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Scientific Tracks & Abstracts

(Day 1)

Abdelaziz Tlili et al., J Biotechnol Biomater 2016, 6:5(Suppl)
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Mutation spectrum of common deafness: Causing genes in patients with non syndromic deafness in UAE population

Abdelaziz Tlili, Abdullah Fahd Al Mutery and **Walaa Kamal Eddine Ahmad Mohamed**
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Congenital genetic disorders are important at all levels of health care due to their significant burden on affected individuals and societies. They may be caused by genetic factors or be triggered by environmental exposures. High prevalence of consanguineous marriages is present in many communities throughout the world, especially countries of the Middle East and North Africa. Due to high consanguinity rates in these populations an increased rate of congenital monogenic disorders, particularly non syndromic autosomal recessive hearing loss (NSAHL) were noticed. This condition accounts for a substantial numbers of birth defects and disabilities among live births in UAE. Therefore, unravelling the genetic causes of NSAHLs is of great value for families and society as a whole. To provide accurate genetic testing and counseling in the UAE population, we investigated the molecular etiology of non syndromic deafness in UAE deaf population. Unrelated affected individuals with hearing impairment (n=60) were recruited for this study. Two common deafness-related genes, GJB2 and mtDNA 12SrRNA were analyzed using all exon sequencing. GJB2 mutations were detected in 15% (9/60) of the entire cohort. The mutation rate of mtDNA 12SrRNA in this group was 5% (3/60). These findings show the specificity of the common deaf gene mutation spectrum in UAE. According to this study, there were specific hotspot mutations in UAE deaf patients. Comprehensive sequencing analysis of the two common deaf genes can help portray the mutation spectrum and develop optimal testing strategies for deaf patients in UAE.

Biography

Tlili received his Ph.D. in biology engineering from National Engineering School of Sfax, Sfax university, Sfax-TUNISIA in 2007. During his Ph.D., he worked on genetic of deafness in Tunisian population. He spent two years as a Postdoctoral Fellow at the Pasteur institute (France). Tlili joined the Department of Applied Biology, University of Sharjah, Sharjah, UAE as a Full-time Assistant professor. He taught several courses in biology including Mendelian genetics, general biology, molecular biology, human molecular genetics and supervised several undergraduate and graduate students to conduct their research projects at his laboratory. Dr. Tlili has published several scientific papers through different research proposals granted as principal and associate investigator, in different abstracted, refereed and indexed Journals. Most of these papers were in the area of human molecular genetics. Also he has participated in several local, regional and international meetings to present his work as a talk or as a poster. Tlili is quite interested in working at a prestigious institute of high standards both in academic and research because this will give him the opportunity to establish a research network involving different laboratories in UAE and abroad.

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Notes:

Glaucia C Pereira et al., J Biotechnol Biomater 2016, 6:5(Suppl)
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A multi-layer non-Newtonian model of cardiovascular inflammation

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Cellular functions related to the maintenance of homoeostasis are regulated by shear forces sensed by endothelial cells. The endothelial cells sense local changes in shear stress. The resulting signals are either transduced into chemical responses or transmitted to the surroundings to regulate the cellular activity. In the current literature, models of blood flow applied to the characterization of atherosclerotic plaques consider blood as a Newtonian fluid because of the characteristic length of the domain. At predilection sites for plaque deposition, the diameter of the blood particles is much smaller than the normal arterial diameter. However, under disease condition, the proportions can dramatically change due to a reduction greater than 80% in the arterial cross-section, in cases of severe stenosis. Here we show that in diseased arteries, the local particle concentration can peak at locations associated to high inflammation. We found that such locations are correlated to the vulnerable plaque phenotype, which is prone to rupture. Our results demonstrate that at locations of high particle concentration, blood particles change the shear stress distribution and magnitude. Therefore, the non-Newtonian blood flow assumption provides new insights in the characterization of plaque built up. These results are combined to *in vitro* experiments that suggest the influence of blood particles in the activity of cytokines. An unbalance in pro and anti-inflammatory cytokines has been associated to an increase in inflammation and, consequently, in the volume of plaques forming. We anticipate our work to be a starting point for a more sophisticated multi-scale model, which combines experimental findings and computational modeling to characterize arterial segments affected by atherosclerosis. Such model includes a coupling between the distending arterial wall and the non-Newtonian blood flow.

Biography

Glaucia C Pereira is a Principal Investigator in Machine Learning and Bioinformatics at the Icelandic Institute for Intelligent Machines. She is a former Member of Imperial College London and a past Researcher Visitor at the University of Cambridge, where she worked with microfluidics and computational bio-fluid mechanics applied to cardiovascular inflammation. She has also worked for both the Spanish and the Brazilian government, as a Researcher. She is currently applying knowledge from biomedical engineering, mathematics and computational systems engineering, while leading projects in the field of biotechnology, aiming at advancing knowledge in basic sciences and translational biomedicine.

