



Joint Conference

International Conference on

ENVIRONMENTAL MICROBIOLOGY AND MICROBIAL ECOLOGY

&

International Conference on

ECOLOGY AND ECOSYSTEMS

September 18-20, 2017 Toronto, Canada

Workshop

Day 1

Joint Conference

International Conference on

ENVIRONMENTAL MICROBIOLOGY AND MICROBIAL ECOLOGY

&

International Conference on

ECOLOGY AND ECOSYSTEMS

September 18-20, 2017 Toronto, Canada

**Gregory B Gloor***University of Western Ontario, Canada***Analyzing 'omics data using compositional data analysis**

We will demonstrate that the microbiome and transcriptome datasets should be analyzed by a combination of Bayesian estimation and compositional data approaches to examine the ratios between features giving robust insights into the structure of high throughput sequencing datasets. Traditional methods of analyzing microbiome or RNA-seq datasets can be misleading, and not use all the available information. This results in many analyses being dominated by either the most abundant, or the rarest features. Data collected using high throughput sequencing (HTS) methods are sequence reads mapped to genomic intervals, and are commonly analyzed as either 'normalized count data' or 'relative abundance data'. One reason for these normalizations is to attempt to compensate for the problem that the sequencing instrument imposes an upper bound on the number of sequence reads. Positive data with an arbitrary bound are 'compositional data' and are subject to the problem of spurious correlation. Thus ordination, clustering and network analysis become unreliable. A second problem is that the data are sparse: i.e., contain many 0 values. A third problem is that the largest measurement error is at the low count margins in these datasets. These issues are all addressed using our approach.

Biography

Greg B Gloor is a professor of biochemistry with broad experience in molecular biology, genetics and genomics. Most recently, he has developed tools to investigate fundamentals of molecular evolution, microbial ecology and meta-transcriptomics. He is currently working on developing and adapting principled methods to characterize correlation and differential abundance in sparse, high throughput sequencing data as generated in 16S rRNA gene sequencing surveys, meta-genomics and meta-transcriptomics. He is the developer and maintainer of the ALDEx2 R package on Bioconductor.

ggloor@uwo.ca**Notes:**



Joint Conference

International Conference on

ENVIRONMENTAL MICROBIOLOGY AND MICROBIAL ECOLOGY

&

International Conference on

ECOLOGY AND ECOSYSTEMS

September 18-20, 2017 Toronto, Canada

Scientific Tracks & Abstracts

Day 1

Joint Conference

International Conference on

ENVIRONMENTAL MICROBIOLOGY AND MICROBIAL ECOLOGY

&

International Conference on

ECOLOGY AND ECOSYSTEMS

September 18-20, 2017 Toronto, Canada

Identification of the relationship between chemical and biological factors impacting corn productivity**Saveetha Kandasamy**

A&L Biologicals, Canada

The definition for soil health as intended for agriculture may be best described as a soil that provides the optimal productivity to a primary crop over an extended time while having the minimum impact on plant, animal, and human health. However, we require a much better understanding of what is a healthy soil agroecosystem, how to identify it, and how to repair damaged sites for optimal crop productivity. Our studies focus on identifying the key drivers associated with soil health at sites where high and poor yields of corn occur within an agroecosystem. The initial project examined the same corn variety grown at a site developed by Mr. Dean Glenney where strips of corn and soybeans are alternated yearly under no till conditions. The yields continued to increase at this site over its twenty plus years of production. Using this site and a farm using conventional corn production and planting the same seed lot, we examined numerous input factors with a focus on identifying the phytobiomes associated with various tissues of corn plants sampled from the two locations. The objectives were to identify when to look, where to look, and how to look. Molecular analysis using TRFLP provided rapid and low cost means of separating the microbial profiles among samples. Both bacterial and fungal microbiomes were found to be similar on comparable tissues at the two sites in the early phases of growth. However, the microbiome found on the roots differed from that of the sap collected from the stems. By the V10 stage there were very significant differences in the microbial profiles of stem sap and leaf tissue from corn collected from the two sites but the microbiomes of the roots were more similar. The differences found at V₁₀ stage became less apparent as the plants aged and became senescent. The changes in the plants microbiology and their relationship to yield will be discussed.

Biography

Saveetha Kandasamy graduated with her Doctoral Degree from Tamil Nadu Agricultural University, India in 2010, Specialized in Plant Microbe Interactions and Biological control. Moved to Canada in May, 2010 with Post-Doctoral appointment at Dalhousie University, worked 4 years and continued her research in Agriculture Canada, as NSERC-Visiting Fellow for another year. Subsequently, she joined as Research Scientist at A&L Biologicals, where she is leading 5-year Agricultural Innovation Program research focusing on plant and soil health from ecological perspectives. Saveetha Kandasamy has published about 25 research papers in refereed scientific journals and 3 book chapters. She is a winner of Dr. M. J. Narasimhan Academic Merit Award for the year 2009 (which is given every year to a young Plant Pathologist in India at the national level), developed a commercial microbial bioformulation. She has participated and presented in several national and international conferences, won some best paper and travel grant awards.

saveetha@alcanada.com

Notes:

International Conference on

ENVIRONMENTAL MICROBIOLOGY AND MICROBIAL ECOLOGY

&

International Conference on

ECOLOGY AND ECOSYSTEMS

September 18-20, 2017 Toronto, Canada

Functional interaction of plant and its microbiome: What are these bacteria doing?**Shimaila Ali**

A&L Biologicals, Canada

Determination of functional genetics of corn microbial community can lead us to find the factors involved in higher corn productivity. Functions imparted to host plants by the microbial community include disease control by production of antibiotics, lytic enzymes, and siderophores and stimulation of host defenses. Many microorganisms can modulate plant hormonal levels by production of indoleacetic acid, ethylene, cytokinins, gibberellins, etc. We developed and standardized protocols for the quantitation of seven different functions in corn microbial community, which include nitrogen fixation (*nif*), phosphate solubilization (*pqqC*), antibiotic production (*srffA* and *fenD* mainly from *Bacillus* sp., *phlD* and *phzF* mainly from *Pseudomonas* sp.), and production of hydrogen cyanide (*hcnAB*). The functional genes were quantified in microbial community DNA extracted from roots, stem, and rhizospheric soil of corn grown in fields selected by aerial infrared photography and identified as having high or average productivity within the same fields. In almost all samples, the abundance of functional genes was directly related to high corn productivity. However, the richness in functional gene(s) in the microbial population associated with corn was not the only factor that correlated with productivity.

Biography

Shimaila Ali graduated with her doctorate from the University of Waterloo. Her research was based on the isolation and characterization of new plant growth-promoting bacterial endophytes. She has worked on identifying how endophytic bacteria impact plant growth and development using both physiological approaches as well as bioinformatics. Dr. Ali has developed identified a small number of proteins predicted to be key elements of endophytic colonization of plants by bacteria. She joined A & L Biologicals in 2014 as NSERC post-doctoral research scientist, where she is leading a part of a research project on functional metagenomic analysis of corn microbiome for identifying main drivers responsible for improved corn yields and other plant productivity.

shimaila@alcanada.com

Notes:

Joint Conference

International Conference on

ENVIRONMENTAL MICROBIOLOGY AND MICROBIAL ECOLOGY

&

International Conference on

ECOLOGY AND ECOSYSTEMS

September 18-20, 2017 Toronto, Canada

Microbial biodiversity in Brazilian semiarid**Fernanda Matias**

Rural Semiarid Federal University, Brazil

When we think of semiarid we always associate with the lack of water, food, agriculture and livestock that end up generating little local development and, in consequence, poverty. However, little is exploring local biodiversity and adapted to that situation. In Brazil, we have a vast area of territory with hot semi-arid climate and only from mid-2010 began to be exploited as the local biodiversity. Microbiological part is even more incipient. In 2014, a previous analysis of microbiome at different times of the year showed a significant difference of 16S rDNA size amplified in the same environment. This year we will start a microbiome work to understand what happens in these environments in different periods of drought. In 2016, lipolytic bacteria from hot springs were isolated. Lipases showed greater activity above 158oF and pH between 10 and 12. Later this year, we began an isolation of phosphate solubilizing, nitrogen fixers and auxin producing bacteria. By the time we succeeded in isolating more than 100 strains, among them was a symbiotic of *Adenium obesum* (desert rose) that is being considered for use as an agricultural inoculant. Furthermore, we developed a mead production method that reduced the months of fermentation timeout to 15 days which enables the industrial production of this beverage and will be the first start-up of the region. These findings suggest that semiarid is really rich in microbial biodiversity.

