The 12th Global Microbial Identifier Meeting, Nanyang Technological University, Singapore
Day 1: Wednesday 12th June 2019

Presentation abstracts and biographies

A Global Database – the vision and action of GMI
Joergen Schlundt, Nanyang Technological University, Singapore

As Next Generation DNA Sequencing (NGS) spreads globally fast, there is an obvious potential to develop a global microbial Whole Genome Sequence (WGS) database to aggregate, share, mine and use microbiological genomic data.

In the not so distant future such data collections will be used as diagnostic tools. In the end, all microbial species, strains, clones will be in the database, enabling any laboratory to upload its sequence and seek the correct answer, meaning species, type (clone) and antimicrobial resistance. If/when all microbiological labs start using this system, it will also enable real-time global surveillance of all relevant communicable diseases (human, animal, plant)
It is important to note that such databases will provide the basis for a platform for WGS investigations of all microorganisms, human and animal pathogens, environmental microorganisms, microorganisms used in food production (probiotics, industrial strains etc.)
This system would promote equity in access and use of NGS worldwide, including in developing countries, but it should be noted that a number of obstacles to open data sharing of WGS data exists.
The Global Microbial Identifier (GMI) an initiative presently involving > 250 researchers from > 50 countries is managed by a Steering Committee, and operates through four Working Groups and annual Global Meetings. The main activities until now includes GMI minimum data requirements for genomic databases (used in NCBI and EBI), three global GMI Lab Proficiency Tests assessing NGS capacity, two letters to Governments of all countries (192) about the potential benefits of microbial DNA sharing.

Joergen Schlundt is Professor Food Science at Nanyang Technological University, Singapore and works at NTU Food Technology Centre (NAFTEC). He has worked at NTU since 2015, but is a Danish citizen with a Ph.D. from the Royal Veterinary University in Denmark in 1983. His work was mainly nationally on food safety 1983-99, including 3 years in Zimbabwe. From 1999-2010 Director Food Safety and Zoonoses at the WHO. 2011-14 Director National Food Institute, Denmark.
JS participated in development of food safety Risk analysis principles, the creation of the WHO International Food Safety Authorities Network (INFOSAN), the first-ever estimation of the global burden of foodborne diseases as well as AMR risk assessment. JS chairs the Global Microbial Identifier, an international initiative suggesting a global database of DNA-sequences of all microorganisms. Throughout his professional life, JS has advocated the lowering of human health risk through effective, science-based action in food production systems.

The air microbiome: A missing ecosystem?
Stephan Schuster, Nanyang Technological University, Singapore

Microbial communities inhabiting terrestrial and aquatic ecosystems have long been studied. With the onset of metagenomics, the degree of diversity and abundance of these communities have become apparent, even on a global scale. In contrast, the atmosphere, despite its enormous planetary volume, has largely been neglected as a habitat for microbial communities, despite providing means of transport with an intercontinental range. We have studied the occurrence of airborne microbial organisms in the tropical climate of Singapore and found robust and persistent assemblages, both on an intra-day and a month-to-month time scales. Plant-associated bacteria and fungi were found to be the major constituent of the air microbiome, in addition to DNA derived from plants and insects. Besides conducting in-depth metagenomics studies that identified the diversity and abundance of airborne organisms, we have sequenced and assembled "100 genomes from air" using single molecule real-time sequencing (SMRT). These genome data, together with organismal and habitat information, are stored in a "DNAir database", which largely extends the organismal range of public databases and also includes previously uncultivatable organisms.

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Prof. Stephan Schuster is Deputy Centre Director (Facilities & Capacities); Research Director (Meta-'omics & Microbiomes), Professor, School of Biological Sciences, NTU; Prof. Stephan Schuster's expertise lies in developing and implementing sequencing platforms with significant discoveries in microbial and human evolution, eukaryotic cell biology and biodiversity. At SCELSE Prof. Schuster is investigating bacterial communities using cutting edge technologies to address structure, function, dynamics and interactions in complex biofilm communities.

