

12th Global Microbial Identifier Meeting Nanyang Technological University, Singapore

12 - 14 June 2019

Lecture Theatre 19A (LT19A), 50 Nanyang Avenue, 639798
<http://maps.ntu.edu.sg/maps#q:lt19a>.



Whole Genome Sequencing - One Health Microbiology

A decorative graphic at the bottom of the page. It features several concentric, semi-circular arcs of varying colors (blue, green, red, purple, cyan) that represent genomic data or sequencing results. The arcs are arranged in a fan-like shape, curving from the bottom left towards the right. In the bottom right corner, there is a scale with tick marks and labels '0.5M' and '1M', indicating a genomic scale in megabases.

AGENDA

Day 1: Wednesday 12th June 2019

08:00-09:00 Registration

TIME	SESSION	SPEAKERS
08:30-08:40	Welcome and Opening Remarks	Peter Preiser, NTU, Singapore
08:40-08:50	Progress of the Global Microbial Identifier Idea at the International Stage	Joergen Schlundt, NTU, Singapore

Singapore's Experience with Next Generation Sequencing (NGS)

Chair: Joergen Schlundt

08:50-09:10	The Air Microbiome: A Missing Ecosystem?	Stephan Schuster, NTU, SG
09:10-09:30	Tracking Antimicrobial Resistance Evolution in <i>Acinetobacter spp.</i> in Whole Genome Sequencing in South East Asia and Globally	Eric Yap, NTU, SG
09:30-09:50	Whole-genome Sequencing Reveals Plasmid-mediated Transmission and Persistent Healthcare Reservoirs of Carbapenemase-producing Enterobacteriaceae	Ng Oon Tek, TTSH, SG

10:00-10:40 Group Photo & Coffee break
Pavilion@TCT LT

10:40-11:00	Recovery of Closed Bacterial Genomes from Complex Microbial Communities Using Long Read Sequencing	Kriethika Arumugam, NTU, SG
11:00-11:20	Cartography of Opportunistic Pathogens and Antibiotic Resistance Genes in a Tertiary Hospital Environment	Niranjan Nagarajan, GIS, SG
11:20-11:30	QA and Discussion	

Developing Country's experience in NGS

11:30-11:50	NGS Training and Application in Southern Africa	Yasmina Fakim, Uni of Mauritius, MA
11:50-12:15	Presentation from Developing Country Representatives	Suraya A. Husin, MY; Vernadette S. Sanidad, PH; Ta Thi Yen, VN

12:15-13:30 Lunch & Illumina Inc. Symposium Pavilion@TCT LT & LT8

13:30-13:50	Presentation from Developing Country Representatives continued	Ernest Bonah, GH; Tapfumane Mashe, ZW
13:50-14:20	Panel Discussion on Developing Country Next Generation Sequencing/Whole Genome Sequencing Experience	
14:20-14:40	WHO Discussions on Implications of Implementation of the Nagoya Protocol on Access and Benefit of Pathogens and Sequence Sharing	Peter Ben Embarek, WHO, CH
14:40-15:00	Highly Accurate PacBio Long Read Sequencing for Microbial Genome Characterization	Zuwei Qian, Pacific Biosciences Inc., SG

TIME	SESSION	SPEAKERS
15:00-15:30 Coffee break Pavilion@TCT LT		
15:30-17:25 Working Group Break-out Session LT 7,8,15 & 16		
17:25-17:55	Summary of Break-out Session	Working Group Chairs (1-4)
17:55-18:00	Closing Remarks	Joergen Schlundt, NTU, SG
18:00 – 19:30 Evening Reception Pavilion@TCT LT		

Day 2: Thursday 13th June 2019

Existing Platforms for Sequencing Analysis and Active Systems and (Barriers to) International Data Sharing

Chair: Eric Stevens

08:40-09:00	Updates on NCBI pathogen Detection Browser	Bill Klimke, NCBI, USA
09:00-09:20	Microbial Genomics in European Food Safety Authority Activities	Mirko Rossi, EFSA, FI
09:30-09:50	Keeping Up with Exponentially Growing Databases and Time Constraints	Bernhard Y Renard, RKI, DE
09:50-10:10	IRIDA: An Extensible and Distributed Bioinformatics Analysis Platform - Working Towards a Global Interoperable Ecosystem for Genomic Epidemiology	William Hsiao, BCCDC, CA
10:10-10:15	QA and Discussion	
10:15-10:45 Coffee break Pavilion@TCT LT		