Biography

Fernanda Matias has completed her Ph.D in biotechnology from Sao Paulo University and post-doctoral studies from Sao Paulo University (Chemistry) and Porto Alegre Health Sciences Federal University (Pathology). She is a professor at UFERSA, School of Biotechnology, and is founding the first company in the university. She has published more than 10 papers in reputed journals.

fernandamatias@ufersa.edu.br

Notes:

Joint Conference

International Conference on

ENVIRONMENTAL MICROBIOLOGY AND MICROBIAL ECOLOGY

&

International Conference on

ECOLOGY AND ECOSYSTEMS

September 18-20, 2017 Toronto, Canada

Safe salad – Is it possible to produce safe baby leaves?**Lars Mogren**

Swedish University of Agricultural Sciences, Sweden

Statement of the Problem: Vegetables are an essential component of a healthy diet. During the last decades, outbreaks of foodborne illnesses have increasingly been linked to fresh and/or minimally processed vegetables. Shigatoxin producing *E. coli*, causing EHEC infections, has been the causal agent for major outbreaks both in Sweden and abroad with leafy vegetables and sprouts. This pathogen is particularly severe due to its severe symptoms and low infectious dose. The major source for contamination is associated with animal or human feces. Contamination can occur in the entire farm-to-fork chain and failure during preharvest may not be counteracted by processing. This project focuses on the whole chain from production to consumer regarding baby leaf crops.

Methodology & Theoretical Orientation: A four year project is called "Safe Salad". It is including several research groups and applies a novel and unique approach, as it focuses on the vector, namely the plant and its microflora. It uses a comprehensive approach from farm to fork. Studies include interactions between cropping and processing environment and the leaf microflora and the prevalence of EHEC are used as a basis for risk assessment and identification of risk factors before harvest and of vegetables at risk. The impact of nitrogen supply to the crop is highlighted. Explanatory models for adhesion on the leaf via the existing biofilm and the significance of the leaf microflora for disease development is studied in animal trials.

Conclusion & Significance: The main conclusion is that there are no single way to prevent and exclude *E. coli* reaching the farm to fork chain but there are several methods to reduce the risks at critical stages.

Biography

Lars Mogren has a background in horticulture and produce quality. His main focus has been the role of pre-harvest factors on post-harvest quality of field grown vegetables. He is Coordinator of a four year research project called safe salad which includes field and greenhouse trials, laboratory analyses, intervention studies and risk assessments.

Lars.Mogren@slu.se

Notes:

Joint Conference

International Conference on

ENVIRONMENTAL MICROBIOLOGY AND MICROBIAL ECOLOGY

&

International Conference on

ECOLOGY AND ECOSYSTEMS

September 18-20, 2017 Toronto, Canada

Secondary metabolites with pesticide activity from plant pathogenic fungi**Kumudini M Meepagala**

USDA-ARSUSDA-ARS (United States Department of Agriculture-Agricultural Research Service), USA

Phytopathogenic fungi produce secondary metabolites that are toxic to host plants. These fungi have evolved to survive in the ecological niche by producing secondary metabolites to compete with other fungi, plants and insects. Thus, these toxins can have various biological activities. As part of ongoing research efforts at USDA, we have investigated some plant pathogenic fungi in search of natural products that can be used as pesticides or can be used as lead compounds in designing such compounds. Phomalactone isolated from *Nigrospora spherica*, a plant pathogenic fungus isolated from *Zinnia elegans* and *Hydrangea macrophylla*, was found to be phytotoxic and mosquitocidal. From the culture medium of *Curvularia intermedia*, $\alpha\beta$ -dehydrocurvularin was isolated as a phytotoxin. *Pyricularia grisea* is a fungus selective to monocots. From the culture broth of this fungus, pyrichalasin was isolated as the phytotoxin. A colony of three fungi was isolated from necrotic leaves of *Basella alba*, commonly known as Malabar Spinach. *Diaporthe eres* was isolated from infected *Hedera helix* leaves. An isocoumarins was isolated from the culture broth of this fungus and found to have phytotoxic and mosquito larvicidal activities. Based on this molecule, several analogs of isocoumarins were synthesized with higher phytotoxic activity. Isolation of active metabolites and synthesis of analogs will be discussed.

Biography

Kumudini M Meepagala has been working in USDA-ARS for over 15 years. She is working on isolation of natural products from plants and fungi that can be used as agrochemicals. She is also involved in synthesis and structure modification of natural products to develop mosquito repellents and larvicidal.

kmeepaga@olemiss.edu

Notes:

Joint Conference

International Conference on

ENVIRONMENTAL MICROBIOLOGY AND MICROBIAL ECOLOGY

&

International Conference on

ECOLOGY AND ECOSYSTEMS

September 18-20, 2017 Toronto, Canada

Diel cycle of the tropical air microbiome**Elena S Gusareva**

Singapore Centre for Environmental Life Sciences Engineering, Singapore

Our understanding of airborne microbial communities including their sources, functions, microbial interplay and ecology is limited despite its relevance for human health, environmental and ecosystems functioning. Few attempts have been made to study air microbial ecosystems to date. Tropical environments, distinct from temperate northern hemisphere systems studied so far, have specific physical/chemical features that impact the structure, function and ecology of the microbial components of their air ecosystems. Moreover, a highly urbanized ecosystem with its unique built environment and extensively processed indoor air, as encountered in Singapore, likely harbors defined yet unknown microbial communities.

To comprehensively describe air-borne microbial ecosystem of Singapore, triplicates air samples were collected within 24 hours for 5 consecutive days in four independent experiments. We used filter-based high volume air sampling instruments to generate samples used for subsequent DNA extraction. A cultivation-free metagenomics next generation sequencing (NGS) was adopted to identify microbial taxa to species level. The air-borne microbial community was found to be remarkably stable with recurrence intervals of high microbial abundance in the dark hours and relatively low abundance in the light hours. Air samples were dominated by DNA of basidiomycota fungi and less frequently of Ascomycota fungi phylum. The microbial air ecosystem was mostly modulated by day/night Biorhythms, temperature fluctuations and rain events. This is one of the highest-resolution researches currently undertaken on any air microbiome and its ecology, worldwide.

Biography

Elena S Gusareva has evolved to be a researcher with a broad knowledge and experience in different aspects of biomedical science and biostatistics. Since joining the team of Prof. Schuster in 2016, she has been involved in a relatively new research field and project on the air microbiome aiming to study microbial diversity and ecology of urban air. So far, the results of the research efforts are remarkable and will certainly generate a series of downstream benefits, including improvements to public health, building design and management.

egusareva@ntu.edu.sg

Notes:

International Conference on

ENVIRONMENTAL MICROBIOLOGY AND MICROBIAL ECOLOGY

&

International Conference on

ECOLOGY AND ECOSYSTEMS

September 18-20, 2017 Toronto, Canada

***In vitro* co-culture of commensal *Escherichia coli* strains enhances Stx2a production by the German *E. coli* O104:H4 outbreak strain**Yongxiang Zhang¹, Lu-Ya Wang¹, Chad Laing¹, Roger Johnson², Cassandra Jokinen¹, James Thomas³ and Victor Gannon¹¹National Microbiology Laboratory at Lethbridge, Canada²National Microbiology Laboratory at Guelph, Canada³University of Lethbridge, Canada

In 2011, a novel shiga toxin-producing *E. coli* (STEC) O104:H4 strain was associated with a large foodborne disease outbreak centered in Germany. The outbreak was characterized by a much higher rate of the hemolytic uremic syndrome (HUS) than typically occurs following STEC O157:H7 infections. Interestingly, this O104:H4 strain produced much lower levels of Stx2a than an STEC O157:H7 outbreak strain in the laboratory. Because the amount of Stx2a produced by O157:H7 strains is correlated with the development of severe clinical illness, such as STEC-associated HUS in humans, we wished to see if Stx2a-encoding phages released by these two STEC strains would increase toxin production by infecting commensal *E. coli*. In this study, we examined the role of commensal non-STEC in amplifying Shiga toxin 2a (Stx2a) production by the toxin-encoding phage released spontaneously from STEC. Co-incubation of *E. coli* K-12 C600 with the STEC O104:H4 strain ON-2011 and O157:H7 strain EDL933 resulted in 21- and 8-fold increases in shiga toxin production, respectively. However, among commensal non-STEC, only isolates of serotypes OR:H19 and O46:H31 from two of ten human fecal samples significantly increased Stx2a production following co-incubation with ON-2011, and no increase was observed following co-incubation of commensal *E. coli* with EDL933. While stable Stx2a phage Φ ON-2011 and 933W *E. coli* C600 lysogens were readily isolated following co-culture with these two pathogens, only Φ ON-2011 lysogens were isolated following co-incubation with the commensal *E. coli*. Two genes encoding putative phage receptor-binding determinants were present in the Φ ON-2011 genome but not that of 933W. While further study is required, it seems likely that differences in 933w and Φ ON2011 commensal *E. coli* host range may result in variability in the levels of Stx2a produced in certain individuals during the course of infection which could contribute to differences in the severity of STEC-associated disease.