Eric Yap, Nanyang Technological University, Singapore - Not available

Whole-genome Sequencing Reveals Plasmid-mediated Transmission and Persistent Healthcare Reservoirs of Carbapenemase-producing Enterobacteriaceae
Ng Oon Tek, Tan Tock Sing Hospital, Singapore

Carbapenemase-producing Enterobacteriaceae (CPE), which is a global, antibiotic-resistant "superbug" threat with 40 to 80% mortality. Infection control, the main intervention to prevent CPE disease spread, is hindered by inability to accurately determine transmission pathways. Recent evidence strongly suggests the inanimate environment as having a major role in CPE spread. We share WGS data over 5 years in Singapore hospitals examining this issue.

Dr Ng Oon Tek is an Infectious Disease Senior Consultant with interest in research integrating public health, laboratory medicine and clinical medicine to improve patient outcomes. He works in the CaPES network on understanding how to stop spread of CPE. He was recently funded by the Singapore Medical Research Council for a study using FMT for CPE gut eradication. His research interest include antimicrobial resistance, emerging infectious diseases and HIV.

Recovery of closed bacterial genomes from complex microbial communities using long read metagenomics

Krithika Arumugam, Nanyang Technological University, Singapore

Metagenome assembly is taking an increasingly central role in the analysis of complex microbial communities, due to the ability of this approach to recover draft genomes of member species, thus providing a rigorous basis for studying the community composition and function. To date most metagenome assemblies have been undertaken using data from short read technologies, but this approach has rarely been able to generate closed genomes. New long read technologies offer huge potential for effective recovery of complete, closed genomes. Here we examine the ability of long read data to permit recovery of genomes from enrichment reactor metagenomes: as they offer a moderate level of complexity compared to their inoculum sourced from full scale wastewater treatment plants. We sampled a bioreactor community designed to enrich for polyphosphate accumulating organisms (PAO), extracting genomic DNA and obtaining both short read (Illumina 301bp PE) and long read data (MinION Mk1B) from the same DNA aliquot. We demonstrate that whole bacterial chromosomes can be obtained from whole community long read data. We provide a straightforward pipeline for processing such data, which includes a new approach to correcting erroneous frame-shifts, as well as descriptive statistical methods for screening associations between short read MAGs and long read chromosome length assembled sequences, in order to identify cognate genomes from both analyses. We conclude that long read metagenomics on medium complexity microbial communities is feasible and can recover closed, complete genomes of the most abundant community members.

Krithika Arumugam studied Computer Science and Engineering at Saveetha Engineering College (Anna University) in Chennai, India. She completed her MSc in Bioinformatics at Nanyang Technological University in 2011. Since then she has been working as a Bioinformatician at the Singapore Centre for Environmental Life Sciences Engineering (SCELSE), NTU. With interests in metagenomics and distributed computing, she designs pipelines and analyses high throughput next generation sequencing data in high performance computing environments. Her primary research focuses on genome recovery from metagenome assembled genomes.

Cartography of Opportunistic Pathogens and Antibiotic Resistance Genes in a Tertiary Hospital Environment