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Protein-protein and peptide-protein interactions to elucidate protein and cell structures as well as to modulate pharmacological barriers

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Pharmacological barriers are formed via extracellular loops (ECLs) of tight junction (TJ) proteins, such as claudins (Cldns). Thus, Cldn petidomimetics were designed as drug enhancer of the blood-brain barrier (BBB). Cldns, transmembrane proteins, limit paracellular permeation of pharmaceuticals. The tightening is achieved by protein-protein interaction between Cldn-ECLs from opposing cells. Consequently, modification of Cldn integrity by the respective peptidomimetics is proposed to enhance drug delivery through the BBB. The Cldn1 and Cldn5 derived peptides C1C2 and C5C2 were tested for structural, binding and barrier modulating properties. C1C2 revealed a beta-sheet flanked by an alpha-helix, a structure modeled in the Cldn1-ECL1 also. C1C2 affected the TJ strand morphology and transiently increased the permeability through a cell culture model of the BBB. Redistribution of various Cldns from TJs to cytosol suggested interactions with other Cldns subtypes also. FRET measurements verified heterophilic interactions between different Cldns isoforms. Analysis in TJ-free HEK-293 cells transfected with Cldn1, -2, -3, -4 or -5 identified Cldn1 and 5 as direct targets. Binding measurements (microscale thermophoresis) with full-length Cldns and recombinant ECLs confirmed these findings with k_d-values in nanomolar range. Association studies of peptides and recombinant ECLs on live-cells further confirmed the target selectivity. Freeze-fracture electron microscopy exhibited alterations in the TJ-architecture of Cldn5 by drastic P to E face transition and altered shape of the Cldn1 TJ-network with enhanced number of parallel strands. C5C2 increased the permeability of a brain endothelial cell barrier. Transmission electron microscopy showed opening of interendothelial TJs. Binding of C5C2 to Cldn5 showed also nanomolar affinity. C5C2 administration in mice resulted in concentration and time dependent BBB opening (marker uptake into brain, magnet resonance imaging). In summary, the Cldn peptidomimetics C1C2 and C5C2 transiently enhanced the paracellular permeability of Cldn1 and Cldn5 expressing cell barriers by affecting TJ localization and structure. The findings recommend Cldn peptidomimetics as templates to elucidate molecular and cellular TJ structures and as candidates to improve drug delivery to the brain.

Biography

Ingolf Blasig studied biology and biochemistry in Leipzig from 1970-74. His diploma thesis was on cancer research at the Robert-Rössle-Hospital in Berlin, his dissertation dealt with the pharmacology of myocardial infarction at the Academy of Sciences (1984). He obtained his venia legendi for investigations on myocardial dysfunction at the University of Halle in 19992. From 1993-95, he was awarded project leader at the NIH, USA. Since 1992 he has been head of the independent research group for Molecular Cell Physiology at the FMP and is teaching at the universities in Potsdam and Berlin.

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Rosana Zau Mafra et al., J Biotechnol Biomater 2016, 6:5(Suppl)
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Alternative extraction of bergenin: A case study of valuation for technology transfer

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This research aimed to evaluate the alternative extraction process of bergenin from *Endopleura uchi*. Valuing a technology means to quantify its monetary value and can be used to sell and/or license technologies, analyze risks of investing in R&D and prioritize R&D projects. There are several methods to Valuate and they vary according to the company, the technology, the strategies adopted, etc. and can be analyzed from the perspective of the buyer or seller. To achieve the goal stated for this research, it was necessary to discuss the technology transfer process, identify the methods of valuation existing, characterize the object of study technology and apply the quantitative data related to the technology (extraction process) to the valuation method chosen. The valuation method used was the Discounted Cash Flow as it is a widely discussed approach and taught at universities, along with the cost approach, among different methods of valuation. It was collected data related to revenues, costs and expenses, taxes, etc., in order to get the required cash flow and their respective discount rates and therefore valuate the technology. Given the uncertainties and risks from the innovative process, it was possible to calculate the terminal value (TV) of technology, which is highly scalable when succeed. Based on its terminal value (TV) (near to U$ 6,000.000) and estimates of revenue (more than U$ 400,000), this technology is highly profitable both for transfer and/or for production.

Biography

Rosana Zau Mafra has completed her Masters in Natural Resources Economics. She is a Professor at Department of Economics and Analysis, Social Studies Faculty of Amazonas Federal University (UFAM), Brazil.

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Sonia Malik, J Biotechnol Biomater 2016, 6:5(Suppl)
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Biotechnological approaches for the production of anticancer compound shikonin and their derivatives from *Arnebia euchroma* (Royle) Johnston

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Shikonin and its derivatives are the commercially most important naphthoquinones pigments, known for their wide range of pharmaceutical properties including anticancer activities. These compounds have also been used traditionally as natural dyes for coloring silk, in cosmetics and as food additives. *Arnebia euchroma* (family Boraginaceae) is considered as one of the sources of shikonin derivatives. It is a perennial herb of alpine belt and distributed between 3000-4200 m in drier areas. Aseptic cultures of *A. euchroma* were established from rhizome buds and shoots were cultured in liquid and agar-gelled medium supplemented with various concentrations and combinations of plant growth regulators. To study the production of shikonin derivatives, cell were cultured in production medium and culture conditions as well as media components were standardized to get the optimum production of compounds. To enhance the production of these compounds from cell culture, attempts were made to genetically transform the cells. Cell suspension cultures of *A. euchroma* were observed to produce increased amount of shikonin derivatives in two phase culture system and their scale up studies in bioreactor showed the possibility of its large scale production to meet its growing demand by various pharmaceutical industries. Thus, the present study would help in conservation of this medicinal plant species which is at the risk of becoming extinct and can meet the ever increasing demand of shikonin derivatives for their commercial production.