Biography

Yongxiang Zhang is a biologist from National Microbiology Laboratory of public health agency of Canada. He has experience in studying the evolution and virulence of shiga toxin-producing *Escherichia coli* and the shiga toxin-encoding phage.

Yongxiang.zhang@canada.ca

Notes:

International Conference on

ENVIRONMENTAL MICROBIOLOGY AND MICROBIAL ECOLOGY

&

International Conference on

ECOLOGY AND ECOSYSTEMS

September 18-20, 2017 Toronto, Canada

Prospect of biofuel in Bangladesh: Bioethanol and biodiesel production at local conditionMohidus Samad Khan¹, Md Mursalin Rahman Khandaker¹, Suman Nandy¹, Anika Ferdous¹, Laila Hossain¹, Samavi Farnush Bint-E-Naser¹, Farid Ahmed¹, John Liton Munshi² and Chapol Kumar Roy²¹Bangladesh University of Engineering and Technology, Bangladesh²BCSIR Laboratories, Bangladesh

In Bangladesh, the demand of fossil fuel has been consistently increasing with the development of its industrial and agriculture sectors. The annual demand of petroleum products in Bangladesh is met primarily by refining imported crude oils from overseas. To meet the future energy demand and to save foreign exchange, it is essential to look for domestically produced renewable fuel sources. Bioethanol from biomass and biodiesel from microalgae could be potential alternate fuels for Bangladesh. Bioethanol, which is generally obtained from the conversion of carbon-based feedstock, is a quasi-renewable energy source. Although Bangladesh does not commercially produce bioethanol till date, there are few initiatives at the private sector in this regard, and therefore, it is important to understand the fuel properties of bioethanol. This study analyzes different fuel properties, namely, specific gravity & API gravity, viscosity, Reid vapor pressure, calorific value, ASTM color, ASTM distillation, copper strip corrosion and water sedimentation, of bioethanol and 5 and 10 percent bioethanol blended with petrol and octane. To make biofuel production from microalgae economically viable and sustainable, it is important to identify microalgae strains with high lipid content and to find an optimized mass culture technique for local condition. This study presents the growth kinetics of microalga *Chlorella vulgaris* grown in Bangladesh, in the parameters of cell count, optical density and dry cell weight cultured in 4 different media, namely CH, BB (Bold's Basal), MLA and CHU (modified). The growth curves obtained from algal growth in all the media were compared with lipid productivity. The extracted lipid was trans-esterified to produce biodiesel and the algal biomass left after lipid extraction was analyzed to quantify protein and other nutrients. This study will be highly useful, providing the baseline properties of locally produced bioethanol and biodiesel as potential alternate fuels for Bangladesh.

Biography

Mohidus Samad Khan is an assistant professor at the Department of Chemical Engineering, Bangladesh University of Engineering and Technology (BUET). He completed his BSc in chemical engineering (2004) from BUET, and Ph.D (2006-10) in bio-surface and biotechnology from Monash University, Australia. He worked as a post-doctoral fellow at the Department of Chemistry, McGill University, Canada to continue his research work on bio-surface engineering (2010-13). Since 2013, He is working as an assistant professor at BUET. He also served as a visiting professor (2015) at McGill University, Canada, and as a visiting research scholar (2016-17) at Texas A&M University, USA.

mohid@che.buet.ac.bd

Notes:

International Conference on

ENVIRONMENTAL MICROBIOLOGY AND MICROBIAL ECOLOGY

&

International Conference on

ECOLOGY AND ECOSYSTEMS

September 18-20, 2017 Toronto, Canada

Cattle Jaguar (*Panthera onca*) attack distribution in Miranda, Pantanal-Brazil**Julio Cesar de Souza¹, Waleria Menezes Barros¹, Rosana Moreira da Silva de Arruda¹, Marcos Paulo Rezende Gonçalves², Genezio Ferreira de Oliveira³, Carolina Fregonesi de Souza⁴ and Scott H Markwith⁵**¹Universidade Federal de Mato Grosso do Sul, Brazil²Università Degli Studi Firenze, Italy³Bodoquena Farm, Brazil⁴Universidade Federal do Pampa, Brazil⁵Florida Atlantic University, USA

Statement of the Problem: The Pantaneira plain is a true sanctuary with strong conservation of fauna and flora. Most of the areas are private and used for livestock production. The objective was geo referencing points where the Jaguar has slaughtered domestic animals; How far away is that in relation to the house of the farm workers; development management suggest actions for the conservation of wild species.

Methodology & Theoretical Orientation: The work was carried out at the Bodoquena Farm which is prized for the conservation of wild animals. The cattle are found in pastures located between reserved of forest and river with protected border. When a characterized carcass killed by jaguar is found, the GPS coordinates were taken and the cameras trails was put there. The research occurs on the period of 12/2015 to 05/2017.

Findings: It was geo referenced 91 points with carcasses. Bovine animals appear to be easier prey than wild animals (tapirs, deer, capybara, peccary, greater rhea, alligators, spotted paca, etc.). When the Jaguar goes out in search of food (natural prey) they first found cattle, for the facility and opportunity of attack, they end up preying the domestic animals. Possibly this jaguar's generations that learned to feed cattle. Many of the wild animals preyed on by the Jaguar now live together cattle or near human homes where they find protection. Recently, cattle were killed by Jaguar within 61m of the residence of a cowboy. There is no record of Jaguar's attack on humans on this farm, however, they are approaching closer to the residences, although to get cattle or capybaras.

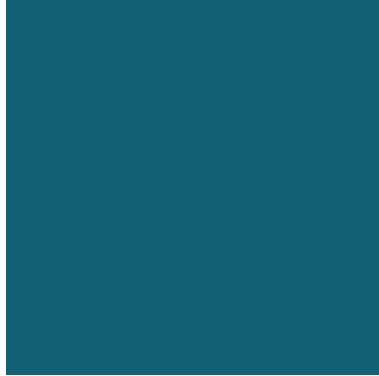
Conclusion & Significance: On the region need create ecological areas, a fauna management project with the purpose of conservation and sustainable. For avoiding the approach of the jaguar near the residences and a possible human accident Brazil public power need to take steps to create ecological reserves and conservation areas to do the fauna in this region. It is important one fauna management program predation control of cattle by Jaguar.

Biography

Julio César de Souza has expertise in animal production and conservation and sustainability. Bachelor's degree in Biological Sciences - Federal University of Mato Grosso do Sul (1986); degree in Animal Science - Federal University of Paraná (2008); a Master's Degree in Genetics and Animal Breeding from the UNESP State University (1992); and Ph.D in Biology (Genetics) at the UNESP (1997). Have two Post Doctoral, one in Animal Science, Missouri University, USA (2006/2007); and other in Florida Atlantic University – USA, in Genetics and Animal Conservation (2012/2013); He is a Full Professor in a UFMS; Has experience in Animal Science, with emphasis on Genetics and improvement of domestic animals, breeding and management of domestic animals, animal production, animal conservation, interaction domestic animals x wild animals, sustainability (buffaloes, horse, beef cattle).

julio.souza@ufms.br

Notes:



Joint Conference

International Conference on

ENVIRONMENTAL MICROBIOLOGY AND MICROBIAL ECOLOGY

&

International Conference on

ECOLOGY AND ECOSYSTEMS

September 18-20, 2017 Toronto, Canada

Special Session

Day 2

Joint Conference

International Conference on

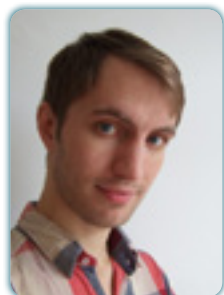
ENVIRONMENTAL MICROBIOLOGY AND MICROBIAL ECOLOGY

&

International Conference on

ECOLOGY AND ECOSYSTEMS

September 18-20, 2017 Toronto, Canada



Nikolaj Sørensen

Clinical-Microbiomics, Denmark

Reference-free shotgun metagenomics for the microbial ecologist

Traditionally, shotgun sequencing of complex microbial communities depends on reference genomes from known organisms. However, reference genomes are missing for the majority of the microbial diversity, making this approach inadequate for surveying complex microbial communities. The metagenomic species (MGS) concept allows detection and functional profiling of unknown species for which reference genomes are absent by clustering genes based on their abundance profiles. This method has already proven successful on the human gut microbiome, where it can identify up to five times more species than reference genomes can. The MGS concept has recently been expanded to include infants, mice, pigs, and marine microbial communities and can likely also be applied to terrestrial environments. Recent tests have found that the MGS concept is much more accurate and sensitive in detecting low-abundance taxa than a reference genome-based approach and, consequently, can provide reliable results at much lower sequencing depths, providing significant savings on sequencing costs. The MGSs typically consists of 1000-2000 genes representing core genomes and annotation of these genes allows identification of the functional potential of each MGS as well as insight into how metabolic pathways are distributed between the members of a microbial community. Furthermore, the majority of the MGSs appears to be only distantly related to known taxa and can provide a vantage point from which to describe new high-level taxa. The MGS concept is a very valuable tool for the microbial ecologist and allows surveying the microbial community at both a taxonomic and functional level of detail not previously possible.