Niranjan Nagarajan, Genome Institute of Singapore, Singapore

There is growing attention surrounding hospital acquired infections (HAIs) due to high associated healthcare costs, compounded by the scourge of widespread multi-antibiotic resistance. Although hospital environment disinfection is well acknowledged to be key for infection control, an understanding of colonization patterns and resistome profiles of environment-dwelling microbes is currently lacking. We report the first extensive genomic characterization of microbiomes (355), common HAI-associated microbes (891) and transmissible drug resistance cassettes (1435) in a tertiary hospital environment based on a 2-timepoint sampling of 179 sites from 45 beds. Deep shotgun metagenomic sequencing unveiled two distinct ecological niches of microbes and antibiotic resistance genes characterized by biofilm-forming and human microbiome influenced environments that display corresponding patterns of divergence over space and time. To study common nosocomial pathogens that were typically present at low abundances, a combination of culture enrichment and long-read nanopore sequencing was used to obtain thousands of high contiguity genomes (2347) and closed plasmids (5910), a significant fraction of which (>58%) are not represented in current sequence databases. These high-quality assemblies and metadata enabled a rich characterization of resistance gene combinations, plasmid architectures, and the dynamic nature of hospital environment resistomes and their reservoirs. Phylogenetic analysis identified multidrug resistant clonal strains as being more widely disseminated and stably colonizing across hospital sites. Further genomic comparisons with clinical isolates across multiple species supports the hypothesis that multidrug resistant strains can persist in the hospital environment for extended periods (>8 years) to opportunistically infect patients. These findings highlight the importance of characterizing antibiotic resistance reservoirs in the hospital environment and establishes the feasibility of systematic genomic surveys to help target resources more efficiently for preventing HAIs.

Dr. Niranjan Nagarajan is Associate Director and Senior Group Leader in the Genome Institute of Singapore, and Associate Professor in the Department of Medicine and Department of Computer Science at the National University of Singapore. His research focuses on developing cutting edge genome analytic tools and using them to study the role of microbial communities in human health. His team conducts research at the interface of genetics, computer science and microbiology, in particular using a systems biology approach to understand host-microbiome-pathogen interactions in various disease conditions. Dr. Nagarajan received a B.A. in Computer Science and Mathematics from Ohio Wesleyan University in 2000, and a Ph.D. in Computer Science from Cornell University in 2006 (Advisor: Prof. Uri Keich). He did his postdoctoral work in the Center for Bioinformatics and Computational Biology at the University of Maryland working on problems in genome assembly and metagenomics (Advisor: Prof. Mihai Pop).

NGS training and application in Southern Africa
Yasmina Fakim, University of Mauritius, Mauritius

The rapid development in sequencing technologies has contributed to a sharp increase DNA sequence data from a wide diversity of organisms. Since 2012, several initiatives have enabled the promotion of NGS in this part of Africa. While sequencing can be paid for and done at commercial institutions, the library preparation and analysis/processing of data require expert training. SANBio and H3ABioNet are two research organisations/networks that have contributed to bringing NGS to researchers in Southern Africa. SANBio- is a network that groups twelve countries in the region and has funded several training events in NGS analysis since 2014 with support from Finland and Sweden. H3ABioNet is a larger consortium of nodes across Africa with UCT, SA as the central node. This presentation will highlight the program of training and research in countries of SW Indian Ocean and Southern Africa where NGS is being applied. Although several research groups across Southern Africa have already started to implement NGS, it is still inaccessible to many because of lack of proper facilities. Different countries are setting up separate programs while a concerted effort towards a coherent strategy would be far more effective. GMI would have a role in assisting institutions developing such a strategy.

Yasmina Jaufeerally Fakim;
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WHO Discussions on Implications of Implementation of the Nagoya Protocol on Access and Benefit of Pathogens and Sequence Sharing

Peter Ben Embarek, The World Health Organization, Switzerland

The Nagoya Protocol is an access and benefit-sharing instrument that governs the international sharing of genetic resources. Implementation of this treaty has implications for public health, notably the timely response to disease outbreaks. These implications include opportunities to advance both public health and the principles of fair and equitable sharing of benefits. WHO, in close collaboration with the Convention on Biological Diversity (CBD) and other international organizations, is working to ensure that public health interests are taking into consideration by the implementation of the Nagoya Protocol. At the recent 72nd Session of the world health Assembly (WHA72), the governing body of the world Health Organisation (WHO), countries received a report from the Director-General of WHO on the *Public Health implications of* the *Implementation of the Nagoya Protocol*. Discussions highlighted countries' strong interest in the matter. They adopted a decision requesting the Director-General of WHO to broaden engagement with Member States, the Secretariat of the CBD, relevant international organizations and relevant stakeholders in order to provide information on current pathogen-sharing practices and arrangements, the implementation of access and benefit-sharing measures, as well as the potential public health outcomes and other implications. The current bilateral based system governing exchange of pathogens and genetic sequence under the Nagoya protocol does not take into account the unique needs of timely and multilateral sharing during disease outbreaks or disease surveillance activities. The presentation will discuss the possibilities of this work leading to a multilateral sharing mechanism for pathogens and/genetic sequences.

Peter K. Ben Embarek is currently working with the World Health Organization (WHO) at its Headquarters in managing the WHO International Food Safety Authorities Network (INFOSAN). He is also Coordinator a.i. for the unit covering risk assessment and risk management work of the department of food safety and zoonoses and interim head of the WHO Task force on Access and Benefit sharing which coordinate the WHO work on the health implications of the implementation of the Nagoya Protocol. Previously from WHO's China Office, he was providing policy and technical advice to the government of China on food safety and nutrition issues. He joined WHO at its HQ in Geneva, Switzerland in 2001 where he worked on how to develop and strengthen integrated and multisectoral national food safety strategies and policies. He was also responsible for the development of microbiological risk assessment work at the international level and assessment and response efforts to new emerging public health issues such as MERS-CoV, Avian Influenza and SARS. Dr. Ben Embarek served with the Food and Agriculture Organization of the United Nations (FAO) from 1995 to 2001. Dr. Ben Embarek received his MSc. Degree in Food Science and Technology and a Ph.D. in Food Safety from the Royal Agricultural and Veterinary University of Copenhagen, Denmark. He is a Fellow of the International Academy of Food Science and Technology (IAFoST) under the International Union of Food Science and Technology (IUFoST) and the 2017 recipient of the Scientific Spirit Award of the Chinese Institute of Food Science and Technology (CIFST).

Highly accurate long read sequencing for microbial genome characterization

Zuwei Qian, Pacific Biosciences Inc., Singapore

To reduce the global disease burden caused by infectious disease, including parasites and bacteria, scientists need better information about mechanisms of virulence, immune evasion, and drug resistance, as well as new insights into parasite and pathogen vector biology and life cycles. One of the longstanding challenges in infectious disease has been the lack of high-quality reference genomes. Parasite genomes in particular have been highly fragmented, as the telomeric regions of their chromosomes are dense with highly homologous genes that cannot be resolved with short read sequencing. Recent developments in genome sequencing, however, are helping researchers overcome this barrier. Recently, highly contiguous genome assemblies of Plasmodium falciparum, Aedes aegypti, and multiple trypanosomes have become available. The number of reference genomes for bacteria that cause infectious disease is similarly expanding rapidly.

PacBio's SMRT sequencing technology has set the standard for fully characterizing complete microbial genomes and populations affordably. The research field is increasingly leveraging the unique advantages of PacBio long read technology characterize microbial communities because it allows for a much deeper understanding of the microbial population that was not attainable previously by NGS technology. I will discuss how these new resources are already yielding new biological insights into critical questions in infectious disease research, including how parasites evade the immune system add how pathogens are adapting to evolutionary pressures. Applications of 16s rRNA as well as shotgun metagenomic studies will be presented which showcase the salient features of long read sequencing uniquely suited for complex microbial mixtures such as those of environmental and health concerns.

Zuwei Qian is the Director of Marketing - Asia Pacific, at Pacific Biosciences. Prior to joining PacBio he spent 14 years at Fluidigm, PacBio and Affymetrix in many a slew of leadership roles ranging from R&D, technical support and sales. Zuwei was a Life Sciences Research Foundation post-doctoral fellow at Howard Hughes Medical Institute with 2017 Nobel Laureate Michael Rosbash and received Ph.D. degree from Rutgers University in the field of molecular genetics and microbiology.