Biography

Sonia Malik is working as a Professor at Biological & Health Sciences Centre, Department of Biology, Federal University of Maranhão, Sao Luis. Her area of research involves *in vitro* production of plant secondary metabolites and metabolic engineering. She is an active member of post-graduate research program at Federal University of Maranhão. She has won many awards and recognitions for her work. Her international experience includes various programs, contributions and participation in different countries for diverse fields of study. She has been awarded with FAPEMA Senior Researcher grants in August 2015. Her research interests reflect in her wide range of publications in various national and international journals. She is the Editorial Board Member and reviewer of scientific journals.

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Iman Emam Omar Gomaa et al., J Biotechnol Biomater 2016, 6:5(Suppl)
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Chlorophyllin derivatives mediated PDT: A new ray of hope in the horizon for cancer treatment

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[3]Friederich Schiller University of Jena, Germany

Photodynamic therapy (PDT) is an approved clinical treatment with minimal invasiveness for different types of cancers. It has the advantage of high selectivity towards tumor tissue and lack of severe and systemic complications with the possibility of harmless repetitive applications. Its mechanism of action involves activation of a photosensitizer (PS) by an appropriate monochromatic light source with long wavelength for deeper tissue penetration. Chlorophylls are photosynthetic pigments present in all organisms that convert light energy into chemical energy. The tetrapyrrolic ring structure of chlorophylls show high level of light absorption in the red region of visible light, activation of chlorophyllin derivatives results into generation of Reactive Oxygen Species (ROS) that cause tumor cells toxicity and subsequent tumor regression. Therefore, PDT has been used for targeting several accessible tumors. It has been also used in treatment of precancerous and cancerous dermatological diseases. In our studies, we were able to prove the distinctive role of chlorophyllin derivatives as highly efficient photosensitizers at both *in vitro* and *in vivo* PDT approaches. In comparison to the conventional chemotherapeutic drugs, no major alterations to the normal physiological condition have been detected. Additionally, successful PDT approaches in tumor cells killing were also achieved via liposomal delivery system of chlorophyllin derivatives. Mechanisms underlying PDT mediated tumor cells killing and *in vivo* tumor regression have been also investigated. Attempts towards the development of an efficient drug delivery system for improved tissue permeation, has been also conducted in an established murine tumor model for possible future clinical applications.

Biography

Iman Emam Omar Gomaa has completed her BSc in Biology at the Faculty of Science, Cairo University. She has obtained her Master's degree from Panum Institute, Copenhagen University and completed her PhD at the Medical School of the Technical University of Munich, Germany. She did four years of Postdoctoral studies at Mount Sinai School of Medicine, NY, USA and the Faculty of Medicine, Marie Curie University, France. Currently she is an Associate Professor of Molecular and Cellular Biology at the Biotechnology Sector, Faculty of Pharmacy and Biotechnology, German University in Cairo. She has published more than 20 papers in reputed journals.

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Rajat Kumar De et al., J Biotechnol Biomater 2016, 6:5(Suppl)
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Modeling ER stress and associated disorders on the onset of obesity

Rajat Kumar De and **Indrani Ray**
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Obesity is an epidemic of the 21st century. It continues to expand in western countries and paradoxically even in the countries where poverty and malnutrition are major problems. No age group is exempted from obesity due to different reasons, i.e., diet, life style and genetic component among others. In this talk we describe how a computational model can be formulated to understand the mechanism of the development of ER stress and associated disorders on the onset of obesity. For this purpose, we collected extensively ER and ER stress related pathways information to construct a set of global pathways by including other related pathways, like apoptosis, diabetes, inflammation, protein degradation and obesity. With all these pathway database and literature, we design an integrated pathway, through mining strategies, to form a biochemical pathway related to ER stress and obesity. We find out the control points regulating the activity (i.e., ON or OFF through feedback inhibition) of the integrated pathway. We also find out the genes coding for the enzymes catalyzing the reactions in the pathway. The talk will also describe design of a database containing all this information. The pathways in the database will then be subjected to network analysis. We use flux balance analysis, control theory and machine learning methodology to develop the model of the pathway as well as to analyze the pathways/networks. The properties of the pathways/networks are very important from therapeutic point of view, as in simple terms, they have the power to control the whole system.

Biography

Rajat Kumar De is a Professor of Indian Statistical Institute, India. He has obtained his PhD degree from the same Institute in 2000. He was a Distinguished Postdoctoral Fellow at the Whitaker Biomedical Engineering Institute, Johns Hopkins University, USA, during 2002-2003. During the last 10-12 years, he has been working in the area of bioinformatics and *in silico* systems biology. Recently, he has started working on Big Data Analytics in the domain of bioinformatics and systems biology. He has published about 85 research papers in international journals, conference proceedings and edited books and co-edited two books.