Biography

Nikolaj Sørensen is a microbial ecologist with experience from a vast range of microbial habitats, including aquatic, terrestrial, and clinical microbial ecosystems. He makes extensive use of high-throughput sequencing in his work and is focused on bridging the gap between bioinformatics and microbial ecology. His holistic approach to microbial ecology comes from being actively involved in all steps of the scientific process, from study planning and sample collection through laboratory work and sequencing to bioinformatics and the ecological interpretation. He is the Director of scientific operations in the contract research organization clinical-microbiomics.

nikolaj@clinical-microbiomics.com

Notes:



Joint Conference

International Conference on

ENVIRONMENTAL MICROBIOLOGY AND MICROBIAL ECOLOGY

&

International Conference on

ECOLOGY AND ECOSYSTEMS

September 18-20, 2017 Toronto, Canada

Scientific Tracks & Abstracts

Day 2

International Conference on

ENVIRONMENTAL MICROBIOLOGY AND MICROBIAL ECOLOGY

&

International Conference on

ECOLOGY AND ECOSYSTEMS

September 18-20, 2017 Toronto, Canada

Exploring the gut microbiota of Lebanese preterm infants with or without necrotizing enterocolitis**Carole Ayoub Moubareck, Tarek Itani and Dolla Karam-Sarkis**
Saint Joseph University, Lebanon

Statement of the Problem: Necrotizing enterocolitis (NEC) is a devastating inflammatory disease which primarily affects preterm infants (PTI). Although its exact etiology remains unknown, gut bacterial colonization is recognized to play a pivotal role in its development. In this study, we hypothesized that differences in bacterial colonization exist between Lebanese PTI with and without NEC.

Methodology & Theoretical Orientation: A total of 11 PTI developing NEC was selected from three Lebanese neonatal intensive care units and matched with 11 controls. Three time intervals were defined: (a) before NEC; (b) most proximate to NEC; and (c) after NEC onset. Fecal samples were analyzed by q-PCR and TTGE.

Findings: By qPCR, all infants were colonized by *Staphylococci* and *Enterococci* with significant differences in colonization before NEC onset. Higher colonization levels by *Staphylococci* ($p=0.034$) and lower colonization levels by *Enterococci* ($p=0.039$) and *Lactobacilli* ($p=0.048$) in the NEC group were noticed indeed. Almost all infants were colonized by *Enterobacteriaceae* at high levels with a trend to higher frequency of colonization in NEC PTI during and after NEC onset. *Bacteroides* and all *Clostridia* (except cluster I) were strongly underrepresented in both groups. Furthermore, throughout the sampling period, comparison of stool samples by TTGE revealed no particular clusterisation suggesting a high inter-individual variability.

Conclusion & Significance: This study did not incriminate a unique causative pathogen but suggested that NEC resulted in part from a perturbation of the intestinal microbiota. It described an abnormal gut microbiota profile in NEC PTI that included high levels of colonization by *Staphylococci* and low levels of colonization by *Enterococci* and *Lactobacilli*. This understanding in NEC etiology might be translated into better prophylactic interventions including the use of pre and/or probiotics in order to reduce the incidence and severity of NEC.

Biography

Carole Ayoub Moubareck is a pharmacist who is specialized in microbiology (Ph.D from the Paris Descartes University) then pursued a Post-doctoral work at the Institute Pasteur of France. She was responsible of the National Reference Center of Antibiotic Resistance in France from 2007 to 2009. She has worked at Saint Joseph University in Lebanon and since 2014 she has been in Zayed University in Dubai as Associate Professor. Her research interests are in controlling infectious diseases by monitoring the emergence and spread of resistant bacteria to antibiotics and characterizing the related resistance mechanisms. She is also interested in food safety by assessing the innocuity of food strains and studying gene transfers from animal to human bacteria in the digestive ecosystem and evaluating the influence of environmental factors. An essential part of her research is about the determination of the intestinal microbiota of preterm infants and the relationship with the establishment of necrotizing enterocolitis.

Carole.AyoubMoubareck@zu.ac.ae

Notes:

Joint Conference

International Conference on

ENVIRONMENTAL MICROBIOLOGY AND MICROBIAL ECOLOGY

&

International Conference on

ECOLOGY AND ECOSYSTEMS

September 18-20, 2017 Toronto, Canada

Effects of bacterial inoculants on soil microbiomes and biodegradation in hydrocarbon contaminated soils**Coppotelli B M**

Center for Research and Development in Industrial Fermentation (CINDEFI) La Plata, Argentina

Over the years, we have collected different bacterial strains belonging to *shingomonadaceae* family, which have in common the ability to degrade PAH (polycyclic aromatic hydrocarbons). Their genomes have been fully sequenced (WGS) showing similarities in genes codifying enzymes involved in PAH degradation. All of them showed different degradation kinetics in cultures with phenanthrene as sole carbon source. This differences were confirmed when were inoculated in soil contaminated with phenanthrene. The bioaugmentation of the strain *Sphingomonas paucimobilis* 20006FA revealed a reduction in genetic and functional diversity of soil, and the accumulation of toxic phenanthrene metabolites reducing efficiency in phenanthrene degradation. This effect was not observed when a similar experiment was performed with *Sphingobium* sp. AM strain, suggesting that despite coding for the same enzymes the genes of the strains would be regulated differently. The effect of the inoculation with strain 20006FA and *Sphingobium* sp. 22B (more resistant to C-starvation and drying conditions) on contaminated soil in a desiccation environment, suggests that strain 22B is the most suitable due to its adaptation to the usual environmental conditions. The effect of bioaugmentation with *Sphingobium* sp. AM strain on different soils microbiomes (chronically and recently contaminated soil) revealed an increase in the richness and diversity (pyrosequencing) in both contaminated microbiomes. An improvement in the elimination of phenanthrene occurred only in recently contaminated soil. In all cases, there was evidence of the establishment of the inoculants, which occurred together with the modification of the microbiome of the soils. It was verified that the establishment of an inoculant in the soil does not necessarily correlate with the increase of the desired catabolic capacities, in our case the degradation of PAH, because it could have been established in function of other resources. We have observed that efficiency of an inoculant in soil is not directly related to its genetic potential but to other physiological properties, which could be translated in a distinctive environmental behavior.

Biography

Coppotelli B M has her expertise in microbial bioremediation and passion in contributing to environmental care. Her studies on hydrocarbon degrading bacterial strains and consortia have contributed to the world of microbial ecology, getting insight into ecology that drives bacterial communities in response to inoculation and biochemical processes of contaminant elimination in soils and sediments and interactions among bacterial community members. It allows contributing our understanding and helping in designing appropriate management and cleanup of contaminated ecosystems.

bibicoppotelli@gmail.com

Notes:

International Conference on

ENVIRONMENTAL MICROBIOLOGY AND MICROBIAL ECOLOGY

&

International Conference on

ECOLOGY AND ECOSYSTEMS

September 18-20, 2017 Toronto, Canada

Pantanal* bird species and their distribution in the Americas*Julio Cesar de Souza¹, Geovane Gonçalves Ramires¹, Marcos Paulo Rezende Gonçalves³, Vanessa Terra Gonçalves¹, Carolina Fregonesi de Souza³ and Scott H Markwith⁴**¹Universidade Federal de Mato Grosso do Sul, Brazil²Università Degli Studi Firenze – Unifi, Italy³Universidade Federal do Pampa, Brazil⁴Florida Atlantic University, USA

Statement of the Problem: The *Pantanal* biome one of the most diverse for avifauna when compared to wetlands such as the Everglades (Florida), Okavango Delta (Africa), Llanos (Venezuela) and Esteros de Ibera (Argentina), where 650, 365, 450, 258 and 343 species are found, respectively. The aim was to survey the avifauna of two routes in the *Pantanal* wetland (BR419 and MS170), Aquidauna (MS), to determine the avifauna of the region and their distribution throughout the Americas.

Methodology & Theoretical Orientation: BR419 (Taboco road) between the coordinates 20°26'49"S 55°47'01"W and 19°52'50"S 55°29'41"W. The other transect was on MS170, Retirinho road, between 20°26'23"S 55°48'10"W and 19°53'13"S 56°01'29"W. The observation times alternated between both routes avoid biasing sampling by time of day, i.e. when MS170 was sampled in the morning, the same or next afternoon the BR419 transect was sampled, the next time the transects were reversed by time of day. Both transects were sampled for a total of 14 sampling events, obtaining a total of 103 hours and 06 minutes of observations.