Advances in the Use of WGS in Clinical, Public Health and Food Virology

Chair: William Hsiao

10:45-11:05	Diagnosis of skin-lesions with NGS-based metagenomic analysis and evaluation of novel diagnostic methods	Andreas Nitsche, RKI, DE
11:05-11:25	The COMPARE Data Sharing Platform	Clara Amid, ENA at EMBL-EBI, UK
11:25-11:45	Intra-host Diversity of Zika Virus in Blood, Urine and Saliva Over Time in an Index Cluster Study in Nicaragua	October Michael Sessions, NUS, SG
11:45-12:00	QA and Discussion	
12:00-13:00 Lunch Pavilion@TCT LT		

TIME	SESSION	SPEAKERS
Advances in the Use of WGS in Clinical, Public Health and Food Bacteriology		

Chair: William Hsiao

13:00-13:20	Integrating the Use of Whole-genome Sequencing in Infectious Disease and Antimicrobial Resistance Surveillance in Europe	Marc Jean Struelens, ECDC, SE
13:20-13:40	First Steps Towards Incorporation of Whole Genome Sequencing Data in Exposure Assessment: Machine Learning and Network-Diffusion Approaches	Pimlapas (Shinny) Leekitcharoenphon, DTU, DK
13:40-14:00	Candida auris: Global Emergence and Transmission of a Multidrug-Resistant Yeast	Rory Welsh, CDC, USA
14:00-14:20	Next-generation Sequencing Applications in the Food Industry – Present Status and Perspectives	Renaud Jonquieres, Merieux Nutrisciences, SG
14:20-14:35	QA and Discussion	

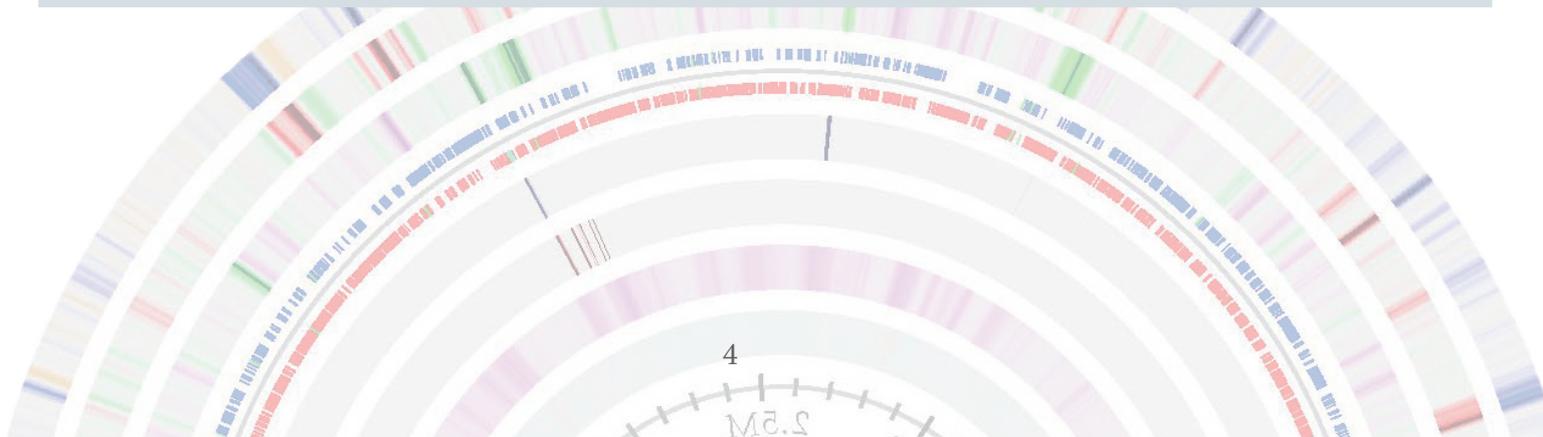
New Molecular/Sequence Based Identification Tool for Organism

Chair: Jianguo Xu

14:35-14:55	Transforming the Future of Genomics, Together: Illumina Solutions for Pathogen Detection and Surveillance	Trang Dahlen, Illumina Inc., SG
14:55-15:15	Oxford Nanopore Technologies at the Bench, in the Field and Beyond	Paola De Sessions, Oxford Nanopore Technologies, SG

