Scientific Tracks & Sessions
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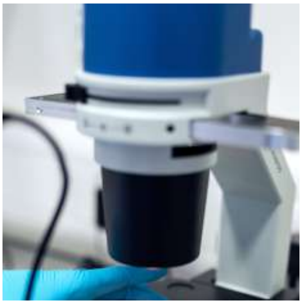
Microbiology 2022



How genomic databases aid clinical mycobacteriology

Alina Minias
Polish Academy of Sciences, Poland

The introduction of high-thruput sequencing allowed for the sequencing of thousands of bacterial strains around the globe. We can currently look into the diversity of genomic composition of bacteria with great detail and on a large scale. We can analyze all mutations present in the entire bacterial genome, and we can do that with many strains. Data availability allows for bacterial population-based studies. We can use large genomic databases to identify DNA sequences that mark specific lineages, important from the clinical point of view. Further, we can analyze the variability of DNA sequences to estimate the level and the direction of evolutionary selection. Such information is valuable to indicate proteins essential for bacterial survival that can be targeted for antibiotics or indicate mutations possibly involved in the generation of drug resistance. Finally, genomic databases provide a holistic view of the bacterial population's composition, drawing meaningful conclusions regarding epidemiology and pathogen transmission. All in all, genomic databases broaden our understanding of bacterial population structure and allow better control of circulating pathogens.

Speaker Biography

She is a polish molecular biologist, currently she is working as a research assistant in department of teacher training and biodiversity studies Poland.

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Synergistic potential of plant growth promoting bacteria and arbuscular mycorrhizal fungi to improve wheat yield and biofortification and characterization of multiple abiotic stress tolerant bacteria

Ramakrishna Wusirika, Radheshyam Yadav and **Parikshita Rathore**
Central University of Punjab, India

The extensive application of inorganic chemical fertilizers on low-yielding agricultural fields is a severe concern. Microbial consortia comprised of native plant growth promoting bacteria (PGPB) and arbuscular mycorrhizal fungi (AMF) could be a potential solution for site-specific sustainable agricultural-management practices, leading to enhanced plant growth and grain yield. Abiotic stresses such as drought, salt and heat cause reduction of plant growth and loss of crop yield worldwide. The use of biofertilizers is the simplest and cheapest method to stimulate plant growth as well as provide protection against abiotic stress. In the present study, the best performing PGPB and AMF for biofortification and improved grain yield and soil health were identified after two-year field trials. Two bacterial isolates belonging to Bacillus species in combination with AMF showed the best results in macro and micronutrients content in grains and root tissue and yield-related parameters compared to the untreated control. Further, consistent improvement in thousand grain weight, biomass, grain iron, and soil organic carbon was observed. Proteomic, metabolomic and protein-metabolite interactions analyses of wheat inoculated with PGPB and AMF provided insights into the role of specific proteins and metabolites. Bacteria with plant growth promoting (PGP) traits and tolerance to multiple abiotic stresses were identified from soil samples and their co-occurrence was studied. Phosphate solubilizing bacteria (PSB) were the most abundant in all types of soils compared to other traits, Cu metal tolerant bacteria (CTB), salt-tolerant bacteria (STB) and antibiotic-resistant bacteria (ARB). Two bacterial isolates with PGP and abiotic stress tolerant traits are being characterized at the molecular level to understand the underlying mechanisms involved in multiple abiotic stress tolerance.

Speaker Biography

Ramakrishna Wusirika has completed his Ph.D. from University of Pune/ National Chemical Laboratory, India. He was a post-doctoral fellow at Purdue University, USA and a faculty member at Michigan Technological University, USA. Currently, he is Professor in Biochemistry department and Dean, Academics at Central University of Punjab, India. He is working on plant growth promoting bacteria and their applications to enhance crop productivity and biofortification as well as the biochemical and molecular mechanisms involved in the process. He has over 75 publications that have been cited over 5270 times, and his publication H-index is 35 and has been serving as an editorial board member and associate editor of reputed journals.

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Novel phytomicrobiome members and their plant-regulatory signals as a sustainable crop production strategy

Donald L Smith and **Dongmei Lyu**
McGill University, Canada

It is increasingly recognized that evolution acts on the combined entity resulting from the plant and its associated microbes, the phytomicrobiome, constituting the holobiont. The plant provides the phytomicrobiome with reduced carbon as an energy source; members of the phytomicrobiome are in the privileged position of being deliberately given a supply recently fixed energy. Because of their relationship, what is good for the plant is good for the members of the phytomicrobiome. We now understand that each plant is generally be accompanied with a substantial, complex and carefully orchestrated population of microbes, most of which are beneficial through performing specific activities for the plant. As climate change conditions continue to develop, field crops are facing the stressful conditions more frequently and the levels of stress will be more extreme. The application of beneficial microbes or their products, microbe-to-plant signal compounds, have the potential to be a very low-input, sustainable mechanism to help plants deal with climate change and, specifically, to help the global crop production sector to continue prospering and producing secure food supplies, as challenging climatic conditions become more prevalent. Given the ability of phytomicrobiome, the biological signals, or the microbes themselves could play a major role in increasing the productivity of crops under extreme growth conditions. Thus, beneficial plant-microbe relationships can not only increase plant productivity through things like nutrient provision, but also can play a role in mitigating climate change effects, enhancing agricultural sustainability and reducing greenhouse gas emissions. At this time we are aware that there is a substantial phytomicrobiome associated with every plant, which regulates the plant and is being regulated by the plant. Thus, there is a capacity to use plant growth promoting bacteria (PGPB) to enhance the climate change resilience of global food production systems. We have developed rapid systems for isolation, screening, characterizing and deployment of beneficial phytomicrobiome members and the plant-growth-enhancing compounds they sometimes produce. From the results of the studies conducted in our laboratory, we have observed the isolated beneficial PGPB and the signal compounds they produce offer enormous potential for a full range of crop species, from corn, soybean, canola to cannabis, under the optimum conditions and stress condition. To date we have isolated and commercialized three materials produced by PBPB. The background to this work and the potential of this area will be synthesized and presented. Beneficial microbe application as sustainable approach should be deployed for the development of more sustainable and climate change resilient crop production and this presentation will outline the route for this effort..

Speaker Biography

Donald L. Smith is distinguished James McGill professor. During his 36 years at McGill, he has conducted research in the production and physiology of crop plants, with an emphasis on plant-microbe interactions. Specific research areas have been: nitrogen metabolism, nitrogen fixation, methods for injection of metabolites into plants, cereal production, plant growth regulators, intercropping, inter-plant competition, plant-microbe signaling, plants and climate change, biofuel crops, crop stress responses, biochar as a soil amendment and cannabis management. He has trained 82 graduate students, ~2/3 at the Ph.D. level, published >360 papers, generated thirteen patents, started a spin-off company (Bios Agriculture Inc.), and commercialized technologies that are now applied to ~100 million ha of cropland per year. He has been cited more than 16,000 times and his current H index is 63 (Research Gate). He has been principal investigator on research grants totaling >$80 million. He currently leads the biofuelnet and Biomass Canada, ($13 M).

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Supranational assessment of the quality of probiotics: Collaborative initiative between independent accredited testing laboratories

Jean-Pol Warzée[1], **Marina Elli**[2], **Daniela Cattivelli**[2], **Abdoulaye Fall**[3] and **Jean-Yves François**[3]
[1]ESLP– European Scientific League for Probiotics, Belgium
[2]Advanced Analytical Technologies Srl, Italy
[3]Food Chain ID Company, Belgium

Recent acquisitions about the role of the microbiota in the functioning of the human body make it possible to envisage an increasing use of beneficial microbes, and more particularly of probiotics as well as their metabolites, as nutritional supplements. National and EU authorities are engaged in assuring the safety and quality of food supplements and in defining rules to assess and communicate their efficacy on human health. The quality of probiotics, intended as strains' identification, viability, and stability over time, is a crucial factor of credibility with consumers and health professionals. Analytical technologies for the quality control of probiotics must also be adapted to new preparations, such as those including new multistrains complex combinations. Accredited laboratories face this relevant challenge on a daily basis. Through its close collaboration with the laboratory commissioned to produce the specifications for its ESLP quality label (identification and quantitative analyses) together with its scientific committee, the ESLP has been focusing on this issue for 10 years. Recently, as part of the internationalization of the ESLP quality label, a new and unique initiative in Europe for the evaluation of the quality of probiotic preparations has been carried out. The collaboration between two accredited laboratories in Belgium and in Italy represented a concrete example of supranational collaboration in the assessment of the quality of probiotic preparations. Results show that both laboratories are in line as expected in terms of performance. Common approaches to the qualitative assessment of probiotic preparations, especially for complex and composite recipes, in terms of number of strains and included substances, should be encouraged and promoted all over the EU.

Speaker Biography

With more than 20 years experience in the microbiota and microbiotics, Jean-Pol Warzée, medical doctor has participated to many research and development projects in this area in human health in collaboration with European Research Centers and Universities. Jean-Pol has collaborated to the development of new microbiotics solutions and is author, co-author of many publications. Co-Founder 10 years ago of the ESLP - European scientific league for probiotics for 2012, Jean-Pol is also the nominated President of ESLP. Member of several international scientific associations, he has been vice-president of the PRI - Pharmabiotics research institute from 2015 – 2017. Jean-Pol participates regularly to international congresses as speaker related to "probiotics quality control" and also "microbiotics in human health" .

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Evaluation of the postbiotic potential of the fermentation of five lactic acid bacteria isolated from aguamiel

Mariel Ortega
UPAEP, Mexico

In Mexico, according to the traditional pharmacopoeia, the consumption of fermented beverages, such as aguamiel, has been associated with numerous nutritional benefits due to the presence of lactic acid bacteria with probiotic potential. Furthermore, the bacteria isolated from aguamiel have shown significant antimicrobial activity, in addition to representing a rich source of iron, ascorbic acid, riboflavin, and bioactive steroid saponins.

One of the main mechanisms of action of these probiotic bacteria is the production of antimicrobial metabolites such as bacteriocins, enzymes and organic acids, which can stimulate the response of the immune system, improve the absorption and digestion of food, and reduce the growth of pathogenic flora. For this reason, the purification of these by-products of fermentation that provide benefits to the host (known as postbiotics) has the potential to be used as adjuvants in the treatment and prevention of infectious diseases.

Speaker Biography

Mariel Ortega completed her studies in biotechnology engineering, with a minor in molecular biology, at the tecnológico de monterrey university in Mexico. Currently, at the age of 24, she is studying a master's degree in biotechnology with special focus on the potential of traditional mexican fermented foods in health.

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Evaluation of cyanobacteria population and mycrocystin detection at billings reservoir (São Paulo, Brazil)

Cristina Souza Freire Nordi, Matheus Santos Freitas Ribeiro, Gregory L Boyer and **Cristina Viana Niero**
Universidade Federal de São Paulo, Brazil

Cyanobacteria are a large group of Gram negative bacteria that perform oxygenic photosynthesis, with cosmopolitan distribution and large distribution in eutrophic environments. In addition, the unrestrained growth trend of some species of the total population produces blooms that are harmful to the aquatic environment, altering the entire balance of the ecosystem. Most flower-forming species are capable of producing cyanotoxins which are toxic secondary metabolites for most eukaryotes and characterized according to their mode of action (neurotoxins, hepatotoxins, cytotoxins and dermatotoxins). Among the cyanotoxins, the microcystin can be highlighted as the most studied among the others, due to its wide distribution in various environments worldwide. Due to their great potential to cause acute or chronic reactions, the presence of cyanotoxins in water bodies used for public supply must be monitored. Some species of cyanobacteria are known to be potential producers of cyanotoxins and their presence in water bodies serves as a warning sign for the possible presence of the toxin in water. The research group of the Laboratory of Ecophysiology and Environmental Monitoring of the Federal University of São Paulo (UNIFESP) has been monitoring the dynamics of cyanobacteria and the presence of microcystins in the Billings Reservoir, the largest water resource in the Metropolitan Region of São Paulo (RMSP) in Brazil since 2014. Monitoring of cyanobacteria is performed by identifying the species present in the sample and counting them under an inverted microscope, later expressed in biovolume, representing the volume that cyanobacteria occupy in one liter of the water sample. The presence of microcystin was monitored by two methodologies: a direct one, performed by high performance liquid chromatography (HPLC), and an indirect one, detecting the presence of the genes responsible for the production of microcystin in the samples by polymerase chain reaction (PCR). The biovolume of cyanobacteria dominated in relation to the other phytoplankton components for most of the studied period, often with values considered extremely high, reaching up to 50 times the limit suggested by Brazilian legislation (1 mm^3/L). This value is the maximum limit for water to be used for public supply. In most cases, potentially cyanotoxin-producing species, such as Microcystis aeruginosa, Plankthotrix isothrix, Woronichinia naegeliana, Dolichospermum sp. and Raphidiopsis raciborskii were dominant or abundant species in relation to other cyanobacterial species. Starting in 2016, the research group started monitoring the presence of genes responsible for microcystin production and such genes were found in all samples studied since the beginning of the study. In 2019, in addition to indirect detection, microcystin quantification was also performed in collaboration with Dr. Gregory Boyer, from the College of Environmental Science and Forestry. Microcystin concentrations ranged from 0.33 ug/L to 50.7 ug/L, the latter value being 50 times greater than the limit established by Brazilian legislation of 1.0 ug/L. The high concentration of microcystin is related to the large biovolume of cyanobacteria observed in the studied period. The dominance of cyanobacteria in the studied periods and the results of the presence of microcystin-producing genes and the detection of values above those allowed by legislation generates a health concern, since several points of the Billings Reservoir are used for public supply.

Speaker Biography

Has a degree in Biological Sciences from the Faculty of Philosophy Sciences and Letters of Ribeirão Preto/USP (1977), a master's degree in Ecology and Natural Resources of São Carlos (1982) and a PhD in Ecology and Natural Resources from the Federal University of São Carlos (1993). Postdoctoral at São Carlos Institute of Physics with a scholarship from the Foundation for Science Support of the State of São Paulo. She has been a professor at the Federal University of São Paulo / Campus Diadema since 2008. She is a permanent member of the Pós-Graduate Program in Ecology and Natural Resources. She has experience in Cryptogamic Botany, working in the following sub-areas: freshwater microalgae, Limnology, EPR and nanostructured films using algal polysaccharides. Currently also working in the area of reservoir monitoring and focusing on cyanobacteria and detection of cyanotoxins through molecular techniques.

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The tetrameric assembly of 2-aminomuconic 6-semialdehyde dehydrogenase is a functional requirement of cofactor NAD+ binding

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The bacterium Pseudomonas sp. AP-3 is able to use the environmental pollutant 2-aminophenol as its sole source of carbon, nitrogen, and energy. Eight genes (amnA, B, C, D, E, F, G, and H) encoding 2-aminophenol metabolizing enzymes are clustered into a single operon. 2-amino muconic 6-semialdehyde dehydrogenase (AmnC), a member of the aldehyde dehydrogenase (ALDH) superfamily, is responsible for oxidizing 2-aminomuconic 6-semialdehyde to 2-aminomuconate. In contrast to many other members of the ALDH superfamily,the structural basis of the catalytic activity of AmnC remains elusive. Here, we present the crystal structure of AmnC, which displays a homotetrameric quaternary assembly that is directly involved in its enzymatic activity. The tetrameric state of AmnC in solution was also presented using small-angle X-ray scattering. The tetramerization of AmnC is mediated by the assembly of a protruding hydrophobic beta-strand motif and residues V121 and S123 located in the NAD+ binding domain of each subunit. Dimeric mutants of AmnC dramatically lose NAD+ binding affinity and failed to oxidize the substrate analogue 2-hydroxymuconate-6-semialdehyde to α-hydroxymuconic acid, indicating that tetrameric assembly of AmnC is functional requirement.

Speaker Biography

Qiuli Shi is studying for Ph.D. at Sichuan University, China.

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