Findings: Were observant 125 species, thus, 58 live just in South America (SA); 17 live in SA and Central America; 19 live the SA at México; 27 live at Mexico plus USA; two arrive Canadian [*Falco sparverius* and *Tyrannus tyrannus*]; and two cosmopolites [*Pandion haliaetus* and *Passer domesticus*]. Using the classification of the IUCN (2017) one endangered species were observed [*Buteogallus coronatus*]; two near threatened [*Pyrrhura devillei*; *Rhea Americana*], and a two vulnerable [*Sporophila maximiliani*; *Anodorhynchus hyacinthinus*].

Conclusion & Significance: Many species in the Aquidauana region live only in SA, but others inhabit the of the Americas. It is important to have a comprehensive understanding of migration of these birds that have large ranges. This information is of paramount importance considering the possibility of dispersal of seeds, eggs, and even diseases. The study area should variety of species classified as endangered, vulnerable and near threatened.

Biography

Julio César de Souza has expertise in animal production and conservation and sustainability. He completed his Bachelor's degree in Biological Sciences - Federal University of Mato Grosso do Sul (1986); also has a degree in Animal Science - Federal University of Paraná (2008); a Master's Degree in Genetics and Animal Breeding from the UNESP State University (1992); and Ph.D in Biology (Genetics) at the UNESP (1997). He has two Post-doctoral degrees, one in Animal Science, Missouri University, USA (2006/2007); and other in Florida Atlantic University – USA, in Genetics and Animal Conservation (2012/2013); He is a Full Professor in a UFMS; he has experience in Animal Science, with emphasis on Genetics and improvement of domestic animals, breeding and management of domestic animals, animal production, animal conservation, interaction domestic animals x wild animals, sustainability (buffaloes, horse, beef cattle).

julio.souza@ufms.br

Notes:

Joint Conference

International Conference on

ENVIRONMENTAL MICROBIOLOGY AND MICROBIAL ECOLOGY

&

International Conference on

ECOLOGY AND ECOSYSTEMS

September 18-20, 2017 Toronto, Canada

In-situ* regeneration of carbon based injectants with endemic biofilms*Dennis Owens**

Sustainable Water Technology, Canada

Background Statement: Activated carbon (AC) has long been used to remove organic impurities from liquids and air. Generally, in the environmental field, we store AC inside vessels and then pump groundwater or air, contaminated with volatile organics, through the carbon vessel. This process injects AC into the contaminated mass itself to remediate the contaminants *in-situ*. AC has an affinity for organic chemicals, such as petroleum hydrocarbons, and organic chemicals will physically bond (absorb) to the micropores of the AC through Van der Waals forces. Once the chemicals are adsorbed to the carbon's surface, the process generally can be reversed only by heating the carbon to very high temperatures, by use of a solvent, or through microbial processes. AC has been found to remain stable under extreme environmental conditions for long periods of time. The purpose of this study is to evaluate methods to stimulate biofilm formation to regenerate *in-situ* AC.

Methodology: Laboratory contaminated soil columns are injected with AC and various additives to stimulate biofilm formation throughout the AC. Each different soil type was then evaluated for types of microorganisms forming the biofilm and their effectiveness in regenerating the AC.

Findings: Different soil types produced the same basic biofilms composed of the same four basic organisms predominating with various subcultures specific to the area and soil type. All biofilms could regenerate the AC *in-situ*.

Conclusion: Biofilms can be formed *in-situ* within the AC area and in the process of biofilm formation the AC is regenerated for continuous remediation *in-situ*. Cost implications are significant for this remedial tool.

Biography

Dennis Owens is the president and senior chemist/microbiologist at Sustainable Water Technology. He has worked in the environmental remedial field since 1985 developing and commercializing remediation technologies for various companies in Canada and the United States.

dennisowens@sustainablewatertech.com

Notes:

International Conference on

ENVIRONMENTAL MICROBIOLOGY AND MICROBIAL ECOLOGY

&

International Conference on

ECOLOGY AND ECOSYSTEMS

September 18-20, 2017 Toronto, Canada

Is offsetting a feasible way to mitigate impacts of coastal reclamation on biodiversity? A case study from China**Shuling Yu and Baoshan Cui**
Beijing Normal University, China

Reclamation of coastal wetlands has a major impact on biodiversity globally. We investigated the feasibility of using biodiversity offsets to mitigate the impacts of coastal reclamation on biodiversity using impacts of reclamation on macrobenthic diversity in the Yellow River Delta region in China as a case study. We estimated 472 km² of coastal wetlands have been reclaimed in the Yellow River Delta between 1980 and 2015, which is an average of 13.5 km² of coastal wetland reclaimed per year. We developed a methodology to calculate biodiversity offset ratios for coastal wetlands using inputs including: biodiversity lost due to development and gained due to restoration offsets, the delay between reclamation and restoration, the amount of biodiversity lost due to leakage and an annual discount rate. Offset ratios were particularly sensitive to the baseline used for the counterfactual. However, the relatively short time it takes for macrobenthos to be restored in coastal wetlands suggests that biodiversity offsets are theoretically feasible for mitigating the impacts of reclamation on this assemblage. However, we estimated that the area of suitable land available within the Yellow River Delta was sufficient to offset 1980-2015 years of reclamation, which suggests that other strategies such as avoiding future reclamation and reducing the impacts of future reclamation on macrobenthos are also necessary if no net loss of macrobenthic biodiversity is to be achieved in the Yellow River Delta Region of China. Our results have important implications for conservation in the face of ongoing coastal reclamation.

Biography

Shuling Yu has her expertise in biodiversity offsetting, wetland ecology, wetland restoration, and wetland management. Wetlands are economically and ecologically important ecosystems, but have been increasingly degraded by anthropogenic impacts. Her current project focuses on optimizing biodiversity offset strategies for degraded habitat from coastal reclamation.

shulingyu@mail.bnu.edu.cn

Notes:

International Conference on

ENVIRONMENTAL MICROBIOLOGY AND MICROBIAL ECOLOGY

&

International Conference on

ECOLOGY AND ECOSYSTEMS

September 18-20, 2017 Toronto, Canada

Effect of varietal feeding on larval duration and cocoon parameters of six strains of eri silkworm *Samia ricini* Donovan in Nagaland, India**L N Kakati**

Nagaland University, India

Rearing of six strains of *Samia ricini* (eri silk worm) i.e. Yellow plain (YP), Yellow spotted (YS), Yellow Zebra (YZ), Greenish blue plain (GBP), Greenish blue spotted (GBS) and Greenish blue zebra (GBZ) was conducted on *Ricinus communis* (Castor), *Heteropanax fragrans* (Kesseru), *Evodia fraxinifolia* (Payam) and *Manihot utilissima* (Tapioca) to evaluate the effect of seasonal pattern on larval duration and cocoon parameters in Nagaland, India. Larval duration during spring season was maximum in all strains in all food plants; however minimum for all strains was recorded during summer season on Castor, Kesseru and Tapioca. Cocoon weight was recorded to be minimum (2.8 ± 0.55 gm) in YP on Kesseru and maximum (4.06 ± 0.68 gm) in GBZ on Castor during spring season; shell weight fluctuated between 0.34 ± 0.08 gm during spring in GBS on Kesseru and 0.58 ± 0.09 gm during summer in YZ on Castor and percentage of silk ratio was found to be minimum and maximum in YP on Payam during spring (11.37 ± 1.29) and in GBS on Castor during summer (16.05 ± 1.59) respectively. The variation in larval duration and cocoon parameters reflected variation in nutrient composition of food plants and dynamic environment conditions prevailing in 1 different seasons of the year. Payam and Tapioca plants could be fed either singly or alternately with Castor or Kesseru to attain the commercial advantage to ensure more value added production. While there were differences in the productivity parameters with respect to strains and seasons, the present study shows that all the strains on four host plants expressed adoptability and suitability for commercial rearing under Nagaland climatic condition.

Biography

L N Kakati is presently Head, Department of Zoology, Nagaland University, Nagaland, India and teaches Ecology & Environmental Biology, Biosystematics, Evolution and Bio statistics in the postgraduate level. He has more than 30 years of research experience of wild silk moth biology and travelled extensively in different hilly states of North Eastern region of India for exploration of wild silk moths. He completed three research projects and presently undertaking two new projects sponsored by different funding agencies in India. Four students have been conferred Ph.D degree under his guidance and four students are presently pursuing research with him. He visited Khonkaen University, Thailand and Tokyo Agricultural University Tokyo for presentation of scientific papers in International seminars. He attended 48 seminars, chaired in technical sessions and delivered lectures in seven seminars as invited Resource person/Keynote speaker. He is presently member of 12 scientific associations and published 70 research papers.

kakati_in@yahoo.com

Notes:

Joint Conference

International Conference on

ENVIRONMENTAL MICROBIOLOGY AND MICROBIAL ECOLOGY

&

International Conference on

ECOLOGY AND ECOSYSTEMS

September 18-20, 2017 Toronto, Canada

Shifting paradigms in coastal restoration: Six decades' lessons from ChinaZe Zheng Liu¹, Baoshan Cui¹ and Qiang He²¹Beijing Normal University, China²Duke University, USA

With accelerating degradation of coastal environment worldwide, restoration has been elevated as a global strategy to enhance the functioning and social services of coastal ecosystems. While many developing countries suffer from intense coastal degradation, current understanding of the science and practice of their coastal restorations is extremely limited. Based on analysis of >1000 restoration projects, we provide the first synthesis of China's coastal restorations. We show that China's coastal restoration has recently entered a rapidly developing stage, with an increasing number of restoration projects carried out in multiple types of coastal ecosystems. While long-term, national-level restorations enforced by the government appear promising for some coastal ecosystems, especially mangroves, restorations of many other coastal ecosystems, such as salt marshes, seagrasses and coral reefs, have been much less implemented, likely due to under-appreciation of their ecosystem services values. Furthermore, the planning, techniques, research/assessment, and participation models underlying current restorations remain largely inadequate for restoration to effectively halt rapid coastal degradation. To promote success, we propose a framework where paradigms in current restorations from planning to implementation and assessment are transformed in multiple ways. Our study has broad implications for coastal environmental management policies and practices, and should inform sustainable development of coupled human-ocean systems in many countries.

