstudio using the Pheatmap package (https://cran.r-project.org) and matplotlib in python (https://www.python.org) were applied for data visualization.

Results: A total of 2731sequences related to waste water samples were submitted to GISAID between April 14 2020 to April 19 2022, from countries including Austria (n=2618), USA (n=72), Liechtenstein (n=22), Brazil (n=15), Italy (n=2), and Mexico (n=1). The GISAID nomenclature revealed the prevalence of clades GK (n=1174), GRA (n=1135), GRY (n=141), G (n=135), GR (n=128), GH (n=9), O (n=5), GV (n=4) in sewage water. According to Nextstrain naming system, the clades circulating in waste water were 21A (Delta) (n=890), 21L (Omicron) (n=607), 21J (Delta) (n=354), 20I (Alpha, V1) (n=265), 20A (n=67), 20B (n=22), 21M (Omicron) (n=13), 21I (Delta) (n=3), 20E (EU1) (n=2), 21H (Mu) (n=1). As per Pango definition, the major lineages comprised B.1.617.2 (n=886), BA.2 (n=591), BA.1 (n=378), B.1.1.7 (n=264), AY.43 (n=132), BA.1.1 (n=88), B.1 (n=50), AY.4 (n=40). The Delta-Omicron recombinant virus (n=24) derived from the GK/AY.4 and GRA/BA.1 lineages, consisted of variants XQ (n=12), XM (n=5), XE (n=2), XF (n=2), XD (n=1), XT (n=1), and XN (n=1). The Delta variant detected from waste water comprised of T478K, D614G, P681R, T19R, D950N, R158G, and G142D (decreasing order of percentage) as the major spike mutations in the overall submitted sequences (range: 76 to 61%, mean±SD: 73±6%). The omicron variant displayed D614G, N679K, N969K, K417N, H655Y, P681H, Q954H, N764K, D796Y, T478K, Q493R, Q498R. Y505H, N440K, S477N, E484A, N501Y, G446S, G496S, G339D, S373P, S375F, S371F, T376A, A27S, G142D, R408S, T19I, V213G, D405N, T547K, A67V, T95I, Y145D, L212I, N856K, and L981F, in descending order of the percentage of waste water based nucleotide sequences deposited in GISAID (range: 99 to 32%, mean±SD: 76±23%). The results showed that the 21J (Delta) and 21A (Delta) clades in Austria were first detected from waste water samples on December 28 2020 and January 16 2021, respectively, at least five months prior to being detected in clinical samples from the same area, i.e., on May 28 2021 and June 18 2021, respectively, implying the significance of wastewater surveillance in the identification and tracking of SARS-CoV-2 in the population.

Conclusions: The spatio-temporal distribution of SARS-CoV-2 genomic variants based on the DNA sequences extracted from wastewater and submitted to GISAID up to April 19 2022, are represented here in this study using three genomic nomenclatures. The associated multiple mutations in Spike protein of SARS-CoV-2 featuring the emerging epidemiological

variants have been determined that help to enumerate the diversity of SARS-CoV-2 strains circulating in the environment.

Audience Take Away:

- Wastewater surveillance approach is important for monitoring variants of concern in the community
- This is important for implementing proper health decisions, organizing and optimizing resources towards management of COVID-19

Biography

Manisha Mandal has her expertise in the field of molecular epidemiology of infectious diseases, data analysis using bioinformatic 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.

Christoph Koppl*[1], Monika Cserjan-Puschmann[1,2], Nico Lingg[1,2], Gerald Striedner[1,2]

[1]ACIB-Austrian Centre of Industrial Biotechnology, Muthgasse 18, 1190 Vienna, Austria

[2]Department of Biotechnology, University of Natural Resources and Life Sciences, Vienna, Muthgasse 18, 1190 Vienna, Austria

Combinatorial fusion tag yields powerful platform process for the production of pharmaceutically relevant proteins

Expression of complex recombinant proteins in E. coli is a major challenge in industrial biotechnology as the protein of interest is often produced with very low titres or misfolded as inclusion body. One possibility to circumvent these problems is the use of fusion partners. Unfortunately, fusion tags can vary greatly in their effectiveness, which is often dependent on the protein of interest. We found that a solubility tag originating from the gene 10 of the T7 bacteriophage can greatly increase recombinant protein titres of multiple relevant biopharmaceutical proteins. Due to its small size of only 22 amino acids, this fusion tag keeps the exerted additional stress on the cellular transcription machinery on a minimal level. The effectiveness of the fusion tag has been evaluated in carbon limited laboratory scale fed-batch fermentations. There, specific recombinant protein titres could be increased by a factor of greater than two compared to expression of the native protein. Since the fermentations were performed under identical conditions, this effect can be attributed solely to the fusion tag which was fused to the N-terminus of the proteins of interest. Furthermore, this fusion tag can be coupled with a pentapeptide cleavage site, resulting in highly efficient and specific cleavage by a human caspase-2 variant. The cleavage is largely independent of the N-terminal amino acid of the protein of interest, which makes this system universally applicable. The combination of the expression enhancing fusion tag with the caspase-2 protease system for efficient tag removal yields a highly capable system to produce challenging recombinant proteins in E. coli, offering an attractive production platform for biopharmaceutical industry.

Audience Take Away:

- Insight into a state-of-the-art fusion protein technology applicable to the production of native pharmaceutically relevant proteins
- Knowledge of a technology that greatly improves the manufacturability of challenging recombinant
- Proteins in Escherichia coli
- Knowledge about fusion tag design, and its influence on recombinant protein production in glucose limited fed-batch fermentations
- Insight into a practical solution that simplifies downstream processing and de-tagging of fusion proteins

Biography

Christoph Koppl graduated from the master's program Biotechnology at the University of Natural Resources and Life Sciences, Vienna as Dipl.-Ing. in 2020. Shortly after, he joined the research group of Univ. Prof. Dr. Gerald Striedner at the Department of Biotechnology (University of Natural Resources and Life Sciences, Vienna). He is currently enrolled in the doctoral study program Bioprocess Engineering (University of Natural Resources and Life Sciences, Vienna) and started his doctoral thesis at the Austrian Centre of Industrial Biotechnology, Vienna in October 2021. So far, he has contributed to three research articles published in SCI (E) journals as co-author.

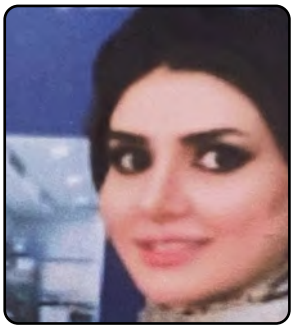
Lopamudra Dey
Heritage Institute of Technology, India

Machine learning techniques for sequence-based prediction of viral host interactions between sars cov 2 and human proteins

The coronavirus disease (COVID-19) pandemic, which is caused by a unique strain of coronavirus called severe acute respiratory syndrome corona virus 2 (SARS-CoV-2) virus infection, is one of the most important diseases in the current situation, according to the World Health Organization (WHO). It has infected over 15 million people in over 200 countries, resulting in the deaths of about 0.6 million people. The disease has put enormous strain on healthcare systems all across the world. The first instance of the new corona virus infection was reported in the Chinese city of Wuhan at the end of 2019. Its fatal effect is now endangering the entire world, from Asia to Europe and America. In addition to many accessory proteins, SARS-CoV-2 contains four primary structural proteins: spike (S) glycoprotein, small envelope (E) glycoprotein, membrane (M) glycoprotein, and nucleocapsid (N) glycoprotein. Understanding how these viral proteins interact with host cells in order to survive and reproduce is critical for therapeutic development. SARS-genetic CoV-2's traits must be fully recognised in order to combat the virus. It is a single-stranded RNA virus with particle sizes ranging from 65 to 125 nm in diameter and a genome size of roughly 27–32 kb. The world's healthcare institutions are frantically hunting for a vaccine to stop the virus from spreading. Aside from that, they segregate the infected patients and treat them with conventional medicine as soon as possible. One method viruses communicate with their hosts is through protein–protein interaction (PPI). The discovery of PPIs between virus and host proteins aids in the understanding of how virus proteins function, propagate, and cause disease. Experimental ways for detecting PPIs have been developed throughout the last few decades. Nonetheless, these high-throughput experimental screens are generally employed to classify intra-species PPIs, leaving inter-species interactomes relatively unexplored. PPI identification in the lab, on the other hand, is typically time-consuming, labor-intensive, and challenging to generate comprehensive protein interactomes. As a result, efficient computational methods for PPI prediction are employed to bridge the gap by offering experimentally testable hypotheses and discarding protein pairs with a low chance of interaction, reducing the number of PPI candidates to be considered. Computational techniques have been popularly used for predicting viral–host interactions previously. To predict the PPIs between corona virus and human proteins, several machine learning models may be created, which are then confirmed using biological tests, gene ontology, and KEGG pathway enrichment analysis. Anti-viral drug discovery can also be aided by the identification of several repurposable medicines that target the expected interactions.

Biography

Lopamudra Dey completed B-Tech from West Bengal University of Technology, Kolkata, India in Computer Science and Engineering in 2009. She received a Bronze medal in her Bachelor degree. In 2011, she completed M.tech. from University of Kalyani, West Bengal India. She obtained her Ph.D. in Computer Science from Kalyani University in 2021. She is also working as an Assistant Professor in the Department of Computer Science and Engineering in Heritage Institute of Technology, Kolkata, India. Her areas of interests include Bioinformatics, Data Mining, and Network Security. She has published more than 10 research articles in SCI(E) journals.)



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

[1]Biophysics, Physics department, Faculty of Science, Mansoura University, Mansoura, Egypt.

[2]Nuclear medicine department, Faculty of Medicine, Kasr Alainy, Cairo University,Cairo, Egypt.

[3]Theoretical Physics, Physics department, Faculty of Science, Mansoura University, Mansoura, Egypt.

Formation and development of liposomes encapsulated radiotracer and assisting the uptake of imaging studies

Liposomes are closed and spherical,l with one or more lipid bilayers, which form an internal cavity that can carry aqueous solutions. Llipid bilayers are composed of two sheets of tightly arranged phospholipids. The ability of liposomes to function as a drug delivery system can be affected by the number and rigidity of the lipid bilayers, as well as their size and surface charge, lipid organization, and surface modification. An animal-stage study of nanoparticle agents with 99mTc aimed to assist in the biophysical characterization and biodistribution of 99mTc labeled with nanoparticles, with the additional aim of demonstrating its toxicity, clearance, distribution, safety, and effectiveness. A further aim was to develop various techniques in order to reduce the size of the nanoparticles, as well as testing the zeta potential, while adding cationic particles to enhance the drug encapsulation. New Zealand rabbits were included in this study after being anesthetized with 2:1 ketamine/xylazine intramuscularly. Neutral liposomes were used in addition to the cationic nanoparticles. Baseline levels were determined to compare the new agents using nanoparticles with tracers without nanoparticles. Static and dynamic images with matrix size of 256x1024 were acquired, using a Symbia gamma camera immediately and one hour after intravenous injection. The biodistribution then was tested by obtaining the count rate of each organ and calculating the organ/organ ratio; the clearance was also studied. Both the neutral and the cationic nanoparticle agents showed fast clearance, as well as better targeting and localization in the organs, compared to the 99mTc tracer without nanoparticles. Further research will aim to test other nanoparticles of different types, with different surface chemistries, surface modifications, and sizes, to support these investigations.

Audience Take Away:

- Audience will be able to identify the liposomal loading techniques using different types of parameters
- Also understanding the factors and methods to use in order to reduce the size of the nanoparticles
- The utilization of liposomal agents encapsulated radiopharmaceutical agents

Biography

Anfal M. Alkandari (Nuclear medicine specialist) 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.

Aakanksha Kalra*, Akansha Mathur, Harshita Jonwal, Vikky Sinha and Aditi Nag

Dr. B. Lal Institute of Biotechnology, India

ESKAPE pathogens in the Indian subcontinent: A comprehensive analysis

ESKAPE pathogens are a group of antibiotic resistant gram positive and gram negative bacteria which are the causative agents for multiple nosocomial and community-acquired infections. ESKAPE refers to E. faecium, S. aureus, K. pneumoniae, A. baumannii, P. aeruginosa, and Enterobacter spp.; top priority pathogens as recommended by WHO which are posing a global threat to human health. Thus, the present study is focussed to consolidate the clinically relevant information on the ESKAPE and epidemiology of these pathogens throughout the Indian subcontinent. In addition to epidemiology, the study is focused on the antibiogram profiling of these pathogenic isolates, a crucial assessment for accurate and appropriate treatment strategies. The epidemiological analysis of these pathogens was done using the data from the clinical sample reports collected via LIS Software in the duration of January 2020 to February 2021, from Microbiology Department of Central Laboratory at Dr. B. Lal Clinical Laboratory Pvt. Ltd. The analysis involved the demographic details of the sampling process as well as the rate of infectivity by these pathogens and their correlation to multiple essential parameters including gender, age, sampling type, temperature and humidity. Similarly, the antibiogram profiling was performed to analyze the pathogenic isolates towards multiple antibiotics belonging to all the four generations. Antibiogram profiling of these clinical isolates were used to compare the susceptibility pattern and monitor the resistance trends over time within the isolates. Surprisingly, it was found that the majority of the isolates were sensitive to 1st generation antibiotics but showed resistance to 2nd, 3rd and 4th generation antibiotics. Majority of the AMR analysis done so far has been in the developed economies with well-planned medical facilities. Thus, the current study would be a case study for an economically weaker set up with compromised medical facilities. The current analysis would be useful to analyze the AMR situation caused by ESKAPE pathogens and would thus highlight the severity of the situation in order to plan appropriate preventive measures.

Audience Take Away:

- Current status of AMR and pathogenic isolates in a developing nation
- It would help the budding researchers to design their study
- It would highlight the importance of statistical analysis and epidemiology in medical sciences

Biography

Aakanksha Kalra, PhD from International Center for Genetic Engineering and Biotechnology, New Delhi, India. She has done her M.Sc. in Life Sciences from Jawaharlal Nehru University, New Delhi, India. She has expertise on various domains of biotechnology including immunology, molecular biology, microbiology, parasitology and animal cell culture technology. She has 7 research articles in international journals focusing on multiple disease causing organisms such as Candida, Plasmodium, etc.

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Marek Koutny*, Jana Sera, Veronika Kucabova
Tomas Bata University in Zlin, Czech Republic

Microbiology of biodegradation with selected biodegradable polymers in soil

Plastic leaking into the environment represents one of the major environmental concerns nowadays. Part of the solution is the replacement of conventional plastics with suitable biodegradable polymers. This especially useful in application where the items cannot be easily retri eved from the environment for example in agriculture. Here the biodegradation of the polymer items is expected to take place in soil, and it is of interest what mechanism and what microorganisms take place in the process. Such knowledge can be useful for further rational design of future polymer materials. Microorganisms related to biodegradation of PBAT, PHB and PBS biodegradable polymers were investigated in soil. All mentioned polymers are essentially polyesters but still they differ substantially in their property which is also translated into differences in the rates of their biodegradation in soil. DNA form the surface of the material was isolated in appropriate time intervals and 16r and 18r RNA genes were amplified and sequenced. Data were further processed to assign abundance and taxonomic categories to individual OTUs. Composition and dynamic of microbial communities for individual materials were observed and compared; especially the participation of bacteria and fungi part of microbial community on the biodegradation process was estimated. Results show that different polymers need slightly different microbial groups for their biodegradation especially in relation to the rate of their biodegradation in soil. Roughly this can be described as a difference between slow and fast degrading polymers. The finding is of interest for certain applications where the polymer product must withstand certain time period in the biotic environment, e.g. in soil, without actual biodeterioration before the biodegradation process is welcomed.

Audience Take Away:

- groups of microorganisms important for the polymer biodegradation in soil
- differences between biodegradation of major biodegradable polymers
- relative importance of bacteria and fungi in the polymer biodegradation

Biography

Marek Koutny obtained master and Ph.D. in biochemistry at Masaryk University in Brno, Czech Republic. From 1999 he joined Brno Technical University and later Tomas Bata university in Zlín. In 2004-2005 he spent as a postdoctoral fellow at Clermont University in France. He then returned to Tomas Bata University where he works up to now finally obtaining a full professor position.

Debabrata Das

FRAI Division, ICAR-CIFRI, Barrackpore, Kolkata

May natural Gene-editing with techie ayurveda science

Today Ayurveda science may be as advanced and authentic with perspective to gene editing or gene-therapy. In past years we find world is full of panicked with every word-goes starting with viruses, their all kind of mutants etc. Later on panicked continued with micro or nano particle of Plastics as a carcinogenic materials in a new civilizations when a time throwing plastic to the environment. A single gram plastic can create a few billion plastic nano-particles harming health and acute environmental damage all around and further destroying a few acres of virgin geography, all turning all very poisonous and damaging worthy the environment for every plastics materials have hazardous roles in every biology as carcinogenic although this may be antivirus but not desirable. However once we take very worthy Isoprene to terpenoids from plants and Fatty biomolecule etc. This may be god gifted biomolecules that can prevent and cure virus attack or even its mutants by damaging their genetic traits. Modern Ayurveda says any anomally in mankind caused by viruses or its mutants can be cured with natural gene-editing plants i.e. Justicia spp, with stated Ayurveda science containing Isoprene, as gene-editing, non-conventional and non protein enzymes by forming isoprene phosphate reversibly, along with all the precursors of desiring genetic base materials such as Purine and Pyrimidine obtainable from very popular alkaloid biomolecules namely Vasicine, Vascineone and Quinazoline, respectively sourced from Justacia spp, Ayurvedic plants since pre-historic era.

Biography

Debabrata Das experienced Senior Scientist skilled in Molecular Biology, Life Sciences, Data analytics science, and Statistics modellings. Strong research professional with a Doctor of Philosophy (Ph.D.) focused in Bio-Statistical and Eco-technological modelling from School of Biotechnology (BHU), Indian Agricultural Statistics Reserach Institute (IARI).

Participants List

Dario Puppi University of Pisa, Italy	07
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Vladimir G. Chigrinov Hong Kong University of Science and Technology, Hong Kong	**27**
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Cornelia Braicu Iuliu Hatieganu University of Medicine and Pharmacy, Romania	**30**
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