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Juliana Ferreira de Santana et al., J Biotechnol Biomater 2016, 6:5(Suppl)
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Linear peptides of *Mycobacterium leprae* antigens identified by SPOT synthesis indicate possible targets for serum diagnosis of leprosy

Juliana Ferreira de Santana, Larissa M Alvarenga, Vanete Thomaz-Soccol and **Juliana de Moura**
Universidade Federal do Parana, Brazil

Leprosy is a chronic granulomatous infection that affects the skin, nasal mucosa and peripheral nerves caused by the Gram-positive and obligate intracellular *Bacillus, Mycobacterium leprae*. The clinical manifestation of the infection with *M. leprae* will depends on the immune condition of the host. To become the multidrug choice therapy easier, according to WHO, the disease is divided into two categories: Paucibacillary and multibacillary leprosy. The paucibacillary patients present low antibody titers and predominant cell-mediated immunity. Contrastingly, multibacillary patients have a cell-mediated immunity inefficient with high antibody titers to *M. leprae* antigens. It will be interesting to identify and characterize biomarkers and antigens for a nearly diagnosis of leprosy of both categories of patients. Thus, our strategy was to realize an epitope mapping of seven proteins from *M. leprae* by using an array-based oligo-pepdide scanning (SPOT synthesis) onto a cellulose membrane probed for reactivity with sera from leprosy patients. No protein has reactivity with sera from healthy volunteers while four proteins have shown reactive spots when assayed with sera from leprosy patients. One of them was the 85B antigen from *M. leprae* previously identified by our group as an immunodominant protein after being mimicked by conformational peptides (mimotopes) by using Phage Display. After chemical synthesis, we hope the linear peptides found here could identify leprosy patients by simple assays like as ELISA, independently of their categories.

Biography

Juliana Ferreira de Santana was graduated in Biotechnology at Universidade Federal de Uberlandia. She has published two scientific papers. Her Master in Bioprocesses and Biotechnology Engineering was initiated in 2015 at Univesidade Federal de Parana.

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A proteomic study on the responses to arsenate stress by an acidophilic fungal strain *Acidomyces acidophilus* WKC1

Wai Kit Chan, Dirk Wildeboer, Hemda Garelick and **Diane Purchase**
Middlesex University School of Science & Technology, UK

An arsenic-resistant fungal strain, *Acidomyces acidophilus* WKC1 was isolated from waste roaster pile of a disused tin mine in Cornwall (UK) that was found to contain 18970 mg kg^{-1} arsenic (As). These tin mining areas are inhospitable due their extreme environmental conditions such as acutely acidity and high concentrations of heavy metals/metalloids, particularly arsenic. The *A. acidophilus* WKC1 strain exhibited remarkable tolerance to high arsenic concentration for instance, it can tolerate As(V) up to 22500 mg L^{-1}. A comparative protein responses analysis of *A. acidophilus* WKC1 exposed to arsenic and its control was performed using hybrid quadrupole-Orbitrap mass spectrometer. This proteomics approach revealed the mechanism behind the outstanding resistance and tolerance of *A. acidophilus* WKC1 against arsenic toxicity. When *A. acidophilus* WKC1 strain was exposed for 24 hours to 500 mg L^{-1} of sodium arsenate (Na_2HAsO_4), the enzymatic activities showed increased glutathione reductase, catalase and superoxide dismutase activities but reduced glutathione transferase activity. A total of 262 differentially expressed proteins were detected, of these 175 were up-regulated and 63 were down regulated following exposure to arsenic. These proteins included ones know to be involved in cellular stress responses, energy production, transport and proteins/enzymes synthesis when exposed to arsenic. In addition, 14 proteins were switched off and 10 proteins were switched on in the presence of arsenic. As far as we are aware this is the first report on proteomic study using *A. acidophilus* strain and next generation semi-quantitative mass spectrometry in arsenic resistance.

Biography

Wai Kit Chan has been captivated by science and environmental issues since in high school and became focused on protecting the environment from pollutants. He is currently pursuing his PhD at the Middlesex University under Dr. Diane Purchase. His research focuses on bioremediation in metalloids contaminated soil using extremophiles species, such as fungi, isolated from an extreme environment and the application of proteomics techniques. Prior to enrolling at Middlesex University, he holds a Master's degree in Environmental Management and BSc in Biotechnology both from University of Sunderland.

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Scientific Tracks & Abstracts

(Day 2)

Vadim R Viviani, J Biotechnol Biomater 2016, 6:5(Suppl)
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Brazilian beetle luciferases: Developing a bright future for cell toxicity assays, bioimaging and environmental analysis

Vadim R Viviani
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Firefly luciferases catalyze the ATP-dependent oxidation of D-luciferin, leading to the production of bioluminescence in the yellow-green region of the spectrum with high quantum yield (41-61%). Thus, they have been extensively used for decades as bioanalytical reagents to measure ATP content, biomass estimation and then as bioluminescent reporter genes to investigate cellular events and bioimaging and biosensors. However, until the nineties, only a few firefly luciferases which produced yellow-green light and were pH-sensitive were used for such bioanalytical purposes. In the past 15 years, we have cloned and characterized 10 new luciferases from Brazilian bioluminescent beetles, which elicit production of different bioluminescence colors, kinetics and pH-sensitivities. Among them *Phrixotrix hirtus* railroad worm luciferase is the only naturally red emitting luciferase (623 nm), *Pyrearinus termitilluminans* larval click beetle luciferase is the most blue-shifted (534 nm) and most efficient one (61%), and *Macrolampis* sp2 firefly luciferase displays a pH-sensitive bimodal spectrum (569/610 nm). With these enzymes, we have investigated the structural determinants of bioluminescence colors, pH-sensitivity and luminescent activity. Based on the acquired knowledge, we have engineered new luciferases with different bioluminescence colors from green to red (534, 550, 564, 575, 590, 605, 615, 628 nm), kinetics and pH-sensitivities, suited for specific biotechnological and environmental purposes. The red emitting luciferase of *Phrixotrix* and *Pyrearinus termitilluminans* green-emitting luciferase are currently used as multicolor reporter gene for mammalian cells assays and cell bioimaging. The luciferases of *Macrolampis* and *Pyrearinus termittilluminans* were shown to be suitable for general toxicity light off whole cell biosensors. Very recently, based on the spectral sensitivity of firefly luciferases, we have developed the first ratiometric intracellular pH and heavy metal-biosensors, being the first dual reporter system using a single luciferase gene to simultaneously monitor intracellular ATP or gene expression based on luminescent intensity (I) and intracellular pH or heavy metals based on the ratio of intensities at different wavelengths (I_{550}/I_{614} nm). Finally, we have developed for the first time a totally new orange emitting luciferase departing from a non-luminescent CoA-ligase, which has potential applicability as carboxylic xenobiotics biosensor for environmental and drug toxicity assays. These luciferases and their modified genes generated patents and products, expanding the range of bioluminescence applications in cell assays and environmental analysis.

Biography

Vadim R Viviani has been completed his degree in Biological Sciences from the Catholic University of Campinas (1990), doctorate in biochemistry from the Institute of Chemistry, University of São Paulo (1996), postdocs in Shizuoka- Japan University (1997-1999) and Harvard University (1999-2002) and professor (2014) by the Institute of Chemistry, University of São Paulo. He is an Associate Professor of Biochemistry at the Federal University of São Carlos, leads the research group "Bioluminescence and Biophotonics" (CNPq), and guest researcher at the Nat. Inst. of Advanced Industrial Science and Technology (Tsukuba, Japan) and Univ. Vanderbilt (Nashville, TN, USA), and president of the International Society for Bioluminescence and Chemiluminescence . Investigates bioluminescence enzymes luciferases and biotechnological and environmental use.

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Carlos Roberto Prudencio, J Biotechnol Biomater 2016, 6:5(Suppl)
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Antigenic profile of humoral immune response against pathogens of interest in public health by next-generation sequencing of phage-displayed peptide libraries

Carlos Roberto Prudencio
Adolfo Lutz Institute, Brazil

Given the growing number of diseases caused by emerging or endemic pathogens in Brazil, like *Ricketsias* and Zika virus, new strategies are urgently required for the development of disease diagnostic markers and vaccines. In this context, identification and development of these markers require high-throughput screening of combinatorial libraries. Phage-display is a powerful technique for selecting unique molecules with selective affinity for a specific target from high-complexity combinatorial phage display peptide libraries. The technology was applied initially to allow identification of high-affinity peptides after *in vivo* and *in vitro* screening. By high-throughput sequencing of the pool of recombinant phage clones following *in silico* analyses amongst hypothetical proteins of these pathogens, all categorized sequences provided the profile of the best candidates. Thus, we heightened the powerful screening capacity of this technique adding complementary approaches based on deep sequencing to identification and characterization of antigen candidates. By combining such approaches, we maximized the selection of molecules potentially relevant for diagnostics and vaccine development for pathogens of interest to public health.

Biography

Carlos Roberto Prudencio has completed his PhD from Federal University of Uberlandia and Postdoctoral studies from University of Sao Paulo and Universidad Castilla-la Mancha, Spain. He is the Coordinator of Immunotechnology Lab of the Center of Immunology at Adolfo Lutz Institute, Secretary of Health of Sao Paulo State; a public health institute with mission focused in research, epidemiological, sanitary and environmental surveillance in Sao Paulo State. He is a Member of the Post-graduation program (CAPES) devoted to Applied Health Sciences. He has published papers in reputed journals and also has been serving as an Editorial Board Member of repute. He is the Inventor holding eight patents related to the field of biotechnology of vaccines and diagnosis with expertise in innovation management and technological transfer focused in health. His research is focused on high-throughput approaches based in phage display technology applied to study host-pathogen interactions and the discovery of targets to develop new diagnosis, drugs and vaccines of interest to public health.

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4F-acts: A strategy to discovery protein interactions *in situ* sensitivity and specifically

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Fast fixation is necessary to study real time protein-protein interactions under physiological conditions. Fast formaldehyde cross linking can fix transient and weak protein interactions, thereby reducing the number of false negatives but producing great complexity. To reduce this complexity, immunoaffinity purification can fish out complexes that include particular target proteins, but affinity based co-purification has a limited capacity to eliminate non specific binding to beads and/or antibodies. To filter out these complexes, SDS-PAGE is used to disrupt non-covalent bonds, thereby eliminating uncross linked complexes and simultaneously providing molecular weight information for identification. We described a 4F-acts strategy to help improve real time ligands discovery based on formaldehyde cross linking, immunoprecipitation and SDS-PAGE separation: Fast Fix, Fish, and Filter, using albumin interactome as an example. The use of gel excision without staining makes this strategy comprehensive and sensitive. The target protein must be identified in the same slice as its ligands. The ligands must be identified in slices for the experimental group but not in the corresponding control slices. Only proteins that appear in the range of molecular weights equal to or greater than the sum of the proteins' theoretical molecular weights, together with the target are considered ligands. In this study, 5 s of cross linking with 10% formaldehyde was achieved in human blood. The use of this strategy identified 35 ligands for albumin. Comparison with four major previous studies of the albuminome revealed that 68.57% of the 35 ligands identified in our study were identified in these other studies. Fast cross linking was achieved. The 4F-acts strategy can be used to identify real time *in situ* interactions without prior intervention and to comprehensively identify ligands of particular target proteins with fewer false positives.

Biography

Youhe Gao is the Professor at Beijing Normal University, China. He has received his MD from Peking Union Medical College, PhD from University of Connecticut and Postdoctoral training from Beth Israel Deaconess Medical Center Harvard Medical School. He was the Professor of Department of Pathophysiology, Institute of Basic Medical Sciences, Chinese Academy of Medical Sciences/Peking Union Medical College from 2001-2014. His research interests include biomarker discovery in urine proteome, protein interaction and related bioinformatics.

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Supported liquid membrane for *in situ* removal of quiral amines produced by biocatalysis in cascade reactions

Bianca Ayres
Lund University, Sweden

The technology of SLM has been explored since 1990s, and it is widely applied for water treatment, and ink systems on printers. Even though, there are many investigations for optimization to removal of key substances in several processes. The application of SLM technology in bioprocess for chiral amines is reported as vanguard group here, in Sweden. The application of this technology for removal of chiral amines was firstly reported regards the higher production of amines within the process with omega transaminase. In the present work, we thoroughly discuss the factors influencing the performance of the SLM system and considerations for its successful use. The hollow fibres inside the membrane contactor is discussed regards to the composition of the polymeric material, lifetime for stability, flow rate of phases, pore size and wall thickness. Moreover, the system is further improved by implementing continuous control of the reactor pH using the amine donor substrate, and temperature of the phases passing through the SLM unit to maintain the extraction performance, allowing the accumulation of 1.0 M (121 g/l) product in the stripping phase during operation for 91 h. This result means improvement of 3-fold in productivity, compared to the process without SLM.

Biography

Bianca Ayres is Biochemical Engineer, has completed her PhD in 2014 from University of Campinas, in São Paulo, Brazil. She has completed Post-doctoral studies from Lund University in Sweden. She has published papers about biocatalysis using renewable resources to produce biopolymers of acrylic and propionic acid with sugars. The application of SLM has been investigated in bioprocess coupling enzymes acting in cascade reactions.

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Root proteome analysis of soybean under phosphorus starvation reveals the genotypic variation in organic acid exudation potential

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Experiments were performed to evaluate a diverse soybean panel for total carbon exudation potential employing shoot labeling with $^{14}CO_2$. Traits contributed to maximum genotypic variability were total ^{14}C exudation, P uptake and total dry weight. The proportion of organic acids was highest among root exuded compounds induced by low P stress. Efficient soybean genotypes exhibited superior growth and P acquisition efficiency under low soil P availability attributed to its higher root exudation potential aiding in mining fixed soil P. To understand the molecular mechanism governing differentially regulating root exudation potential in contrasting genotypes, root proteome analysis at low P stress was carried out. Among the total proteins visualized by 2D-gel electrophoresis, 105 (32%) were differentially expressed between sufficient and low P levels. A total of 44 (14%) proteins were down regulated by more than two-fold under low P while 61 (15%) proteins were up-regulated by more than two-fold at low P. Several key enzymes in organic acid synthesis and glycolytic bypass pathways were differentially regulated under low P stress in the P efficient soybean genotype, EC-232019. Alterations at the metabolite and protein level of EC-232019 suggest the cross talk between various metabolic pathways conferring higher P acquisition efficiency to plants under stress. Characterization of 17 proteins with unknown function might reveal roles of novel genes under low P stress. The identified genotypes have potential to be used as donors in crop improvement programs to develop high yielding P efficient cultivars, which may be an asset to low input sustainable agriculture.

Biography

Renu Pandey has completed her PhD (2001) from ICAR-Indian Agricultural Research Institute, New Delhi and Postdoctoral training in Molecular Biology from Donald Danforth Plant Science Center, USA. She is working as a Senior Scientist in the Division of Plant Physiology on understanding the basic mechanisms of phosphorus uptake and utilization in crops at physiological and molecular levels. Influence of climate change on phosphorus nutrition is also her area of interest. She has published 40 papers in reputed journals and serving as a Treasurer in Indian Nitrogen Group-Society for Conservation of Nature and Editor of *Indian Society for Plant Physiology*.

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MicroRNA: A small non-coding RNA, an efficient biomarker for prostate cancer

Khanmi Kasomva[1,2], **Savarimuthu Ignacimuthu**[1], **Michael Gabriel Paulraj**[1] and **Arnab Sen**[2]
[1]Loyola College, India
[2]Indian Council of Agriculture RC-NEH, India

Prostate cancer is the second leading cancer for men in America and Europe. Prostate cancer development is a slow process in men commonly over the age of fifty years. There are still poor in tools or biomarkers to identify in its early stage of development. Currently clinicians are using prostate specific antigen testing (PSA) and digital rectal examination (DRE) as early diagnostic tools for identifying prostate cancer but it shows ineffective due to low specificity and poor sensitivity. Therefore a novel biomarker for diagnosis of prostate cancer is required. A large quantity of microRNAs (miRNAs) is built up of 18-23 nucleotide; they are small non-coding and single-stranded and are important in post-transcriptional regulation of gene expression by degrading or suppressing target gene mRNAs. MiRNAs are implicated in the pathogenesis of prostate cancer; however they also act as novel target for the therapeutic intervention and circular microRNAs are shown potential biomarker for the prostate cancer diagnosis and show more specificity and sensitivity compared to available tools/biomarkers.

Biography

Khanmi Kasomva is currently a PhD scholar at Entomology Research Institute, Loyola College, India. He has completed his Master's degree in Biotechnology in 2014 from Loyola College, India. He is the recipient of 2013 Summer Research Fellowship of Indian Academy of Sciences and recipient of 2016 Young Professional-II from Indian Council of Agriculture Research and also received a Best Diplomacy Award at 1st session of North East Indian International Model United Nation Conference 2013. The main focus of his research is to understand the mechanism of microRNAs in prostate cancer, to examine the gene regulation by microRNA and to determine microRNA as a biomarker in prostate cancer. Recently, he has published a paper in *Clinica Chimica Acta* entitle "MicroRNA in Prostate Cancer".

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Notes:

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Adjuvant potential of outer membrane vesicles from *Neisseria lactamica*

Mariana Watanabe Garcia[1,2]
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Outer membrane vesicles or OMVs are derived from evaginations of Gram-negative bacteria outer membrane and they have gained immunological interest especially in relation to their ability to modulate biological functions and to be an alternative to the development of new vaccine strategies and combinations thereof. OMVs from commensal bacterium *Neisseria lactamica* induce antibodies which have cross reactivity with *N. meningitidis* and may be both antigen to meningococcal disease and a potential mucosal adjuvant. The objective of this study was to evaluate the adjuvant function of *Neisseria lactamica* OMVs using the surface protein PspA5 from *Streptococcus pneumoniae* as antigen model. OMVs were obtained from cultivations of the bacteria in bench scale bioreactor. The immunoassays were performed with OMVs *in natura* formulation (pure) and OMVs purified with sodium deoxycholate (DOC) at 0.3% and 0.5% in order to remove part of its lipopolysaccharide (LOS). The immunization groups were divided into 5 control groups: (1) Non, (2) PspA5, (3) pure OMV (OMV_{pure}), (4) OMV purified with DOC 0.3% ($OMV_{0.3\%}$), (5) OMV purified with DOC 0.5% ($OMV_{0.5\%}$) and 3 vaccinated groups: (6) PspA5 in combination with OMVpure, (7) PspA5 in combination with $OMV_{0.3\%}$ and (8) PspA5 in combination with $OMV_{0.5\%}$. The schedule set 2 intranasal fortnightly doses in murine model. It was evaluated the induction of anti-PspA5 IgG antibodies (IgG, IgG1 and IgG2a) and the protective potential of the different formulation. Initial immunological tests showed determinant adjuvant activity of all OMVs using the heterologous protein PspA5 as antigen model and protection against survival challenge.

Biography

Mariana Watanabe Garcia is Biological Scientist who graduated from Mackenzie University (2011). She was honored to have been the best student of Biological Sciences from 2008 to 2011. She is completing her PhD in Biotechnology from University of São Paulo in a project that has been developed in partnership with Butantan Institute, Brazil. She is also working at Merck Life Science as Biotechnology Application Specialist.

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Screening E3 Substrates Using a Live Phage Display Library

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Outer membrane vesicles or OMVs are derived from evaginations of Gram-negative bacteria outer membrane and they have gained immunological interest especially in relation to their ability to modulate biological functions and to be an alternative to the development of new vaccine strategies and combinations thereof. OMVs from commensal bacterium *Neisseria lactamica* induce antibodies which have cross reactivity with *N. meningitidis* and may be both antigen to meningococcal disease and a potential mucosal adjuvant. The objective of this study was to evaluate the adjuvant function of *Neisseria lactamica* OMVs using the surface protein PspA5 from *Streptococcus pneumoniae* as antigen model. OMVs were obtained from cultivations of the bacteria in bench scale bioreactor. The immunoassays were performed with OMVs *in natura* formulation (pure) and OMVs purified with sodium deoxycholate (DOC) at 0.3% and 0.5% in order to remove part of its lipopolysaccharide (LOS). The immunization groups were divided into 5 control groups: (1) Non, (2) PspA5, (3) pure OMV (OMV_{pure}), (4) OMV purified with DOC 0.3% ($OMV_{0.3\%}$), (5) OMV purified with DOC 0.5% ($OMV_{0.5\%}$) and 3 vaccinated groups: (6) PspA5 in combination with OMVpure, (7) PspA5 in combination with $OMV_{0.3\%}$ and (8) PspA5 in combination with $OMV_{0.5\%}$. The schedule set 2 intranasal fortnightly doses in murine model. It was evaluated the induction of anti-PspA5 IgG antibodies (IgG, IgG1 and IgG2a) and the protective potential of the different formulation. Initial immunological tests showed determinant adjuvant activity of all OMVs using the heterologous protein PspA5 as antigen model and protection against survival challenge.

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Screening E3 Substrates Using a Live Phage Display Library

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Ubiquitin ligases (E3s) determine specificity of ubiquitination by recognizing target substrates. However, most of their substrates are unknown. Most known substrates have been identified using distinct approaches in different laboratories. We developed a high-throughput strategy using a live phage display library as E3 substrates in in vitro screening. His-ubiquitinated phage, enriched with Ni-beads, could effectively infect E. coli for amplification. Sixteen natural potential substrates and many unnatural potential substrates of E3 MDM2 were identified through 4 independent screenings. Some substrates were identified in different independent experiments. Additionally, 10 of 12 selected candidates were ubiquitinated by MDM2 in vitro, and 3 novel substrates, DDX42, TP53RK and RPL36a were confirmed ex vivo. The whole strategy is rather simple and efficient. Non-degradation substrates can be discovered. This strategy can be extended to any E3s as long as the E3 does not ubiquitinate the empty phage.

Biography

Youhe Gao Professor Beijing Normal University. He received his MD from Peking Union Medical College, his Ph.D from University of Connecticut and postdoctoral training from Beth Israel Deaconess Medical Center Harvard Medical School. He was the professor of Department of Pathophysiology, Institute of Basic Medical Sciences, Chinese Academy of Medical Sciences/ Peking Union Medical College from 2001-2014. His research interests include biomarker discovery in urine proteome, protein interaction and related bioinformatics.

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Biotechnology World Convention

August 15-17, 2016 Sao Paulo, Brazil

Workshop

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Biotechnology World Convention

August 15-17, 2016 Sao Paulo, Brazil

Sonia Malik
Federal University of Maranhao, Brazil

Biotechnology and plant secondary metabolites production

Secondary (also known as natural) compounds derived from plants have been used for various purposes, such as, pharmaceuticals, agrochemicals, flavors, fragrances, pigments, dyes, cosmetics, food additives etc. Although some of these compounds are synthesized chemically but due to their complex chemical structures and complicated biosynthetic pathways, most of them are obtained from plants. Biotechnology offers a valuable tool to produce these compounds of interest in a desired amount and an eco-friendly way. By employing biotechnological techniques, it is possible to regulate the biosynthetic pathway of plant in order to enhance/decrease the synthesis of particular compound. Despite, the advances in biotechnology techniques, there are only a few successful examples of secondary compounds production at an industrial level. The symposium addresses the new challenges and emerging researches in the area of biotechnology and plant secondary metabolism. The focus is to highlight the various strategies to increase the quality as well as quantity of secondary compounds. The topics covered under the symposium include: Chemistry and pathways of secondary compounds derived from plants, phytochemistry, phytotherapy, quality control of natural products, production of secondary compounds using biotechnological means, *in vitro* culture (cell, organ or tissue culture), various factors affecting production of secondary compounds, immobilized culture, two-stage and two-phase culture systems, hairy root culture, genetic modifications, metabolic engineering, nanotechnology and nanobiotechnology, green syntheses of metallic nanoparticles using plant extracts, modifications in endogenous pathways and stable transfer as well as integration of gene involved in flux-limiting steps of biosynthetic pathways, characterization of genes and proteins involved in secondary metabolic pathways, transcriptomics, proteomics and metabolomics studies with respect to secondary metabolism, and industrial production of secondary compounds. The event will bring together the academia and industry in a common international platform to exchange the knowledge, experience and research innovations among researchers working in the area of Biotechnology. This symposium will provide an opportunity for scientists, researchers from academia/industries, graduate and post-doctoral researchers as well as young researchers to explore their knowledge and face to face talk with experienced researchers.

Biography

Sonia Malik is working as a Professor at Biological & Health Sciences Centre, Department of Biology, Federal University of Maranhão, Sao Luis. Her area of research involves *in vitro* production of plant secondary metabolites and metabolic engineering. She is an active member of post-graduate research program at Federal University of Maranhão. She has won many awards and recognitions for her work. Her international experience includes various programs, contributions and participation in different countries for diverse fields of study. She has been awarded with FAPEMA Senior Researcher grants in August 2015. Her research interests reflect in her wide range of publications in various national and international journals. She is the Editorial Board Member and reviewer of scientific journals.

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