Biography

Ze Zheng Liu has his research interests in wetland ecology and hydrology, wetland restoration, and wetland management. Currently, he is particularly interested in how the interactive processes of ecological communities, such as competition, facilitation, and food web interactions, to structure their environments and influence fundamental ecosystem processes such as plant growth and productivity. Such fundamental theories on community assembly and ecosystem functioning has important implications for the restoration of damaged habitats.

zzliu@mail.bnu.edu.cn

Notes:

International Conference on

ENVIRONMENTAL MICROBIOLOGY AND MICROBIAL ECOLOGY

&

International Conference on

ECOLOGY AND ECOSYSTEMS

September 18-20, 2017 Toronto, Canada

Insight into the diversity of soil fungi in Changbai mountain by high-throughput sequencingGuozhong Lyu¹, Dongning Shi^{1,2}, Zhihui Zhao¹ and Hong Yang¹¹Dalian Nationalities University, China²Liaoning Normal University, China

Soil fungi are an important group of microorganisms in forest ecosystem, they play pivotal roles in cycling of organic compounds and further affect the below-ground and above-ground ecosystems. In contrast to soil bacteria, soil fungi have been poorly understood in forest ecosystem. The rapid development of molecular technologies offers an effective method to access more functional information on soil fungal diversity. We applied the technique of Illumina Miseq High-Throughput Sequencing to investigate the soil fungal diversity and community structures in the northern slope of Changbai Mountain, Jiling Province, China, which is characterized with an evident vertical vegetation distribution pattern along with the altitude. The metagenome sequence analysis was conducted by targeting ITS1f-ITS2 fragments for 80 soil samples collected in the four characteristic forest vegetation bands ranging from the root of 700 m to the top of 2600 m in altitude, it reveals a tremendous abundance of soil fungi in Changbai mountain forest. Totally 2,294,552 rDNA fragments of reads are grouped into 25,282 operational taxonomic units (OUTs), they belong to 1056 species, 622 genera, 195 families, 87 orders, 24 classes and 5 phyla of fungi. Among which 182 genera are of *Basidiomycota* (48.72%), 411 genera of *Ascomycota* (31.67%), 13 genera of *Zygomycota* (10.21%), 13 genera of *Chytridiomycota* (0.27%), 3 genera of *Glomeromycota* (0.04%), and the left 9.09% are unclassified taxa. The species of *Basidiomycota* are the predominant components of the soil fungi in the mountain, especially the genera of *Laccaria* (6.17%), *Inocybe* (5.54%), *Hygrocybe* (3.06%), and *Russula* (2.37%) of *Agricales*. While the genera of *Mortierella* (6.73%) and *Inocybe* are most widely distributed in all altitude sampling soils in the mountain. The soil fungal richness evidently tends to decrease from the root to the top of the mountain, and the fungal compositions vary in the four characteristic vegetation bands of the mountain. The novel profile of soil fungi in the mountain uncovered by means of metagenome technique could not be obtained by conventional fungal research methods.

Biography

Guozhong Lyu has completed his Ph.D from Shenyang Agricultural University. He is the Dean of College of Environment and Resources, Dalian Nationalities University, China. He has published 150 papers mainly about fungal biodiversity, plant diseases and biocontrol of invasive weeds in academic journals.

lvz@dlnu.edu.cn

Notes:

International Conference on

ENVIRONMENTAL MICROBIOLOGY AND MICROBIAL ECOLOGY

&

International Conference on

ECOLOGY AND ECOSYSTEMS

September 18-20, 2017 Toronto, Canada

Large variations of salinity and dissolved oxygen and their effects on macrobenthic communities in Lake Sihwa, the west coast of Korea**Bon Joo Koo**

Korea Institute of Ocean Science & Technology, Republic of Korea

Since the dyke construction the lake Sihwa has undergone unstable environments such as large fluctuation of salinity and oxygen due to irregular exchanges of water between the outer saline zone and the inner brackish one, inflow of a good deal of pollutants from non-point and point sources and water stagnancy. It indicates that the lake ecosystem has a variability of species composition and species density. Especially, benthic organisms lack the ability to cope up with changes in the environment because most of them are sedentary and have limited mobility, thus the variation gives rise to change in the community structure. The Sihwa macrobenthos have responded to the severe environment, which was reported in some previous studies. However, these studies referred to the succession of macro fauna for only three years of the initial stage after the dyke construction. In the present paper, I report on the long-term responses of the macrobenthos to the large variation in salinity and dissolved oxygen for fifteen years after the birth of the lake.

Biography

Bon Joo Koo, Ph.D. Principal Research Scientist, Professor in UST Biological Oceanography & Marine Biology Division, Korea Institute of Ocean Science & Technology (KIOST)

bjkoo@kiost.ac.kr

Notes:

International Conference on

ENVIRONMENTAL MICROBIOLOGY AND MICROBIAL ECOLOGY

&

International Conference on

ECOLOGY AND ECOSYSTEMS

September 18-20, 2017 Toronto, Canada

Hexavalent chromium induces testicular dysfunction in small Indian mongoose (*Herpestes javanicus*) inhabiting tanneries areas of Kasur District, Pakistan**Shaista Andleeb and Tariq Mahmood**
PMAS-AAUR, Pakistan

Hexavalent chromium (Cr-VI), widely used in tanning industries, is a potent toxic metal whose accumulation in the animal body can adversely affect the reproductive organs. District Kasur, Pakistan, is famous for having tanneries industry where Cr (VI) is directly discharged untreated into the adjoining water nullahs. Resultantly, wildlife species, reliant on these water sources, are exposed to chromium toxicity, which enters into the animal body through drinking water and food chain. The current study investigated toxic effects of Cr(VI) on testicular tissue of adult small Indian mongoose inhabiting the study area from February 2015 to January 2016. Average Cr-concentrations, in experimental area soil and water, and the blood and tissue samples of the species were found significantly higher compared to control. Average body and testicular weights of experimental animals were found reduced. Histological analysis revealed seminiferous tubules disorganized in experimental animals, depleted germ cells and hyperplasia of the Leydig cells. Sperm counts were found reduced. Serum testosterone and LH levels were found reduced while FSH levels increased in experimental animals. The study concludes that Cr being discharged from tanneries into the environment is up taken by small Indian mongoose leading to severe testicular tissue damage and potential impairment of reproductive function of the species.

Biography

Shaista Andleeb is Ph.D Scholar at the department of Wildlife Management, Pir Mehr Ali Shah-Arid Agriculture University Rawalpindi, Pakistan. She secured her MPhil degree from the same department, by conducting research work on the ecology of endangered Indian Pangolin (*Manis crassicaudata*) in the Margallah Hills National Park, Islamabad, Pakistan. Recently working on the toxic effects of chromium on the reproductive physiology of small Indian mongooses, inhabiting the tannery areas of Kasur District, Pakistan. District Kasur is famous for having leather tannery industries and the surrounding environment is highly contaminated with chromium, being discharged by these industrial effluent, eventually the wildlife residing this contaminated area poses serious health problems.

shaistaandleeb444@gmail.com

Notes:

International Conference on

ENVIRONMENTAL MICROBIOLOGY AND MICROBIAL ECOLOGY

&

International Conference on

ECOLOGY AND ECOSYSTEMS

September 18-20, 2017 Toronto, Canada

Diversity dynamics of cotton infecting *Begomovirus*, a serious threat emerged due to assorted agro-climate of Pakistan**Muhammad Javed Iqbal, Muhammad Zia-Ur-Rehamn, Usman Hameed and Muhammad Saleem Haider**