15:15-15:45 Coffee break Pavilion@TCT LT

15:45-16:05	Comprehensive Microbial Detection by the Combination of Next Generation Sequencing and Microbiome Array Developed by Thermo Fisher Scientific	Arjun Kandalam, Thermo Fisher Scientific, SG
16:05-16:25	MitochonTrakr and Metagenometrakr	Padmini Ramachandran, FDA, USA
16:25-16:45	Reverse microbial etiology: new strategy for prevention of emerging infectious diseases in future	Jianguo Xu, CDC, CN
16:45-17:05	Whole-genome Sequence Based Species Identification Using K-mer Alignment	Pimlapas (Shinny) Leekitcharoenphon, DTU, DK
17:05-17:25	Genomic Biomarkers to Advance Food Safety	Maria Hoffmann, FDA, USA
17:25-17:45	Update from the EUCAST Sub-committee on WGS for Antimicrobial Susceptibility Testing	Matthew Ellington, Public Health England, UK
17:45-17:55	QA and Discussion	
17:55-18:00	Closing Remarks	Joergen Schlundt, NTU, SG



Day 3: Friday 14th June 2019

TIME	SESSION	SPEAKERS
Advances in the Use of Metagenomics		
Chair: Andreas Nitsche		
08:25-08:45	Mapping Everything Against Everything	Frank Aarestrup, DTU, DK
08:45-09:05	The Successes and Pitfalls of Metagenomics for Clinical, Public Health, and Food Safety Application – a Canadian Perspective	Natalie Knox, PHAC, CA
09:05-09:25	Metagenomics Profiling for Analysis of Sequencing Data from Foods	Luca Cocolin, University of Torino, IT
09:25-09:45	Progression of Metagenomics as a Tool for Routine Diagnostics	Robert Schlaberg, University of Utah, USA
09:45-10:10	Culture-independent Genome Sequencing of Mycobacterium Tuberculosis	Nathan Bacchman, University of Sydney, AU
10:10-10:40 Coffee break Pavilion@TCT LT		
10:40-11:00	COMPARE Food Proficiency Testing based on a Salmon Matrix - Wet Lab Part	Alessandra De Cesare, University of Bologna, IT
11:00-11:20	COMPARE Food Proficiency Testing based on a Salmon Matrix - Dry Lab Part	Dirk Hoper, FLI, DE
11:20-11:30	QA and Discussion	
NGS in One Health – Surveillance and Investigation		
Chair: Marc Struelens		
11:35-11:50	Investigating a Listeriosis Outbreak in South Africa	Anthony Smith, NICD, ZA
11:50-12:10	Establishing Integrated Genomic Outbreak Investigation and Surveillance Systems in Germany: Players, Challenges and Chances	Maria Borowiak, BfR, DE
12:10-12:30	Typing Reveals an Invasive Clone of Streptococcus agalactiae in South East Asia, Missed for Decades	Timothy Barkham, TTSH, SG
12:30-13:30 Lunch Pavilion@TCT LT		
13:30-13:50	How Whole Genome Sequencing is Used for Foodborne Pathogens: a Regulatory Perspective	Eric Stevens and Ruth Timme, FDA, USA
13:50-14:10	Epidemiological Considerations Concerning the Use of Whole Genome Sequencing Data for Foodborne Outbreak Investigation	Heather Carleton, CDC, USA

14:10-14:30	The Modernization of Foodborne Disease Surveillance in Canada: How We Made it Happen	Celine A. Nadon, PHAC, CA
14:30-14:50	Application of Whole Genome Sequencing in Surveillance and Risk Assessment for Foodborne Pathogens	Kalliopi Rantsiou, University of Turin, IT
14:50-15:00	QA and Discussion	

**15:00-15:30 Coffee break
Pavilion@TCT LT**

**15:30-17:15 Working Group Break-out Session
LT 7,8,15 & 16**

17:15-17:45	Summary of Break-out Session	Working Group Chairs (1-4)
17:45-17:55	Finalization of Potential Singapore Statement	
17:55-18:00	Closing Remarks	Joergen Schlundt, NTU, SG

NICD: National Institute for Communicable Diseases
 BfR: Federal Institute for Risk Assessment
 CDC: Centers for Disease Control and Prevention
 DTU: Technical University of Denmark
 ECDC: European Centre for Disease
 EFSA: European Food Safety Authority
 FDA: Food and Drug Administration
 FLI: Friedrich-Loeffler-Institut
 GIS: Genome Institute of Singapore
 MHCC: Ministry of Health and Child Care
 MOH: Ministry of Health
 NCBI: National Center for Biotechnology Information
 NICD: National Center for Biotechnology Information
 NIFC: National Institute for Food Control
 NMIS: National Meat Inspection Service
 NTU: Nanyang Technological University
 NUS: National University of Singapore
 PHAC: Public Health Agency of Canada
 RKI: Robert Koch Institute
 SCELSE: Singapore Centre for Environmental Life Sciences Engineering
 TTSH: Tan Tock Seng Hospital