University of the Punjab, Pakistan

Pakistan is an agriculture based mono-crop economy largely dependent on cotton with 4th rank in production and 3rd in consumption globally. For last few decades cotton leaf curl disease (CLCuD) caused by a group of *Begomovirus*, is been proved to be havoc for cotton production in Pakistan with two major epidemic outbreaks after 1990s (\$5 billion loss in less than five years) and still a nightmare for country as they possess great evolving potential due to diverse and changing climate and cropping practices in cotton growing zone. Globally this virus has been reported from India, and several countries of Africa after Pakistan and now from China and Philippine too threatening the Australia and America with Large infestation of *Begomovirus* vector, White fly (*Bemisia tabaci*). The targeted virus has great recombination and resistance breaking capabilities specially therefore a constant eye is required on it to predict its genetic behavior and possible recombination. In current study diversity dynamics of *Begomovirus* has been study in different wild and cultivated hosts along with cotton with coat protein marker, to evaluate the host range of virus, either are they restricted to hosts or have multiple or shared host, in same way the viruses in cotton and non-cotton regions of Pakistan are evaluated. From 25 plant samples 13 different *Begomovirus* were identified. Six different samples were with mix viral infection, 7 different wild weeds were proved to be reservoir of *Begomovirus*. 7 viruses were common in different locations 4 plants were hosting different viruses in different locations, 7 viruses were found in multiple locations and There were 13 new reports of viruses and host which were not known before. Facts revealed that in favoring multiple cropping *Begomovirus* have developed utmost important infection patterns which favor them to recombine and evolve better to overcome host resistance in short time.

Biography

Muhammad Javed Iqbal is a Ph.D Scholar at University of Punjab, Lahore, Pakistan. He is working on diversity of plant viruses especially on *Begomovirus* (A genus of ssDNA virus family, *Geminiviridae*) and on RNAi based endogenous resistance development against these viruses. He is much interested in evolving potential of these viruses in the changing climate and agro-ecological systems. This work can be helpful for a large scientific community who are fighting these pathogens for global food and agriculture security.

javed786_pk@yahoo.com

Notes:



Joint Conference

International Conference on

ENVIRONMENTAL MICROBIOLOGY AND MICROBIAL ECOLOGY

&

International Conference on

ECOLOGY AND ECOSYSTEMS

September 18-20, 2017 Toronto, Canada

Young Researchers Forum

Day 3

International Conference on

ENVIRONMENTAL MICROBIOLOGY AND MICROBIAL ECOLOGY

&

International Conference on

ECOLOGY AND ECOSYSTEMS

September 18-20, 2017 Toronto, Canada

Immobilization of murine noroviruses in a cultivated phaeozem soil and its reversibilityVincent Tesson¹, Gael Belliot², Line Capowiez¹ and Pierre Renault¹¹INRA, France²University of Dijon, France

Wastewater reuse in irrigation may contaminate soils with human enteric viruses that can be internalized in plants via their roots. Experiments have shown that virus immobilization in soils varies with virus, soil and soil solution; results were mostly obtained at saturation and the reversibility of immobilization was not clearly assessed. Models generally use a partition coefficient, although colloid immobilization is often assumed kinetic and non-reversible. Our objectives were to explore other contexts, assess the reversibility of immobilization and the relevance of equilibrium or kinetic models. Columns of phaeozem soil aggregates were saturated with soil solutions optionally enriched with MgCl₂ or fulvic acids, under vacuum or air to affect air trapping. For immobilization, the solutions circulated at different temperatures between the columns and reservoirs contaminated with murine noroviruses. For remobilization, contaminated columns were stored between 0 and 6 days at some moistures and then rinsed by - virus-free - soil solutions, sterilized wastewater or underground water. Solutions were sampled in the reservoirs or at the column outlets; half aliquots were filtered at 0.45 µm. Viruses retained in soils were extracted. Immobilizations were also monitored on stirred soil suspensions. Viruses were quantified by RT-qPCR and cell culture. The relevancies of models combining flow and immobilization were evaluated. Except after MgCl₂ enrichment, the weak virus immobilization over 1 day - i.e. about 40% of the brought viruses - could be quantified only from remobilization experiments. When saturated conditions are kept for 6 additional days, most of viruses are progressively immobilized, only a few being remobilized later with virus free soil solution. Fulvic acids increase virus remobilization. By contrast, the partial drying of soil columns after the initial immobilization day increases the irreversibility of the immobilization. Models considering inter- and intra-aggregate pore spaces as well as reversible and irreversible virus immobilizations fitted to experiments.

Biography

Vincent Tesson has his expertise in the environmental fate of human enteric viruses. After working on the detections of equine and *Bovine coronavirus* by RT-qPCR and FTIR spectroscopy, respectively, he undertook a Ph.D on the environmental fate of human enteric viruses by analyzing their fate after wastewater discharge in river or reuse in agricultural irrigation. He has completed a work on the fate of viruses in the soil that contributes to a project on green onion contamination. He is currently working on the simulation of virus discharge in rivers from regional acute gastroenteritis epidemiological data.

vincent.tesson@inra.fr

Notes:

International Conference on

ENVIRONMENTAL MICROBIOLOGY AND MICROBIAL ECOLOGY

&

International Conference on

ECOLOGY AND ECOSYSTEMS

September 18-20, 2017 Toronto, Canada

Bacillus megaterium*: A potential swimmer and an efficient bio-degrader of an organophosphorus pesticide*Shweta N, Jadhav S K and Keshavkant S**
Pt. Ravishankar Shukla University, India

Agriculture sector is largely dependent on the use of synthetic agrochemicals (pesticides) for increasing the crops productivity and to protect it from pests. Chlorpyrifos is one of the globally and popularly exploited pesticides, but continuous and unethical use of it has become a major threat to soil contamination due to high soil adsorption coefficient, comparatively longer half life and persistence nature. The Diffusion chamber method targeted one of the bacterial strains from the soil samples of identified paddy growing field which showed significant growth and tolerance against higher (600 mgL^{-1}) concentration of Chlorpyrifos and having potency of its degradation. Morphological and molecular characterization identified the strain as *Bacillus megaterium*. Further, micro-capillary assay revealed Chlorpyrifos as chemo attractant for the *Bacillus megaterium* and chemotactic response was seen to be induced by both 600 and 800 mgL^{-1} concentrations of this pesticide. Moreover, the results of HPLC analysis pertaining to Chlorpyrifos degradation efficiency revealed that 600 mgL^{-1} of it is the most suited concentration for degradation by *Bacillus megaterium*, and about 81% of it was metabolized within 10 days of incubation. Concentration dependent decrease in peak area as well as emergence of new peak(s) was also observed which could be assumed as metabolites of this pesticide. Moreover, SDS-PAGE of the *Bacillus megaterium* cell lysate revealed appearance of new bands over the gel in response to Chlorpyrifos. Thus, overall study suggested that *Bacillus megaterium* could be well exploited for bioremediation of Chlorpyrifos contaminated sites.

Biography

Shweta N is pursuing her Ph.D from School of Studies in Biotechnology, Pt. Ravishankar Shukla University, Raipur, India. She is working as an environmental microbiologist and has expertise regarding isolation of the microbes using the modern cultivation approaches. She has been testing the microbes for biodegradation purpose of pesticides for achieving sustainability also testing the sensory response of bacteria. She has been working in this area for three years. Achievements of her include isolation of positive and responsive pollutant (especially pesticides) degrading bacteria. In relation to this, she has published one paper and others are in communication.

shwetanistala@gmail.com

Notes:

International Conference on

ENVIRONMENTAL MICROBIOLOGY AND MICROBIAL ECOLOGY

&

International Conference on

ECOLOGY AND ECOSYSTEMS

September 18-20, 2017 Toronto, Canada

You are what you eat: Get mature faster by foraging on your parents, the discus fish example**Francois-Etienne Sylvain**
Laval University, Canada

The Discus fish (*Symphysodon aequifasciata*) is an Amazonian ornamental fish with a unique parental behaviour. After hatching, the fry feeds exclusively on a cutaneous mucus secretion from both parents during three weeks. Studies have documented a differential protein pattern on the mucus layer of discus in reproductive phase, suggesting that specific elements are vertically transferred from parents to their offspring to stimulate fry growth. The aims of our study were (1) to characterize the ontogenesis of discus fish gut microbiota; (2) to determine if reproduction phase induced a differential shift of cutaneous mucus microbiota composition on parental fish; and (3) to assess the impact of parental feeding on the compositional dynamics of discus fry gut microbiota. To achieve these goals, we sampled thoroughly one brood of *S. aequifasciata*, during four months post-hatch. We sampled fry and parental feces, parental mucus and aquarium water. We sequenced the hypervariable region V4 of the rRNA 16S to characterize bacterial communities in all samples. The results show that (1) there is a convergence of the gut microbiota composition of the fry towards the gut microbiota of their parents as soon as the fry starts feeding on their parents cutaneous mucus; (2) there is a differential shift of the parental mucus microbiota composition when the parents get in reproductive phase; and (3) the taxonomic structure of the fry gut microbiota stabilizes earlier than what has been observed for the shorter-lived zebrafish. Our results highlight the beneficial influence of vertical parent-offspring transfer of parental bacteria via skin mucus feeding.

Biography

Francois-Etienne Sylvain completed his Master's thesis at Laval University (Quebec). His longtime passion for the underwater world led him to work on fish-associated microbiomes. Francois-Etienne is particularly interested in understanding what are the factors that shape the structure of Amazonian fish microbiota, as the Amazon River Basin contains the highest fish biodiversity in the world, as well as very contrasted aquatic environments (e.g. black and white water). Francois-Etienne and his thesis advisor, Nicolas Derome, have established a research collaboration with the National Institute of Research of the Amazon (Brazil), where two collaborative research projects were completed. For his research on the discus fish gut microbiota ontogeny, Francois-Etienne received the JC Bill Costerton Award, for "Research that best involves new theories in microbial ecology and wider inter-disciplinary significance" at the 16th International Symposium of Microbial Ecology (ISME 2016).

francois-etienne.sylvain.1@ulaval.ca

Notes:

Joint Conference

International Conference on

ENVIRONMENTAL MICROBIOLOGY AND MICROBIAL ECOLOGY

&

International Conference on

ECOLOGY AND ECOSYSTEMS

September 18-20, 2017 Toronto, Canada

Biodiversity monitoring in Sno valley (Georgia, Caucasus)**Eter Abulidze**

Iliia State University, Georgia

The valley of Sno in Georgia (Caucasus) is reach with its biological and landscape diversity (<http://www.apa.gov.ge>) and is one of the most popular destinations for tourists. Currently hydro-electric stations and pylons are planned to deploy in Sno valley, which is supposed to have an impact on the biodiversity of the area. Previous studies have shown that the development of high voltage electro-power transmission system could affect local biodiversity either by destruction of physical environment and by direct influence of electro-magnetic field on plants and animals (<https://electricalnotes.wordpress.com> 2012.02.17). The direct effects on biodiversity could be numerous. As power lines are particularly bright and their Ultra Violet light is visible for most of the animal species, it will become physical barrier for them which in turn could pose a problem during the migration (<https://www.theguardian.com> 12 March 2014). Some bird species (Great Rosefinch (*Carpodacus rubicilla*), Guldenstadt's Redstart (*Phoenicurus erythrogaster*) and Chiffchaff, (*Phylloscopus collybita*) spend their lifetime on Sno valley (N. Paposhvili et al., 2016). In winter, they use the Sea-buckthorn for feeding which is mostly occurring in the areas where the pylon will be deployed. The large part of this wintering habitat is already destroyed which means that, specific bird species will face to significant problems. High voltage electro-magnetic field have also shown to affect animal and plant species health, development and germination (Balaji, A. 2015; Dib & Mordjaoui, 2014). Hence, monitoring of local biodiversity is an important issue for its maintenance and conservation. The proposed research will help to develop biodiversity database that could serve as a baseline for future biomonitoring of the impact of hydro-electric constructions. In particular, from April I am doing to accurately evaluate the forest coverage in the valley and generate distributional database for wooded plants, bird, large mammal and reptile species.

Biography

Eter Abulidze from Georgia (Caucasus), is a 3rd year Ph.D student at the Iliia State university, Faculty of Natural Sciences and Engineering, She is working as a Researcher at the Institute of Ecology (2013–2014/2016-2017). Also She has the financial support as a Researcher for the biodiversity monitoring program from German NGO GIZ (2017). During two years She was studied in Italy University of Tuscia, Department of Dafne, as an Ph.D exchange student (Erasmus Mundus program) molecular genetics' laboratory and worked molecular-genetic analysis of Nordman's Fir (*Abies nordmannian*) and Eastern spruce (*Picea orientalis*) in Caucasus region (2014-2016). She was involved in "Spiral Methodology Seminar" at Greece City of Kavala. She has a Master's Degree in Ecology and Conservation Biology and Bachelor's Degree in Biology and Ecology.

eter.abulidze.1@iliauni.edu.ge

Notes:

International Conference on

ENVIRONMENTAL MICROBIOLOGY AND MICROBIAL ECOLOGY

&

International Conference on

ECOLOGY AND ECOSYSTEMS

September 18-20, 2017 Toronto, Canada

Monoclonal and polyclonal antibodies directed toward *Tsukamurella pulmonis* polysaccharide

Adnan Saeed, Mariola Paściak, Jerzy Szkudlarek, Marek Drab and Andrzej Gamian

Ludwik Hirsztfeld Institute of Immunology and Experimental Therapy, Poland

The genus *Tsukamurella* includes aerobic Gram-positive and modified acid alcohol-fast-positive rods belonging to the aerobic actinomycetes, usually found in soil, sludge and arthropods. *T. pulmonis* is a rare human pathogen associated with oncologic and immunosuppressed patients, and a variety of infections have been associated with this bacterium: pneumonia, conjunctivitis, keratitis and catheter-related bacteremia. The strain of *T. pulmonis* was obtained from Polish Collection of Microorganisms (PCM 2578). The bacteria were identified morphologically by Gram staining, scanning electron microscopy and MALDI-TOF mass spectrometry. The polysaccharides were extracted by trichloroacetic acid from dry bacterial cell mass and purified by anion exchange and gel permeation chromatography. Sugar composition was determined by gas-liquid chromatography-mass spectrometry (GLC-MS). The monoclonal antibodies against polysaccharide of *T. pulmonis* were obtained by the hybridoma technique. Rabbit polyclonal immune sera against *T. pulmonis* were obtained by immunization with *T. pulmonis* whole cells. The scanning electron microscopy showed a variation of the rod shape of the bacteria. Purified polysaccharide of *T. pulmonis* consists of arabinose and mannose also traces amounts of glucose and galactoses were detected. Two hybridomas 5 and 23 producing mAbs against polysaccharide antigen were IgM class. The ELISA test allowed to detect cross reactivity of these monoclonal antibodies with some other Actinomyces spp antigens. Reactivity in double immunodiffusion test of polysaccharide antigen of *T. pulmonis* with polyclonal sera against *T. pulmonis*, *T. tyrosinosolvans*, *T. inchonensis* and *T. paurometabola* cells was observed. Cross reactivity of EPS were seen with all *Tsukamurella* antisera studied. Results indicate that monoclonal and polyclonal antibodies and polysaccharide could serve as tools for diagnostic purposes but their diagnostic potential should be further studied regarding the specificity and structure of epitope recognized.

Biography

Adnan Saeed is researcher in Department of Immunology and Infectious Diseases, Ludwik Hirsztfeld Institute of Immunology and Experimental Therapy, Polish Academy of Sciences, Weigla 12, Wrocław, Poland.

Adnan.m14.m14@gmail.com

Notes:



Joint Conference

International Conference on

ENVIRONMENTAL MICROBIOLOGY AND MICROBIAL ECOLOGY

&

International Conference on

ECOLOGY AND ECOSYSTEMS

September 18-20, 2017 Toronto, Canada

Video Presentation

Day 3

International Conference on

ENVIRONMENTAL MICROBIOLOGY AND MICROBIAL ECOLOGY

&

International Conference on

ECOLOGY AND ECOSYSTEMS

September 18-20, 2017 Toronto, Canada

Effect of inoculation with phosphate solubilizing fungus on growth and nutrient uptake of wheat and mungbean plants fertilized with tri-calcium phosphate in alkaline soilsRachana Jain¹, Jyoti Saxena², Vinay Sharma³ and S N Naik¹¹Indian Institute of Technology, New Delhi, India²BT Kumaon Institute of Technology, India³Banasthali University, India

Thirty-two isolates were recovered from farmland soil samples of the Banasthali region, Rajasthan, India, out of which 16 showed phosphate solubilizing potential. These microorganisms were further screened based on solubilization efficiency of inorganic phosphate sources in Pikovskaya agar and broth media containing tricalcium phosphate as an insoluble source of phosphorus. Isolates S33 showed the highest phosphate solubilizing potential, and later identified as *Aspergillus tubingensis*, was selected for further work. This isolate could solubilize other inorganic forms of phosphorus (P) viz. dicalcium phosphate, ferric phosphate and Udaipur rock phosphate. The efficiency of *Aspergillus tubingensis* S33 was further studied in semi-arid soils in a pot experiment to evaluate the effects of this fungus on the enhancement of P uptake by plants, available P status in the soil, dry matter production and grain yield of wheat (*Triticum aestivum* L.) and mung bean (*Vigna radiata*). Inoculation of *A. tubingensis* S33 significantly improved dry matter and grain yield in both crops. In general, there was a significant improvement in P uptake by plants and extractable P status in the soil. The results suggested that *A. tubingensis* S33 can play an important role in wheat and mungbean growth promotion and increase in soil available P.

rachana_nbs@yahoo.co.in

Notes: