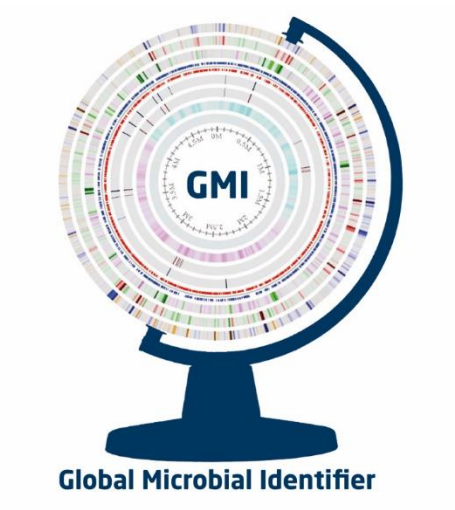
12th Global Microbial Identifier Initiative Meeting Report



12-14 June 2019

Nanyang Technological University, Singapore

Contents

Acronyms

BCCDC	British Colombia Centre for Disease Control
BfR	German 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
FAO	Food and Agriculture Organization of the United Nations
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
NAFTEC	Nanyang Technological University Food Technology Centre
NCBI	National Center for Biotechnology Information
NGS	Next generation sequencing
NICD	National Institute for Communicable Diseases
NIFC	National Institute for Food Control
NMIS	National Meat Inspection Service
NTU	Nanyang Technological University
NUS	National University of Singapore
OIE	World Organisation for Animal Health
PFGE	Pulsed Field Gel Electrophoresis
PHAC	Public Health Agency of Canada
PT	Proficiency test
RKI	Robert Koch Institute
TB	tuberculosis
SCELSE	Singapore Centre for Environmental Life Sciences Engineering
TTSH	Tan Tock Seng Hospital
USFDA	US Food and Drug Administration
WGS	Whole genome sequencing
WHO	World Health Organization

Acknowledgments

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Executive Summary

Sequencing technology is presently revolutionizing monitoring, surveillance and management of disease threats across the animal, environmental, food and human sectors. The equal access and implementation of such technologies and the global sharing of sequencing results can dramatically reduce national, regional and global burdens of communicable disease. The Global Microbial Identifier is a not-for-profit international consortium of more than 270 scientists from 55 countries in support of a framework for coordinating the sequencing data collection and analysis of microorganisms, and open sharing of sequence data.

On the 12th -14th June 2019, the Global Microbial Identifier Initiative hosted its 12th annual meeting at Nanyang Technological University, Singapore. The event which was organized in conjunction with an NGS training workshop (10th - 11th June 2019), attracted over 250 registrants from 40 countries, among which sponsorship was provided for 27 developing country participants. In addition to an observed increase in participation rate compared to previous meetings i.e. 11th and 10th annual meeting, the 12th annual meeting also attracted the attention of media, resulting in news articles on Singapore's daily broadsheet newspaper, The Straits Times, and TV reports on Channel News Asia (English, 7 min. interview with Joergen Schlundt), Channel 8 (Chinese) and Vasantham (Tamil). The programme included more than 40 presentations - from scientists, public health professionals and industry representatives - on the advances of sequencing technology, sequencing use in food, environment and human sectors, updates on the available data-sharing platforms and addressment of existing legal and technical barriers to genomic data sharing. The programme also held two working group break-out discussion sessions whereby clear progress and future goals were made known.

GMI's key achievements include drafting letters of support to 192 governments (ministries of health and agriculture), the near finalization of three GMI lab proficiency tests and the addition of epidemiological metadata in NCBI using GMI/NCBI minimum epi date requirements. The outcome of the GMI 12 event also included the development of a Singapore Sequencing Statement, prepared for a broad audience i.e. everyone with an interest in public health and food safety, and for the intention to increase public debate and potential political action.

The rapid evolution of sequencing technologies over the past eight years since GMI's inception has prompted a need for the Steering Committee to re-examine the vision and mission of the Global Microbial Identifier. This, together with the preparation of GMI13 in Vancouver, and GMI14 in Barcelona, is currently under way.

Meeting Programme

Day 1 – Wednesday 12th June 2019

07:45-08:30 Registration of delegates		
08:30-08:40	Welcome and Opening Remarks	Peter Preiser, NTU, Singapore
08:40-08:50	Political 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 *Acinetobacter spp.* 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
09:50-10:00	QA and Discussion	
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	Krithika 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 **Chair: Joergen Schlundt**		
11:30-11:50	NGS Training and Application in Southern Africa	Yasmina Fakim, University of Mauritius, MA
11:50-12:15	Presentation from Developing Countries	Suraya Amir Husin, MOH, MY; Vernadette S. Sanidad, NMIS, PH; Ta Thi Yen, NIFC, VN
12:15-13:30 Lunch & Illumina Inc. Symposium Pavilion@TCT LT & LT8		
13:30-13:50	Presentation from Developing Countries *continued*	Ernest Bonah, Food and Drugs Authority, GH; Tapfumanei Mashe, MHCC, ZI
13:50-14:20	Panel Discussion on Developing Countries Next Generation Sequencing/Whole Genome Sequencing Experience	S.A. Husin, MY; V.S. Sanidad, PH; T.T. Yen, VN; E. Bonah, GH; T. Mashe, ZI
14:20-14:40	Update on the Recent World Health Assembly Discussions on the Public Health Implications of the Implementation of the Nagoya Protocol on Access and Benefit of Pathogens and Sequences Sharing	Peter Ben Embarek, World Health Organization, CH
14:40-15:00	Highly Accurate PacBio Long Read Sequencing for Microbial Genome Characterization	Zuwei Qian, Pacific Biosciences Inc., SG
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 Use of Whole Genome Sequencing to Better Understand the Human Health Risks of Zoonotic Diseases from Wildlife and Agricultural Production Systems	Gavin Smith, Duke-NUS Medical School, SG
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		
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	Lakshmi Madabusi, 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

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

Presentation Abstracts and Main Messages

Day 1: Wednesday 12th June 2019

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.

Main messages

- A global DNA database of all microbiological strains enables simple identification of all microorganisms through faster, cheaper, more correct characterization + antimicrobial resistance pattern;
- The enabling of real-time global (*and national*) surveillance of disease and AMR;
- The enabling of a **giant resource for genomic knowledge** about all microorganisms – global scientific collaboration

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) 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 pilot WGS data and analysis over 5 years in Singapore hospitals examining this issue.

Main messages

- Bacterial and plasmid linked CPE transmission was studied between 2010-2015, at 6 Singapore hospitals involving 805 subjects.
- Plasmid-mediated transmission may account for a large proportion of CP gene transmission.
- Persistent hospital reservoirs may account for ongoing CP gene transmission.
- There is a need for further work to define plasmid-mediated CPE transmission to target infection prevention measures

Tracking Antimicrobial Resistance Evolution in *Acinetobacter spp*. in Whole Genome Sequencing in South East Asia and Globally
Eric Yap, Nanyang Technological University, Singapore
Main messages

- AMR of Acinetobacter spp. has increased dramatically over the last two decades
- AMR genes were found to be clustered in resistance islands which exists in a few airborne genomes
- AMR found possible through intra- and inter- species and perhaps inter-genera transmission through plasmids and possibly through phages
- Studying clinical resistance should not just be limited to the human environment but also the natural environment, as well as other aspects of the environment

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 scale. 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.

Main messages

- The air microbiome is characterized by a larger diversity of organisms during the day
- The time specific nature of airborne organisms is also reflected in healthy indoor environments
- The use of metagenomics has enabled understanding of the air microbiome, and will aid in increased understanding of the impact of changes to the environment e.g. climate change, pollution, environments affected by climate change as well as the impact of the environment on respiratory and gut health.
- These studies prompt the inclusion of biological components in air quality assessment i.e. not only physical and chemical parameters
- Use of metagenomics has enabled greater understanding of the air microbiome, and the potential to improve the understanding of fungal pathology

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 metagenome-assembled genomes (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.

Main messages

- Recovering complete bacterial chromosomes from an enriched microbial community using long read sequencing is feasible
- Feasibility in more complex communities is still unclear
- Correction for sequencing error rate remains a priority e.g. improving MEGAN-LR frame shift correction algorithm
- All data from this study are publicly available in NCBI: SRX5120474, SRX5126404

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.

Main messages

- High quality nanopore sequencing is feasible for patient samples and environmental samples
- Long reads help with:
  - Assembly
  - Strain genomes
  - Transmission analysis
  - Study of resistance gene combinations
  - Novel phages and plasmids
- Real-time capabilities make it a very attractive platform with optimized workflows

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 in DNA sequence data from a wide diversity of organisms. Since 2012, several initiatives have enabled the promotion of NGS in Southern 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 University of Cape Town, 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.

Main messages

- Online bioinformatics courses have proven successful in reaching out and training a number of participants in Southern Africa
- Very few sequencing facilities lie outside of South Africa and are characterized with poor infrastructure, limited internet connectivity, lack of human resources
- Very few sequencing projects on foodborne bacteria and contaminants presently exist

Presentation from Developing Country Representatives
Suraya A. Husin, Malaysia; Vernadette S. Sanidad, Phillipines; Ta Thi Yen, Vietnam; Ernest Bonah, Ghana; Tapfunamei Mashe, Zimbabwe

Main messages

- An example of a one health project using sequencing technology in Malaysia was presented
- As of this stage there is no implementation of NGS in the food regulatory agencies but the NGS capacities are available in the academic sector in the Philippines
- Food security is the priority of many of developing countries and as a result, lack of funding and support is available to implement NGS in regulatory sectors

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 taken into consideration in 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. This work will be important in efforts attempting to achieve a multilateral sharing mechanism for pathogens and/genetic sequences.

Main messages

- As of Dec. 2018, 116 countries have presently joined the Nagoya Protocol (NP)
- NP implementation has resulted in delay of public health event and emergency response e.g. delay in receiving influenza strains to make vaccines
- NP's public health implications will be further assessed by information on current pathogen-sharing practices, access and benefit-sharing measures, documented examples of current delay/constraints in sharing pathogens/sequences, and documented benefit of future multilateral microbial DNA data sharing mechanisms.

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 to characterize microbial communities because it allows for a much deeper understanding of the microbial population that was not attainable previously by NGS technology. These new resources are already yielding new biological insights into critical questions in infectious disease research, including how parasites evade the immune system and how pathogens are adapting to evolutionary pressures. Applications of 16s rRNA as well as shotgun metagenomic studies can show the salient features of long read sequencing uniquely suited for complex microbial mixtures such as those of environmental and health concerns.

Main messages

- Sequencing technologies are enabling better understanding of microbial communities, with new models enabling faster data generation through increased capacity

Day 2: Thursday 12th June 2019

Updates on NCBI pathogen Detection Browser
William (Bill) Klimke, NCBI, USA
The NCBI Pathogen Detection pipeline takes raw sequencing data from a surveillance network of public health labs sequencing food and clinical pathogen isolates and generates publicly available reports. The pipeline takes the raw sequencing data, assembles, annotates, and clusters the isolates into phylogenetic trees to aid outbreak and traceback investigations. The annotated assemblies are checked for the presence of antimicrobial resistance genes/proteins using a process built by NCBI called AMRFinder. AMRFinder uses a set of curated proteins and hidden markov models (HMMs) to assign functional names to proteins.

Main messages

- NCBI Pathogen Detection project serves two key functions – to provide real-time detection of isolates for traceback and outbreak investigations, and to detect AMR genes and proteins
- NCBI aims to have 500,000 pathogens, fully annotated, assembled and available to the public by the end of the year 2019
- NCBI Pathogen Detection team can be reached by email at pd-help@ncbi.nlm.nih.gov.

Microbial Genomics in European Food Safety Authority Activities
Mirko Rossi, European Food Safety Authority, Finland
Implementation of whole genome sequencing (WGS) as a molecular typing technique has shown clearly its strength to enhance laboratory-based surveillance of communicable diseases at the local, national and international levels. Genome-based typing of foodborne pathogens is replacing traditional methodologies in several countries, revolutionizing outbreak detection and investigation, and becoming a relevant tool for trace back investigations, source attribution, detection and surveillance of foodborne pathogens, as well as for monitoring of antimicrobial resistance. The findings of the relevant activities sponsored and coordinated by the European Food Safety Authority (EFSA) related to the use of WGS in microbial food safety, with particular focus on existing bioinformatic solutions, was presented.

Main messages

- Recent WGS activities in EFSA (2018-2019) include final reports from the INNUENDO and COMPARE projects, and a technical report on the WGS data collection and analysis system from the ECDC-EFSA working group
- 'Strategic elements' have been identified as a guide in enabling future EC mandate on implementation of WGS in the joint ECDC-EFSA molecular typing database

Keeping up With Exponentially Growing Databases and Time Constraints
Bernhard Renard, Robert Koch Institute, Germany
With the continuously increasing use of next-generation sequencing in time-critical applications such as disease outbreak analysis, there is a high demand for novel concepts to overcome the limitations of traditional approaches for data analysis. We observe exponential growth of commonly used reference databases for metagenomics. Daily or weekly updates of computational indices from these references become almost impossible even on large scale computing resources. At the same time, while reference collections continue to grow, there is strong bias towards few overrepresented species and resulting incompleteness of these collections. While runtime of data analysis software, e.g. for read alignment, have significantly decreased and more powerful computational resources have become available, the overall turnaround time from sample arrival to availability of analysis results have remained nearly the same due to the sequential paradigm of data production and analysis. As part of our work at Robert Koch Institute, the German national public health institute, we have developed and routinely applied a collection of tools for sequence analyses. These include (i) steps to modularize reference genome indices, allowing updates and recomputations within few minutes, (ii) deep learning approaches to predict phenotypes such as pathogenic potential for sequences which are not assessable via sequence homology and (iii) approaches for analyzing Illumina data, while the sequencer is still running. In doing so, intermediate results can be obtained for four crucial steps in time-critical analysis workflows: read alignment, read filtering, metagenomic classification and viral diagnostics.

Main messages

- Interleaved bloom filters (IBF) explores larger sets of references, is easy to update and offers short turnaround times suitable for outbreak investigations
- Compared to Kraken, Ganon updates (addition/removal) in a fraction of time to build the indices
- The collection of bioinformatics projects developed by RKI are available at https://gitlab.com/rki_bioinformatics

IRIDA: An Extensible and Distributed Bioinformatics Analysis Platform - Working Towards a Global Interoperable Ecosystem for Genomic Epidemiology

William Hsiao, BCCDC, CA

The Integrated Rapid Infectious Disease Analysis (IRIDA) project is a Canada-led initiative to build an open source, end-to-end platform for public health genomics. The Integrated Rapid Infectious Disease Analysis (IRIDA) platform is a user-friendly, distributed, open source bioinformatics and analytical web platform, developed to support real-time infectious disease outbreak investigations using whole genome sequencing data. IRIDA is designed for use in public health, food safety, and clinical microbiology labs, and is also suitable for general infectious disease comparative microbial genomics.

While IRIDA was initially created to support the Canadian public health system, instances can be independently installed on local computing resources, enabling private and secure analyses according to organizational policies and governance. IRIDA supports controlled, collaborative data sharing and data analysis for users on its platform and for users on other IRIDA platforms. IRIDA's data management capabilities enable secure upload, storage and management of all sequences and metadata, and provides data provenance and auditability as required by clinical laboratories. Easy to run pipelines for quality control, assembly, annotation, variant detection, *in silico* serotyping and cgMLST, make sophisticated genomics analyses accessible to lab analysts, while providing power-users with modularity and customizability.

The IRIDA platform enables fast, scalable, private (and shareable) analytics and visualizations for WGS-based microbial pathogen investigations, and is currently transforming the Canadian public health ecosystem.

Main messages

- IRIDA's ultimate goal is to have process interoperability which is in line with GMI's vision, where information fed into one platform is interpreted and processed consistently across all platforms in a distributed network
- Funding for the next three years will allow IRIDA to focus on benefit-sharing challenges and how to build trust in this distributed system
- IRIDA is freely available at https://github.com/phac-nml/irida and www.irida.ca.

Diagnosis of skin-lesions with NGS-based metagenomic analysis and evaluation of novel diagnostic methods

Andreas Nitsche, Robert Koch Institute, DE

Main messages

- In response to the problems arising with metagenomics sequencing i.e. high human background in samples, a targeted sequencing approach for viruses was developed
- The novel approach is rapid, user friendly to laboratory personnel with limited bioinformatics knowledge and as it is specific to the target of interest, poses less problems with data management and data protection
- Given emerging and re-emerging viruses occur approx. once a year and are not always a completely new sequence and in 2025 the consequences of digitalization are estimated to be responsible for 8% of the total greenhouse gas production (cf. to 2% as a result of international air traffic), one may need to start considering whether sequencing should be done for everything or adoption of new aforementioned methods would be a better approach.

The COMPARE Data Sharing Platform

Clara Amid, EBI, United Kingdom

Data sharing is a prerequisite to making the most use of research data but also one of the biggest challenges scientific communities face. Areas of public and animal health as well as food safety would benefit from rapid data sharing when it comes to emergencies. Challenges to overcome are not only ethical, regulatory, or institutional, but also due to lack of suitable platforms which provide an infrastructure for data sharing in structured formats. In this presentation we will describe an informatics platform that includes workflows for structured data storage, managing and pre-publication sharing of pathogen sequencing data and its analysis interpretations with relevant stakeholders.

Main messages

- The COMPARE data sharing platform offers users increased choice and control, including privacy protection for pre-published data

Intra-host Diversity of Zika Virus in Blood, Urine and Saliva Over Time in an Index Cluster Study in Nicaragua
October Michael Sessions, National University of Singapore, Singapore

Main messages

- The study focused on the 2016 Zika virus outbreak in Nicaragua
- Certain genes (1 specific amino acid chain) were found to be overrepresented over time – that being the genes responsible for the viral replication
- Deep sequencing enabled detection of minority variance whereby first generation transmission events appeared to be of long range interaction/relatedness
- Sequencing provided high resolution for analysis and looking at epidemic trajectories
- First generation transmission events involved a long range interaction/relatedness
- Future work seeks to link up apparent variations/mutations, provide genetic linkage and elucidate the significance of co-variation e.g. are specific mutations dependent on other ones?

Integrating the use of whole-genome sequencing in infectious disease and antimicrobial resistance surveillance in Europe.
Marc Struelens, European Center for Disease Prevention and Control, Sweden

Since 2015 ECDC's vision on whole genome sequencing (WGS) fosters its frontline use for outbreak investigations and public health surveillance across the European Union (EU) by 2020.

EU capacity mapping surveys in public health reference laboratories showed that the pace of WGS uptake varies between pathogens, diseases and countries. WGS-based typing use for routine surveillance increased from no countries in 2013 to 20 in 2017. By the end of this year, all EU countries intend to use WGS for public health surveillance. From 2015 to 2018, ECDC helped investigate 41 presumptive multi-country foodborne outbreaks caused by *Salmonella enterica, Listeria monocytogenes* or Shiga-toxin producing *E. coli* (STEC). As part of this work, more than 2,000 bacterial genomes were sequenced. Investigations confirmed 31 multi-country outbreaks and identified the food source for 12 outbreaks.

ECDC is supporting the national reference laboratories so they can participate by 2021 in joint operations at European level for:

• Multi-country outbreak investigations: outbreaks of any bacterial pathogen or emerging multi- or extensively drug-resistant bacteria, new pathogens or new modes of transmission of healthcare-associated or community pathogens.

• Control-oriented EU-wide continuous surveillance: influenza virus, *Listeria monocytogenes*, MDR TB, *Neisseria meningitidis*, *Salmonella enterica* and Shiga-toxin producing *E. coli*.

• Strategy-oriented EU-wide sentinel surveillance or surveys: antibiotic-resistant *Neisseria gonorrhoeae*, *Bordetella pertussis*, carbapenem- or colistin-resistant Enterobacteriaceae and *Acinetobacter baumannii*, HIV drug resistance and *Streptococcus pneumoniae*.

ECDC is developing a set of technical solutions available in house and/or externally for safe sharing, storage, analysis of WGS typing data and visualisation of integrated genomic and epidemiological data analysis for risk assessment.

Main messages

- EU has rapidly expanded national reference laboratory capacities for WGS-enhanced surveillance and outbreak investigations
- EU has standardized WGS data sharing between EU countries
- The use of WGS has already proven successful in resolving international outbreaks of foodborne disease and multi-drug resistant pathogens e.g. TB, Klebsiella

First steps towards incorporation of whole-genome sequencing data in exposure assessment: Machine Learning and Network-Diffusion approaches
Pimlapas (Shinny) Leekitcharoenphon, National Food Institute, DTU, Denmark

Exposure assessment of microbiological hazards in food is a major part of the four components of the microbial risk assessment (MRA) process. This step involves the assessment of the qualitative and/or quantitative likely intake of microbial hazards via food or other relevant sources. In this presentation, approaches will be presented incorporating whole genome sequencing, machine learning (ML) and network-diffusion based analysis of *Listeria monocytogenes* genomic profiles for exposure assessment considering response to the four stress conditions: desiccation, salt concentration, pH and low temperature storage. A total of 7348 accessory genes in amino acid sequences were used as model input to predict and differentiate each of the stress categories using supervised ML models. A matrix of percent similarity between accessory genes and the *Listeria* genomes was generated and subsequently used as input for ML. ML algorithms random forest, support vector machine gradient boosting, logit boost and neural network were evaluated for their prediction accuracy with 10-fold cross validation. Random forest was chosen as appropriate model for the cold (Accuracy: 96%; CI: 90-99%), salt (Accuracy: 86%; CI:79-92%) and desiccation stress (Accuracy: 91%; CI:85-96%) responses although it performed as good as other choices for some stress responses. Support vector machine (radial kernel) (Accuracy: 88%; CI: 81-94%) emerged as best model in prediction of acid stress response. Top genes contributing to the predictions were selected. Next steps towards incorporation into microbial risk assessment, validation and interpretation of completed modelling outputs will be presented.

Main messages

- Predictive models based on WGS data may greatly reduce the need for future validation of models in the lab and in food

***Candida auris*: Global Emergence and Transmission of a Multidrug-Resistant Yeast**
Rory Welsh, CDC, USA

The emerging multidrug-resistant pathogenic yeast *Candida auris* represents a serious threat to global health. *C. auris* went from an unknown pathogen a decade ago to being reported in over thirty countries on six continents. The origins and potential environmental reservoirs of this globally emerging multidrug-resistant yeast remains a mystery. *C. auris* is of particular importance because, unlike most Candida species, it is easily transmitted and often causes healthcare-associated outbreaks. In addition, *C. auris* tends to have a high associated mortality rate and is difficult to treat as it is more often than not resistant to one or more antifungal agent. A more detailed understanding of the diversity and distribution of this pathogen is critical to aiding infection control. The rapid rate at which *C. auris* emerged creates unique challenges for infection control efforts. To better understand its emergence and transmission dynamics and to inform clinical and public health responses, we used whole genome sequencing to assess the genetic similarity between isolates collected from patients in the United States and those identified in several other countries. Whole genome sequence analysis indicates the known worldwide *C. auris* population consists of four phylogenetically distinct clades that are strongly associated with geographic region, which suggests near-simultaneous emergence.

Main messages

- There is a need to identify the origins and potential environmental reservoirs of *C.auris*
- More data is required to enhance disinfectant efficacy and decolonization strategies
- Work is in progress to add *C. auris* to the NCBI Pathogen Detection pipeline's list of organisms

Next Generation Sequencing Application in the food Industry: Present Status and Perspectives
Renaud Jonquieres, Merieux Nutrisciences, Singapore

In recent years the breakthrough of next generation sequencing (NGS) allowed to decode genomes of microorganisms with unprecedented speed. NGS has been widely adopted by Epidemiology labs and Public health institute to help track foodborne outbreaks. Large International food brands now pave the way for adoption of this technology in routine food safety monitoring programs. The two most common applications of NGS in food industry are the Whole Genome Sequencing (WGS) and Metabarcoding.

WGS helps to fully identify a microorganism by comparing its genome with other sequences. This analysis allows to do root cause analysis when a pathogenic or unwanted microorganism is detected. Also, in food bio-processes where organisms play a crucial role to bring organoleptic attribute or health claims to the product, WGS can fully characterize process strains in conjunction with their phenotype.

Metabarcoding allows to discover which species of organism are present in a given sample at a given time of the shelf life or at different moment of the manufacturing process. Such knowledge may help identify spoilage organism that may degrade the product.

As the technology continues to improve with faster cheaper and more compact equipment, the NGS will certainly play an increasing role in food safety programs. The depth of the analysis allowed by this tool should help achieve quicker corrective actions when food processes are out of control. Also, NGS will help better understand the resistance of microorganism to decontamination in plants as well as help prevent spread of antibiotic resistant organisms in our foods.

Main messages

- NGS application offers opportunities for:
  -systematic plant flora mapping e.g. is Listeria monocytogenes ST6 in the manufacturing environment?
  -onsite quick investigations
  -central database for pathogens
  -combatting food fraud
  -combatting antibiotic resistance e.g. checking if incoming animal products are free of antibiotic residues and antibiotic resistance genes
  -GMO testing

Transforming the Future of Genomics, Together: *Illumina Solutions for Pathogen Detection and Surveillance*
Trang Dahlen, Illumina Inc., Singapore

Main messages

- NGS is a powerful tool that enables increased knowledge of microbes and communities of microbes that exist in and around us

Oxford Nanopore Technologies at the bench, in the field and beyond
Paola Flórez de Sessions, Oxford Nanopore Technologies, Singapore
Oxford Nanopore Technologies aims to disrupt the paradigm of biological analysis by making high performance, novel DNA/RNA sequencing technology that is accessible and easy to use. Our novel, electronics-based DNA/RNA sequencing technology is being used in more than 80 countries, for a range of biological research applications. These include large scale human genomics, cancer research, microbiology, plant science and environmental research. Nanopore sequencing is also being explored beyond research, where it has the potential to provide rapid, meaningful information in the fields of healthcare, agriculture, infectious disease, metagenomics, food and water surveillance and education. We provide complete bacterial, fungal, and viral (DNA or RNA) genomes with long-read nanopore sequencing. In addition, we identify and characterise microbes from environmental or single organism samples, with rapid methods for pathogen detection — whether at the bench or in the field. Biology for anyone, anywhere

Main messages

- Several cases of the effective use of sequencing technology were provided e.g. identifying real time Ebola and Zika virus transmission

Comprehensive Microbial detection by the combination of Next Generation Sequencing and Microbiome array developed by Thermo Fisher Scientific
Lakshmi Madabusi, Thermo Fisher Scientific, Singapore
The microbial community is essentially another organ of the body that plays a crucial role in human physiology and disease. It has now been demonstrated that altered microbial compositions and/or activities in the intestine, also known as dysbiosis, bear relation to a number of ailments such as inflammatory bowel disease, diabetes, allergies, asthma, autism, obesity, cardiovascular disease and even certain cancers. The microbiome modulating strategies with which most people are familiar are probiotics and prebiotics. The ultimate goal should be stimulating the growth and activity of only those microbes that can help the human host in order to achieve specific health benefits. This creates the potential for food and pharmaceutical companies to precision engineer the microbiome to improve human health. The Rapid adoption of Metagenomics and Next Generation Sequencing Technologies has increased focus on microbiome research. Thermo Fisher Scientific's 16s Metagenomics assay enables the detection of bacteria using the primer sets designed for hyper-variable regions like V2-4-8 and V3-6,7-9 regions. Additionally, Thermo Fisher Scientific has launched a new Microbiome array that can detect the presence of all classes of microorganisms such as bacteria, Fungi, Virus, Protozoa and Archea in different variety of samples. The array consists of more than 12000 microbial species and the content is sample-type agnostic, suitable for applications in nutrigenomics, agrigenomics, and animal research and modelling. This array enables species- and strain-level detection and RNA virus detection using cDNA template with ease to use analysis software (Axiom MiDAS).

Main messages

- Sequencing provides solutions to a multitude of challenges in the food and pharmaceutical sectors and it is a matter of training future scientists and physicians to fully realize the potential of such technologies

MITOChonTrakr and MetagenomeTrakr.
Padmini Ramachandran, FDA, USA
Full understanding of the microbial load in our food and the impact of the food matrix itself is of vital importance to public health. The promise of culture-independent next generation sequencing (NGS) technologies – or metagenomics - have fueled a renaissance in our understanding of foods and the impact on our own human microbiome. Both targeted and target-independent metagenomic data has been used to describe microbial and viral ecologies from soils to water to foods, helping us in our understanding of the foods we consume and the complex microbial ecologies along the farm to fork continuum – important both for food safety from pathogens and for issues of nutrition, allergy, and immunology. Food microbiome data will contribute to improved understandings of important ecologies for questions surrounding pathogenicity, food quality (spoilage), and nutrition. These data are advancing recommendations for data based Good Agricultural Practices and FSMA regulations. The convenience and affordability of NGS technologies, improved bioinformatic pipelines, and converging reference databases will further rapidly increase the uptake of this technological application. Important questions remain to ensure that we harness the full potential of this technology. Metagenomics could help us build a better and more effective food safety management systems.

Main messages

- Reference genomes will facilitate target-independent sequence-based detection methodologies, providing sufficient information for discriminating closely related eukaryotes and creating new avenues for rapid detection and identification of filth in foods

Reverse microbial etiology
Jianguo Xu, CDC, China
The major challenge of emerging infectious diseases in the future is to timely identify new pathogens. Many emerging infectious diseases in the future will be caused by new microorganisms. However, most likely over 99% of all bacterial or viral species on earth have not been discovered yet. Therefore, we propose a reverse microbial etiology. The main contents include: 1. discovering, isolating and naming new microorganisms; 2. evaluating the potential pathogenicity or public health significance of newly discovered microorganisms; 3. To propose the catalogue or list of the new microorganisms that may cause outbreaks in future; 4. To study the mechanism, methods, techniques and strategy for detection, diagnosis, treatment, prevention and control; 5. To prevent SARS-like outbreaks in future.

Main messages

- Scientists have studied microorganisms from wild animals i.e. bats, ticks, rats, mosquitoes, marmots etc. and have identified potential emerging infectious disease outbreaks in China: west nile virus, zika virus, SARS-like emerging coronavirus, anaplasma ovis-like bacteria, Wenzhou virus, Escherichia albertii, Rickettsia sibirica subspecies sibirica BJ-90, Candidatus Rickettsia tarasevichiae etc.
- A full review on reverse microbial etiology has been published in the *Journal of Biosafety and Biosecurity*.

Whole-genome sequence based species ID using K-mer alignment
Pimlapas (Shinny) Leekitcharoenphon, National Food Institute, DTU, Denmark
Species identification is one of the first steps in microbiological study. Traditionally, bacterial species identification is based on 16S rRNA and BLAST alignment. There are limitations using one gene and BLAST for species identification. We are presenting a new aligner program called KMA (k-mer alignment). KMA has been used in KmerFinder, a tool for bacterial species ID. KmerFinder uses all information in the WGS data to identify the species. KmerFinder was validated using a training data (database) from 1,647 completed and almost completed genomes from NCBI containing 1,009 different species and evaluation data (testing data) from 695 draft genomes from NCBI (151 species) and 10,407 draft genomes from SRA (168 species). The evaluation result showed that KmerFinder has greater accuracy than 16S rRNA and other methods included. Other applications of KMA includes herbal authentication and metagenomics identification .

Main messages

- KMA has applications for resistance genes identification, metagenomics and herb authentication

Genomic Biomarkers to Advance Food Safety
Maria Hoffmann, FDA, USA

Main messages

- FDA is not only interested in using WGS for trace-back but also in studying genes that are able to evade preventative control measures during food processing e.g. heat processing, disinfectant and cleaning processes
- Future efforts include the development of more standards, particularly for biocide resistance

Update from the EUCAST Sub-committee on WGS for Antimicrobial Susceptibility Testing
Matthew J Ellington, Public Health England, United Kingdom
WGS offers the potential to predict antimicrobial susceptibility from a single assay. The European Committee on Antimicrobial Susceptibility Testing (EUCAST) subcommittee has reconvened the sub-committee examining the development status of WGS for bacterial antimicrobial susceptibility testing (AST). Previously, the sub-committee found the use of WGS-inferred AST for guiding clinical decision was not supported by the evidence base. The current re-examination process has identified significant progress for some species, it is reconsidering same areas and aspects of WGS use described last time, as well as new sections on the use of machine learning algorithms, the use of long-read sequencing and the development of metagenomics for use in AST. It is expected that the revised report will be available for consultation in the last quarter of 2019.

Day 3: Thursday 14th June 2019

Mapping Everything Against Everything
Frank Aarestrup, DTU, Denmark
Recap of the original goals of GMI, summarizing the sequencing landscape since then, including work that is currently been done at DTU.

Main messages

- NGS is rapidly transforming current microbial diagnostic and surveillance
  -We should remember all pathogens and both data-sharing and analytic tools/infrastructure
- Combining NGS data with other "omics" data has enormous potential
  -We can benefit from integrating bioinformatics with epidemiology
- DTU attempts - with limited resources - to contribute to the global community:
  -CGE-tools
  -Evergreen phylogeny
  -Processed metagenomic data and combining with epidemiological information

The Successes and Pitfalls of Metagenomics for Clinical, Public Health, and Food Safety Application – A Canadian Perspective
Natalie Knox, PHAC, Canada
The current gold standard for pathogen detection relies on laborious culture-dependent techniques or rapid culture-independent diagnostic tests which are highly targeted and often require supplementary tests for further pathogen characterization. In contrast, metagenomics, a culture-independent method, offers an attractive avenue for detection and characterization of known pathogens, mixed infections, and the discovery of novel microorganisms directly from a sample. With the adoption of whole genome sequencing for routine foodborne surveillance activities and outbreak response, many Canadian public health laboratories already have access to high-throughput sequencers and staff trained to generate sequence data. Though we remain far from operationalizing metagenomics into routine public health practice, the feasibility of implementing this technology as a validated and accepted test for pathogen detection is rapidly approaching. The Public Health Agency of Canada and its partners have been evaluating this technology for its applicability across the fork to farm continuum with some successes and challenges. With improved analytical methods and training, metagenomics has the potential to improve infectious disease diagnostics as well as public health and food safety surveillance and outbreak response.

Main messages

- Culture independent diagnostic tests (CIDT) used at point of care facilities do not present public health labs with cultures aided in future detection of outbreaks and contaminated foods and the suggested solution of reflex cultures is considered an additional burden
- Metagenomics offers solutions to CIDT drawbacks, but is not without its own challenges
- In studies using metagenomics to classify acute gastroenteritis, regardless of classifier or coverage, ~50% of pathogens can be identified
- There is a need to address host data in food i.e. unsuccessful removal of host DNA
- There is a need to standardize wet and dry lab analytical workflow and reference databases fit for purpose
- Guidelines are currently being developed for the need of physicians to obtain patient informed consent, what to do with incidental findings and patient rights to knowledge of incidental findings
- Guidelines are also in development for secondary sample use

Metagenomic profiling for analysis of sequencing data from food
Luca Cocolin, University of Torino, Italy
The way the microbial ecology of food has been investigated has dramatically changed in the last 30 years. We switched from culture-dependent methods, based on cultivation, isolation and identification, to culture-independent approaches, where microorganisms are identified directly in the food matrix without the need of their cultivation.
This big change has been achieved with technologies that either are able to profile the populations in electrophoretic gels or sequence, with high efficiency, mixtures of DNA extracted directly from the food samples. These approaches highlighted from their first applications that what could be seen on agar plates was only a fraction of the total microbial populations involved in the fermentation process. With the development of the next generation sequencing methodologies, we have now in our hands techniques, that are able to deeply investigate the diversity of microorganism and how they are interacting in a very dynamic ecosystem. Not only can we reconstruct the taxonomic map of the microbes present in a given food, but we can also monitor the metabolic activities that are expressed at a specific time point. This huge amount of new data can be analyzed through bioinformatic tools to fully understand the role of the microorganisms.

Nowadays we do have to concentrate our attention and our efforts on the study of whole interactive microbial communities, since the classic approach to focus on a specific population has been demonstrated to be not valid on several occasions.

Main messages

- Metagenomics provides understanding of the ecosystem in which food fermentation processes take place e.g. in sausages and cocoa beans

Progression of Metagenomics as a Tool for Routine Diagnostics

Robert Schlaberg, University of Utah, USA

Current infectious disease molecular tests are largely pathogen-specific, requiring test selection based on the patient's symptoms. For many common syndromes caused by a large number of viral, bacterial, fungal, and parasitic pathogens this necessitates large panels of tests and has limited yield. In contrast, metagenomics can be used for detection of both expected and unexpected pathogens. While proof-of-concept has been extensively shown, implementation of metagenomics tests in routine diagnostic practice is challenging. We have performed extensive performance evaluation of a metagenomics test for use in a large reference laboratory setting. This presentation will provide an overview of remaining challenges, potential solutions, and lessons learned.

Main messages

- Existing challenges need to be addressed before metagenomics can be used as a tool for routine diagnostics
- One obvious challenge is as the target species in a culture is diluted, more contaminants will appear in the results

Culture independent genome sequencing of Mycobacterium tuberculosis

Nathan L. Bachmann, University of Sydney, Australia

Critical to the control of tuberculosis (TB) is early and effective diagnosis that can also detect antibiotic resistance. Current TB diagnostics uses acid-fast staining of sputum, however, microscopy is unable to provide species-level identification or resistance profile and the culture-based methods that are used to overcome these limitations are still labor-intensive and slow. Therefore, culture independent genome sequencing methods are being developed to sequence *Mycobacterium tuberculosis* directly from sputum samples in order to determine species-specific information and drug resistance without having to rely on culturing an isolate. In order to sequence *M. tuberculosis* straight from sputum it is necessary to deplete host DNA to ensure sufficient read coverage for the bacterial genome. Sputum samples collected by the Mycobacterium Reference Laboratory (MRL), Westmead Hospital in Australia and Manipal Academy of Higher Education in India were subjected to differential lysis to burst the human cells and liberate host DNA, while keeping the mycobacterial cells intact. The human DNA is then depleted following by bead beating extraction of *M. tuberculosis* DNA. To assess the effectiveness of host DNA depletion, qPCR using human and mycobacterium specific primers are used to measure the levels of host and microbial DNA after extraction. Six samples have been sent for deep sequencing and produced full-length genomes with approximately 25x coverage. Continued improvements are required to increase read coverage for reliable antibiotic resistance testing. Optimizations of culture-independent genome sequencing for TB will provide drug susceptibility results seven weeks sooner than traditional approaches.

Main messages

- A combined selective lysis and CTAB protocol may improve the success rate of culture-independent genome sequencing for TB
- Low pathogen load is a major issue and enrichment methods are complex and expensive
- DNA concentration vary widely between samples
- Further "deep" sequencing will give more coverage
- This procedure increases cost but not by as much as straight metagenomics deep sequencing

COMPARE food PT based on a salmon matrix - wet lab part

Alessandra De Cesare, University of Bologna, Italy

Due to the importance of foods in the transmission of zoonotic agents, a ring trial was organized with the aim to check which microorganisms of a mock community experimentally spiked in a food matrix each Participant was able to detect using shotgun metagenomic sequencing. The food matrix was cold-smoked salmon spiked with bacteria, viruses, one yeast and one parasite. Each Participant performed their own sample handling, nucleic acid extraction, library preparation and sequencing protocol. A total of 36 data file(s) (i.e., 27 by spiked smoked salmon, 4 smoked salmon not spiked and 5 negative controls) were uploaded in a dedicated ENA data hub and analyzed using MGmapper, MG-RAST and OneCodex. The wet lab protocols followed by the Participants were very different but both MGMapper and MG-RAST performed well in terms of bacteria, parasite and yeast detection, while both DNA and RNA viruses were not detected. Specific correlations between sequencing outputs and wet lab variables were identified.

Main messages

- The wet lab protocols followed by the Participants were different but except for the RNA viruses the microorganisms of the mock community were traced back in the metagenomes submitted as part of the PT using the selected data analysis tools.
- For viruses there probably was an inappropriate balance between bacteria, parasite and yeast cells vs virus genomes in the mock community and the whole dataset will be tested with data analysis tools more tailored to viruses.

- The sample handling and the nucleic acid extraction protocols largely affected the normalized counts of the microorganisms of the mock community; sequencing platform, sequencing yield and read length influenced the normalized counts of the yeast and specific bacteria.
- The dataset built in this PT is the first one obtained by shotgun metagenomic sequencing of real food samples and shows that microorganisms belonging to different kingdoms can be traced back using this genome technology.
- Further PTs must be done to come out with standardized protocols for the wet lab part and to check which concentrations of potential foodborne pathogens can be detected in food ecosystems containing also their background microflora.

COMPARE Food Proficiency Testing – Dry Lab Part
Dirk Höper, FLI, Germany
The purpose of the COMPARE metagenomics proficiency test – dry lab – was (i) testing the interpretation of results obtained from the software analysis by the participants, i.e. the recognition of potentially dangerous species and (ii) the awareness of artefacts occurring in the sample processing and sequencing. Using ARTIllumina (Q Version 2.5.8), a synthetic data set with approx. 1E+7 reads was created from EST and coding sequence data retrieved from the NCBI databases. It was designed as Illumina dataset sequenced with an Illumina MiSeq instrument using v3 chemistry in single end 250 bp mode. The dataset resembled sequencing of a sample of contaminated trout, analyzed by shotgun RNA sequencing. Participants performed the bioinformatics analysis and assessment of an artificial metagenomics dataset provided by FLI and submitted a results table and/or a report to FLI. This ring-trial showed that despite shortcomings in some analyses (namely usage of incomplete databases or improper data pre-processing), overall the used software appears to have matured over the last years. However, for a truly beneficial effect of diagnostic metagenomics for the detection of potentially present pathogens, it is especially necessary to put more effort into the training for the assessment of the results delivered by the different software pipelines for the analysis of metagenomics data.

Main messages
- most software reliably classifies reads
- the software used does not affect the outcome as much as the databases
- sensitivity is compromised by unsuitable incomplete databases or improper data pre-processing
- MOST IMPORTANTLY
  - critical assessment of the obtained results is necessary
  - classification at species or strain level may be misleading for the assessment
  - training is necessary

Investigating a listeriosis outbreak in South Africa
Anthony Smith, NICD, South Africa
In South Africa, a progressive increase in listeriosis cases was noted from mid-June 2017, heralding what was to become the world's largest listeriosis outbreak. A total of 1060 cases were reported for the period 1 January 2017 to 17 July 2018. We describe laboratory activities, experiences, and results of whole-genome sequencing (WGS) analysis of *Listeria monocytogene*s isolates associated with this outbreak. WGS was performed using Illumina MiSeq technology. WGS data was analyzed using CLC Genomics Workbench Software and free-to-use open source on-line analysis tools/pipelines/databases. Multilocus sequence typing showed that 91% of clinical isolates were sequence type 6 (ST6), determining that the outbreak was largely associated with *L. monocytogene*s ST6. Epidemiological and laboratory findings led to investigation of a large ready-to-eat processed meat production facility in South Africa, named Enterprise Foods. *L. monocytogenes* ST6 was found in environmental sampling swabs of the production facility and in ready-to-eat processed meat products (including polony, a product similar to bologna sausage) manufactured at the facility. ST6 isolates, sourced at the Enterprise Foods production facility and from Enterprise food products, were shown by single nucleotide polymorphism (SNP) analysis to be highly related to clinical isolates; these non-clinical ST6 isolates showed <10 SNP differences as compared to clinical ST6 isolates. Core-genome multilocus sequence typing showed that clinical ST6 isolates and Enterprise-related ST6 isolates had no more than 4 allele differences between each other, suggestive of a high probability of epidemiological relatedness. WGS data interpreted together with epidemiological data concluded that the source of the listeriosis outbreak was ready-to-eat processed meat products manufactured by Enterprise Foods.

Main messages
- Since the 2017 outbreak, South Africa has added listeriosis to the list of mandatory notifiable medical conditions
- Surveillance systems have strengthened to facilitate prevention and early detection of listeriosis outbreaks

Establishing integrated genomic outbreak investigation and surveillance systems in Germany: Players, challenges and chances
Maria Borowiak, German Federal Institute for Risk Assessment, Germany

In Germany, foodborne pathogens caused approximately 380 detected outbreaks with more than 2200 cases in 2017. However, linking an outbreak to a certain food product often proves to be difficult. In order to improve outbreak detection, trace back investigations and real-time surveillance of foodborne diseases, Whole-Genome Sequencing (WGS) is currently integrated in routine diagnostics in food, veterinary and clinical laboratories in Germany. WGS provides an unprecedented level of strain discrimination. Consequently, it is possible to trace and track pathogenic subtypes within the food chain, and to support outbreak investigations by matching suspicious highly similar or identical isolates. Furthermore, WGS is used in food safety to predict antimicrobial resistance, virulence and environmental stress behaviour of isolates and consolidates the numerous different methodologies currently in use by allowing a rapid and cost efficient characterization of foodborne pathogens regardless of the species by following a universal workflow. Taking into account that there are more than 40 official laboratories legally responsible for detecting and typing of foodborne pathogens in the federal states in Germany, the transition from conventional subtyping to WGS comes with a lot of challenges. Microbiologists, bioinformaticians and epidemiologists have to collaborate at national and international level to successfully implement an integrated genomic outbreak investigation system. International standards are required to ensure the generation of high quality data, which has to be validated, stored and made available for national and international outbreak detection.

Main messages

- There is a transition in Germany to investigate outbreaks using WGS technologies
  → WGS is implemented in public health & food safety authorities on national level and in some federal states
- Standardization and harmonization of data generation and metadata nomenclature is needed to ensure data comparability
  → national working groups are created
- Accreditation of data generation and analysis is necessary before WGS can replace standard methods
- There is a need to rethink the use of open data
- Efforts are under way to establish a common database system for improved investigation of European outbreaks (EFSA and ECDC)

An invasive clone of *Streptococcus agalactiae* in SE Asia, …missed for decades.
Timothy Barkham, TTSH, Singapore

Sepsis with *Streptococccus agalactiae* (group B streptococcus (GBS)), seemed more prevalent in Singapore in 2015. Sanger based multi locus sequence typing (MLST) showed an increase in GBS sequence type (ST) 283. Case control studies associated disease with consumption of raw freshwater-fish. This was the first reported foodborne GBS outbreak globally. It came to an abrupt halt when an advisory was issued to the public to avoid eating raw freshwater-fish. There were three prior reports of ST283 in the literature, of 20 sepsis cases in Hong Kong, two bone infections in France, and one infected tilapia in Thailand. We hypothesised there was unrecognized ST283 disease in humans and fish across Southeast Asia. We used an ST283 specific PCR test to look for ST283 amongst GBS collections from Singapore, Malaysia, Thailand, Vietnam, Cambodia, and Lao PDR. We found that ST283 has been causing unrecognized disease in humans and farmed tilapia across SE Asia for at least twenty years. This investigation demonstrates that current practices, of extremely limited bacterial typing in human and animal health, allowed this unusual One Health epidemiology to persist unrecognized in many countries for decades. It prompts us to wonder what else we might be missing. The Singapore and regional pictures were resolved with microbiological common sense and MLST, because ST283 is a highly unusual ST. Whole genome sequencing, as a single and highly discriminatory and robust typing method, of bacterial isolates on a routine basis, from humans and animals, might reveal other ongoing transmission events unsuspected by traditional surveillance measures.

Main messages

- WGS helped with BEAST analysis (Bayesian Evolutionary Analysis Sampling Trees) and the development of an ST283 specific PCR
- With enough data, WGS could determine direction of ST283 regional spread
- WGS offers a unified method for routine typing with adequate discrimination
- WGS will answer the question. 'where have you been, what have you done, with whom?'

How Whole Genome Sequencing is Used for Foodborne Pathogens: a Regulatory Perspective
Eric Stevens and Ruth Timme, FDA, USA

Main messages

In the U.S. the application of WGS data is used in combination with other evidence (e.g. traceback, epidemiology, etc). Each case is different so no one-size fits all approach exists on SNP cutoff or number of samples, etc. The use of WGS within a foodborne outbreak investigation and response helps in:

-pointing to potential sources of contamination
-defining scope of contamination and illness
-effectiveness of cleaning and sanitation i.e. preventative control in industry
-providing a piece of the information used in regulatory action i.e. still requires traceback, epi info etc.
-understanding the root cause

- FDA supports public sharing of data e.g. via NCBIWGS:
  - allows for a refined outbreak investigation approach i.e. matching isolates with environmental/inspection data followed by epidemiological investigation
  -helps solve persistent/complex problems on a farm or in a facility
  -supports preventative controls by enabling internal comparisons to a public database of food/environmental isolates
  -can help identify suppliers who ship contaminated products
  -identifies whether a contaminant is resident or transient to a facility
  -proved to identify outbreaks, enabling quicker response to outbreaks, rapid response to ensure contaminated food is not on the market for consumers thus resulting in fewer sick people
- Future data flow will follow an independent submission model i.e. labs working with Bionumerics 7.6 will submit data directly to NCBI
- SOP, best practices for submission through Bionumerics 7.6 document will be made available in September 2019

Epidemiological Considerations Concerning the Use of Whole Genome Sequencing Data for Foodborne Outbreak Investigation
Heather Carleton, CDC, USA

The WGS-based analysis tools used at CDC can be used to compare bacteria associated with foodborne illness, the sequence data is translated into epidemiological databases for outbreak detection and tracking, and WGS is thus used in identifying potential outbreaks and sources.

Main messages

- PulseNet has been detecting foodborne outbreaks for over 20 years, originally they used PFGE but now use WGS as the primary molecular subtyping method
- PulseNet uses allele codes to integrate with epidemiological databases like SEDRIC
- Allele codes help identify which isolates are closely related
- Allele codes can generate histrograms in SEDRIC to track trends and manage outbreaks
- WGS is just the first step for PulseNet, next stop is culture independent subtyping methods like metagenomics

Applications of whole genome sequencing in surveillance and risk assessment for foodborne pathogens.
Kalliopi Rantsiou, University of Turin, Italy

Whole Genome Sequencing (WGS) is progressively being adopted as the molecular typing method by competent authorities. It has contributed in advancing food safety through enhanced epidemiological investigation of foodborne outbreaks and surveillance. Food industries are also investigating its application mainly within environmental monitoring programs to elucidate contamination routes. WGS has been shown to be of extreme importance when applied to delineate microbial population structures and for source attribution within the risk analysis context.

It is envisioned that WGS will also upgrade microbiological risk assessment. Describing the microbial biodiversity, in terms of survival and adaptation within the food chain and virulence, is fundamental for improving hazard characterization. Comparing genomic features with phenotypic data may provide insights into the molecular mechanisms that underlie microbial behaviour. There should be particular emphasis on how it is foreseen that WGS and next generation sequencing will function within microbiological risk assessment.

Main messages

- Omics data currently too complex to be readily implemented into the current risk assessment paradigm
- Risk assessment moving beyond taxonomic hazard identification/characterization to a function based approach

Poster Abstracts

[1] Comparative genomics of 16 strains of *Leuconostoc carnosum* isolated from cooked ham

Francesco Candeliere
PhD Student, Dept. of Life Sciences, University of Modena and Reggio Emilia, Modena, Italy

Leuconostoc carnosum is a lactic acid bacterium often used in meat industry as bioprotective starter due to production of bacteriocins against *Listeria monocytogenes.* This work aims to conduct a genomic diversity analysis on the genomes of 16 strains of *Leuconostoc carnosum* isolated from cooked ham packaged in modified atmosphere, manufactured by different European producers. These samples were isolated during the product shelf-life for a previous work and taxonomically characterized through 16S rRNA sequencing. For this work, their genomes have been analysed through whole genome sequencing, genes have been annotated and clustered into functional categories using RAST. Their pangenome was calculated with Roary. WGS analysis revealed that 4 strains belong to a different *Leuconostoc* species, *L. mesenteroides.* The pangenome of twelve *L. carnosum* strains consist of 2810 total genes; 1407 represent the core genome, 871 the shell genome, 532 the cloud genome. In order to identify bacteriocin-producing strains effective against *L. monocytogenes*, both on plate tests and *in silico* analysis using BAGEL4 were conducted. On plate test allowed to identify six strains, two *L. carnosum* and four *L. mesenteroides. In silico* analysis confirmed the results from plates, and it also identified another *L. carnosum* strain that possess the gene for bacteriocin but lacks the gene for a bacteriocin transmembrane transporter. This work is still in progress and its goal is to provide a better comprehension of *L.carnosum* genomics.

[2] PulseNet USA Transition to Whole Genome Sequencing as Gold Standard Method for Foodborne Disease Surveillance in the United States

Heather Carleton* and Peter Gerner-Smidt,
Enteric Diseases Laboratory Branch, Division of Foodborne, Waterborne, and Environmental Diseases, Centers for Disease Control and Prevention, Atlanta, GA, USA

PulseNet, the national molecular subtyping network for foodborne disease surveillance in the United States, has transitioned in 2019 from using the previous gold standard of Pulsed Field Gel-Electrophoresis (PFGE) to Whole Genome Sequencing (WGS) as its primary subtyping method. PulseNet is a network of over 80 state, local, and federal public health laboratories that perform molecular subtyping on foodborne bacteria. PulseNet CDC has developed an analysis workflow including core and whole genome multilocus sequence typing (cg/wgMLST), genotyping tools to identify serotyping, virulence, plasmid, and resistance genes, as well as tools including an allele code built on single linkage trees to name each sequence for outbreak detection and easy communication. These tools and schema are integrated from open source tools available through the Center of Genomic Epidemiology (CGE), PubMLST, Institut Pasteur, and EnteroBase and all sequence data generated by the states is uploaded in real time to NCBI and included in the GenomeTrakr databases. To access these tools, PulseNet members must participate in a certification and proficiency testing process that certifies that members can perform the WGS lab workflow to generate sequence data for all PulseNet organisms to meet quality standards and to accurately analyze the sequence data to determine whether it can be uploaded to a national database as well as NCBI. So far, over 50 PulseNet members have become laboratory and analysis certified, over 100,000 read sets for PulseNet organisms including *Salmonella, Escherichia, Vibrio, Listeria, Yersinia, and Campylobacter* has been uploaded to the PulseNet national databases and NCBI.

[3] Nanopore Whole Genome Sequencing for One-health: Identification of Pathogens, Antibiotic Resistance, and Virulence Factors

Olga Francino[a]*, Joachim Vines[a,b], Anna Cusco[b], Lourdes Migura-garcia[c], Armand Sanchez[a]
[a] SVGM, Molecular Genetics Veterinary Service, Universitat Autònoma de Barcelona, 08193 Bellaterra, Barcelona, Spain
[b] Vetgenomics, Edifici EUREKA, PRUAB, 08193 Bellaterra, Barcelona, Spain
[c] IRTA, Centre de Recerca en Sanitat Animal (CReSA, IRTA-UAB), 08193 Bellaterra, Barcelona, Spain

Nanopore sequencing is a flexible alternative to public health in-depth characterization of pathogen genomes, and their antimicrobial resistance and virulence factors. The long reads have the potential to assemble the entire genomes, even from complex metagenomics datasets. We are collaborating with reference groups in microbiology, and in human and animal health from a One-Health approach, to validate the use of nanopore sequencing from isolates, from clinical samples (clinical metagenomics) or even from complex metagenomics samples. As a proof-of-concept, we have sequenced with MinION (1) 18 strains of *Staphylococcus pseudintermedius* isolated from pyoderma in dogs, and (2) 18 *Escherichia coli* positive for mcr-1 isolated from a mixed farm (13 from calves, 4 from pigs and 1 from human). Unicycler was used to perform genome assembly and Abricate, along with different databases (CARD, NCBI and PlasmidFinder), to characterize the contigs. Nanopore sequencing allowed us to obtain the whole genome sequences of (1) the 18 *S. pseudintermedius* strains and to confirm their phenotypic resistance profiles at the genomic level; and (2) to identify the presence of colistin resistance due to mcr-1 gene in 17 out of 18 *E.coli* strains and to locate it in the chromosome (2 strains) or at different replicon-harbouring contigs (potential plasmids): IncX4 (14), IncI2 (1), and IncHI2 (1).

The lower accuracy of nanopore reads is overcome using a hybrid approach (e.g., Unicycler from Wick et al., 2017) with both long (nanopore) and short (Illumina) reads for the best assembly completeness and accuracy.

[4] Microbiological Criteria and Food Safety

[a]Dr Nesrine Gharbi*, [a]Monia Bouktif, [a]Hichem Mechichi
[a]Agence Nationale de Contrôle Sanitaire et Environnemental des Produits

Currently Tunisia don't have a regulatory text that describe the microbiological criteria and their limits and that constitute a legislative reference for inspectors and controllers. Knowing that the contamination of food with microbiological agents is a public health problem worldwide, most countries have shown a significant increase over the past decades in the incidence of diseases caused by the presence of microorganisms in foods, including pathogens such as *Salmonella* and *E-coli*. Diseases caused by food-borne pathogens are a major burden for consumers. As a result, the prevention and control of these diseases have become public health goals internationally. These objectives depended in part on the establishment of parameters such as microbiological criteria, which reflect the knowledge and experience of good hygienic practices (GHP) during production, processing, handling, distribution, storage, sale, preparation and use, in conjunction with the implementation of the HACCP system. Microbiological criteria have been used for many years and have contributed to the improvement of food hygiene. It is within this framework that this project is integrated with the aim of producing a regulatory text setting the microbiological criteria and their limits applicable to all foodstuffs.

[5] Empowering local to global WGS-based surveillance and investigation: The Integrated Rapid Infectious Disease Analysis (IRIDA) Platform

Emma Griffiths[1*], Thomas Matthews[2], Aaron Petkau[2], Josh Adam[2], Damion Dooley[1], Dan Fornika[3], Geoff Winsor[4], Finlay Maguire[5], Brian Alcock[6], THE IRIDA CONSORTIUM, Andrew Mcarthur[6], Rob Beiko[5], Morag Graham[3], Fiona Brinkman[4], Gary Van Domselaar[3], William Hsiao[1,2]
[1] Department of Pathology and Laboratory Medicine, University of British Columbia, Vancouver, BC, Canada
[2] National Microbiology Laboratory, Public Health Agency of Canada, Winnipeg, MB, Canada
[3] BC Centre for Disease Control Public Health Laboratory, Vancouver, BC, Canada
[4] Department of Molecular Biology and Biochemistry, Simon Fraser University, Burnaby, BC, Canada
[5] Faculty of Computer Science, Dalhousie University, Halifax, NS, Canada'
[6] Department of Biochemistry and Biomedical Sciences, McMaster University, Hamilton, ON, Canada

Specialized analytical tools and highly trained personnel are needed to analyze complex genomics data. Yet these resources are not always available in public health organizations. While centralized web services are available, these require users to upload potentially sensitive data to un-vetted servers, an action prohibited by some institutions and jurisdictions. The IRIDA platform is a decentralized, user-friendly, open-source bioinformatics and analytical web platform custom-designed to support multi-jurisdictional infectious disease outbreak investigations using genomic sequence data. IRIDA can be installed on institutional servers, enabling users to perform secure and local analyses, while also permitting data sharing with 'trusted' partners and public sequence repositories. IRIDA provides data management, secure data sharing, analytics and visualizations, and incorporates quality control, genomics assembly and annotation, in silico serotyping, multi-locus sequence typing, and outbreak phylogenomics. The platform also directly incorporates results into visualizations for hypothesis generation during epidemiological investigations. IRIDA supports customization through its new plugin architecture - connecting users to additional 3rd party tools, such as the Resistance Gene Identifier with its state-of-the-art AMR detection methods for genomes and metagenomes, as well as others in Galaxy Toolshed. Community development of IRIDA is encouraged and has led to customization success in Italy (ISS), and in South Africa to support LMIC (SANBI). Recent enhancements include preliminary ontology integration, and a data sharing ring trial. Future IRIDA augmentations include "containerizing" pipelines, cloud deployability, creating ontology-based fine-grained access controls, and developing a data attribution system. IRIDA is freely available at https://github.com/phac-nml/irida and www.irida.ca.

[6] Phenotypic and Genotypic Characterization of Antimicrobial Resistant *Escherichia coli* Isolated From Ready-to-eat Food in Singapore Using Disk Diffusion, Broth Microdilution and Whole Genome Sequencing Methods

Siyao Guo[1,2]*, Moon Tay[1,2], Kyaw Thu Aung[1,2,4], Kelyn Seow Lee Ghee[1,2], Lee Ching Ng[3,4], Rikky W. Purbojati[5], Daniela I. Drautz-Moses[5], Stephan C. Schuster[5], Joergen Schlundt[1,2]
[1] Nanyang Technological University Food Technology Centre (NAFTEC), Singapore
[2]School of Chemical and Biomedical Engineering, Nanyang Technological University, Singapore
[3] School of Biological Science, Nanyang Technological University, Singapore
[4] Environmental Health Institute, National Environment Agency, Singapore
[5] Singapore Centre for Environmental Life Sciences Engineering (SCELSE), Nanyang Technological University, Singapore

Antimicrobial resistance (AMR), especially multidrug-resistance, of bacteria is posing a great threat to public health. This study aimed to determine the antimicrobial resistance profiles of *Escherichia coli* isolated from ready-to-eat food sold in retail food premises in Singapore. In this study, a total of 99 *E. coli* isolates from poultry-based dishes (n=77) and fish-based dishes (n=22),

obtained between 2009 and 2014, were included for disk diffusion testing. Of the 99 isolates, 24 (24.2%) were resistant to at least one antimicrobial agent. These isolates were then subjected to broth microdilution testing against 33 antimicrobial agents to determine the minimum inhibitory concentration (MIC) of isolates. Finally whole genome sequence (WGS) was carried out on the strains in order to correlate resistant phenotypes to putative antimicrobial-related genes. Of the 24 isolates, 15 (62.5%) were found to be resistant to three or more classes of antimicrobials and thus were defined as multi-drug resistant strains. Two isolates (8.3%) were confirmed as Extended-Spectrum β-lactamase (ESBL)- producing *E. coli* by double disk synergy test. Based on WGS data, online analysis tool ResFinder detected 7 classes of antimicrobial resistance genes and resistance-related chromosomal point mutations in 19 of the 24 *E. coli* isolates. By analyzing the WGS contigs using BLASTn and KmerFinder, ESBL genes and transferable colistin resistance gene *mcr*-1 and *mcr*-5 were determined to be located on plasmids, which could pose a greater risk of AMR transfer among bacteria. This study showed the presence of antimicrobial resistant *E. coli* isolates in ready-to-eat retail food, and raises a concern on the possible transmission of antimicrobial resistant bacteria from food to humans.

[7] Characterization of the Phenotypic and Genotypic Properties of Carbapenemase-producing *Vibrio* spp. Isolates in Germany

CLAUDIA JÄCKEL[1], ECKHARD STRAUCH[1] and JENS ANDRE HAMMERL[1,*]
[1] German Federal Institute for Risk Assessment, Department of Biological Safety, Max-Dohrn Str. 8-10, 10589 Berlin, Germany

Vibrio isolates are widely distributed in coastal waters and sometimes associated with wound infections and diarrheal diseases in humans. Some years ago, antimicrobial resistance testing of potentially pathogenic *Vibrio* species recovered from coastal waters of Germany indicated that some of the isolates exhibited carbapenem resistance. Recently, a *V. parahaemolyticus* isolate from imported Asian seafood intended for consumption in Germany exhibited also a non-wildtype phenotype against carbapenems. To determine the genetic basis of the carbapenemase-producing *Vibrio* spp., the isolates were subjected to whole genome sequencing and bioinformatical analysis. Sequence determination was performed by long- and short-read sequencing via PacBio RSII and MiSeq, respectively. Bioinformatic analysis revealed that carbapenem-resistant *V. cholerae* carried $bla_{\text{VCC-1}}$, while the *V. parahaemolyticus* isolate comprises $bla_{\text{NDM-1}}$. Further analyses, i.e. PFGE-profiling, DNA-hybridization as well as conventional PCR were used to reveal the organization of the $bla_{\text{VCC-1}}$ or $bla_{\text{NDM-1}}$ gene within the *Vibrio* genomes. Initial MiSeq sequencing of all prevailing isolates did not definitely revealed the genetic localisation of $bla_{\text{VCC-1}}$ and $bla_{\text{NDM-1}}$ within the genomes. However, PFGE profiling indicated that the $bla_{\text{VCC-1}}$ resistance gene is chromosomally located, while $bla_{\text{NDM-1}}$ is plasmidal encoded. Interestingly, some of the $bla_{\text{VCC-1}}$ isolates carried more than one copy of the carbapenem-resistance gene on its chromosomes. The genetic basis of the $bla_{\text{VCC-1}}$ and $bla_{\text{NDM-1}}$ carrying genomes will be presented in detail. Our study indicates that carbapenemase-producing *Vibrio* spp. are frequently present in different regions of the German coastline and imported seafood. Therefore, the question arises if *Vibrio* species are a common reservoir for carbapenem resistance genes.

[8] Genetic variability and Antimicrobial Resistance of *Klebsiella* spp. Isolates from Sewage Water of Swine and Poultry Slaughterhouses

MICHAEL SAVIN[1], CLAUDIA JÄCKEL[2], SILVIA SCHMOGER[2], MARIJO PARCINA[3], JUDITH KREYENSCHMIDT[1], ANNEMARIE KÄSBOHRER[2,4] and JENS ANDRE HAMMERL[2,*]
[1] University of Bonn, Faculty of Agriculture, Institute of Animal Sciences, Katzenburgweg 7-9, D-53115 Bonn, Germany
[2] German Federal Institute for Risk Assessment, Department of Biological Safety, Max-Dohrn Str. 8-10, 10589 Berlin, Germany
[3] University of Bonn, University Hospital, Institute of Medical Microbiology, Immunology and Parasitology, Sigmund-Freud Strasse 25, D-53105 Bonn, Germany
[4] Institute for Veterinary Public Health, University of Veterinary Medicine, Veterinärplatz 1, 1210 Vienna, Austria.

Klebsiella spp. are Gram-negative opportunistic pathogens prevalent on plants, in water and soil but also colonizing a wide range of livestock/wildlife animals. Klebsiellae were recognized as an important threat to global public health due to their high level of antimicrobial resistance, mainly associated with the presence of mobile genetic elements. In this study, ESBL-producing *Klebsiella* isolates from sewage water of poultry and swine slaughterhouses were characterized by whole genome sequencing and antimicrobial resistance testing. Antimicrobial susceptibility testing of *Klebsiella* spp. isolates was performed using broth microdilution following CLSI guidelines and EUCAST epidemiological cut-off values. Whole genome sequencing and bioinformatics were performed to reveal the genetic basis of the observed resistances and the diversity of the isolates in different processing stages of slaughtering. Bioinformatic analyses revealed that prevailing isolates represented a high genetic diversity in its MLST-type and virulence profile. Overall, the isolates exhibited many plasmid sequences, that carried various antimicrobial resistance genes. The majority of the isolates harbor bla_{SHV} genes causing its ESBL-phenotype. Some of them also comprise determinants involved in the development of a carbapenem-resistance phenotype. The genetic basis of the isolates, their antimicrobial resistances and the content of mobile genetic elements will be presented in detail. Our study confirms that characterized klebsiellae comprises diverse mobile genetic elements that may be important vectors for the transmission of antimicrobial resistances. Some of the plasmids are closely related to plasmids of clinical *Klebsiella* isolates from humans. However, up to now their impact on human health is unknown and needs to be assessed.

[9] Dissection of the Genetic Basis of *mcr-4/mcr-5* carrying *Escherichia coli* Isolates from Food and Livestock in Germany

J.A. Hammerl[1]*, K. Juraschek[1], D. Shamoun[1], M. Borowiak[1], S. Schmoger[1], B. Malorny[1], A. Irrgang[1], and A. Käsbohrer[1,2]
[1] German Federal Institute for Risk Assessment, Department of Biological Safety, Max-Dohrn Str. 8-10, 10589 Berlin, Germany
[2] Institute for Veterinary Public Health, University of Veterinary Medicine, Veterinärplatz 1, 1210 Vienna, Austria.

According to the recommendation of the WHO, colistin belongs to the highest priority critically important antibiotics, which should be used only to treat severe human infections caused by multidrug- and/or carbapenem-resistant Gram-negative bacteria. In 2017, Carattoli *et al.* and Borowiak *et al.* simultaneously reported on the identification of two novel mobilizable colistin resistance genes in *Salmonella enterica* serovar Typhimurium, designated *mcr-4* and *mcr-5*, respectively. In the National Reference Laboratory for Antimicrobial Resistances in Germany, *mcr-4* and *mcr-5* carrying *E. coli* isolates from the German national monitoring program for antimicrobial resistance in zoonotic agents from the food chain were subjected to whole genome sequencing for determination of its genetic basis.
Molecular detection and typing of mobile colistin resistance genes among colistin-resistant *E. coli* recovered between 2010 and 2017 was performed using multiplex PCR analysis according to Rebelo et al. (2018). For genetic characterization whole genome sequencing using an Illumina MiSeq-benchtop sequencer was conducted *in house*. Comprehensive bioinformatical analyses were performed to identify and characterize the localization of the *mcr*-genes within the genomes and the genetic variability of the isolates.
Out of 800 colistin-resistant *E. coli*, *mcr-4* and *mcr-5* was detected in 13 and three isolates, respectively. Molecular analyses, whole genome sequencing and bioinformatics revealed that two variants of *mcr-4* (*mcr-4.2* and *mcr-4.3*) and *mcr-5* (*mcr-5* and *mcr-5.2*) are prevalent in German *E. coli* isolates. Overall, the isolates differ in their MLST-, sero- and fim-type but carry highly conserved *mcr-4* and *mcr-5* plasmid prototypes that showed some variability in size and genetic composition. Detailed information on the genetic features of the isolates and *mcr*-carrying plasmids will be summarized. Our findings indicate that the mobile colistin resistance genes *mcr-4* and *mcr-5* are located on closely related plasmids that are non-self-transmissible. However, both *mcr*-genes are located in transposable elements that might be disseminated by transposition to other mobile genetic elements. Up to now, the impact of these resistance genes is unknown. Further information on the stability of *mcr-4/mcr-5* harboring genetic elements, their transmission routes as well as their distribution in livestock, food products and humans are needed to assess the potential impact of this resistance determinant on public health.

[10] Dynamic Time Warping Assessment and Sensitive High Resolution Melting Analysis for Subtyping *Salmonella* Isolates from Northern Thailand

KRITCHAI POONCHAREON
Division of Biochemistry, School of Medical Sciences, University of Phayao, 19 Moo 2, Tambon Maeka, Amphur Muang, Phayao, 56000, Thailand

Nontyphoidal *Salmonella spp*. transmitted through various routes are a major concern of food poisoning due to the consumption of contaminated food. To establish a molecular-based protocol for simple and rapid subtyping of *Salmonella* isolates from various sources. Sensitive High-Resolution Melting-curve analysis (S-HRMa) and Dynamic Time Warping assessment (DTW) were applied for serotyping forty *Salmonella* spp. isolates from various origins and locations in seven provinces in the north of Thailand; the results were compared to those from conventional serotyping and ERIC- PCR. HRM serotyping of 40 *Salmonella* spp. initially produced 14 melting-curves with 2 predominant clusters: C1 (n=18) and C2 (n=9). Applying S-HRMa and serogroups generated 25 sensitive clusters. Conventional serotyping revealed that cluster C1 and C2 comprised of 6 different *Salmonella* serotypes with *S.* Weltevradent (n=14) as the predominant one. The S-HRMa also suggested the possible subtyping in some serotypes. In addition, DTW was performed to cluster those 40 *Salmonella* spp. into 28 clusters, assigned into different 4 clades corresponding to S-HRMa. The two clustering methods indicated that the S. Weltevreden was the predominant subtype (DTW4-S1, n=6). Three ERIC clusters at 92% similarity index also corresponded to the results of those two clustering methods. With important and related epidemiological data, *S.* Derby and *S.* Monophasic were suggested to be related to the slaughterhouse and swine. In this study, the ERIC cluster 10 comprising 2 *Salmonella* isolates of *S.* Weltevraden suggested the transmission route was likely to be farm-to-farm in the same province. The DTW assessment and S-HRMa effectively increased the discriminatory power of clustering to the same level as that of ERIC - PCR and were a simple and rapid protocol to perform *Salmonella* subtyping for the epidemiological research.

[11] Implementation of Next Generation Sequencing for Pathogen Typing in Routine Analysis - Evaluation of DNA Fragmentation Methods

L. MURR*, M. PAVLOVIC, U. BUSCH, I. HUBER, P. GUERTLER
Bavarian Health and Food Safety Authority, Veterinärstr. 2, 85764 Oberschleißheim, Germany

Next Generation Sequencing (NGS) currently represents the highest-resolution method for strain typing. In combination with a suitable data analysis, NGS has the potential to differentiate bacterial isolates of a species much more precisely than with the typing methods previously used in routine. The implementation of NGS in routine analysis, as part of the official monitoring of food, requires an optimization of the corresponding workflow with regard to sequencing quality and time/cost ratio. A crucial factor in NGS applications is the choice of method for DNA fragmentation used to produce DNA libraries. The prerequisite for a high coverage of the genome is the generation of random and uniform strand breaks. Coverage can vary depending on the type of fragmentation method selected and the DNA sequence of the organism. In order to evaluate the susceptibility of different methods to the sequence-induced generation of irregular fragment sizes, their application to bacterial DNA with different GC contents (*Campylobacter coli* with ~30 % GC content and *Salmonella enterica* with ~50 % GC content) was tested and evaluated in terms of time, cost and size distribution. Fragmentation was performed physically by ultrasonic on the one hand, and enzymatically by tagmentation or two alternative enzymatic methods on the other hand. The generated fragments were separated by capillary electrophoresis and the size distributions of the individual isolates were compared before and after size selection. When enzymatic kits were used, the DNA could be overfragmented due to sequence-specific fragmentation, while physical fragmentation is easier to standardize due to less fragmentation bias.

[12] High Throughput Whole Genome sequencing for Molecular Surveillance using a Certified Process

RADONIC A., GOLLNOW K., KURZENDOERFER P., BARZ D., THUERMER A.*
*Robert Koch-Institute, Department of methodology and research infrastructure, Division Genome Sequencing, Berlin, Germany

Whole genome sequencing with Next Generation Technology (NGS) is a wide-spread method that is used in many laboratories as a “gold standard” for genome analysis. There are several methods available that can be used for the NGS library preparation, as well as for the sequencing procedure. Due to the different methods and instruments the generated sequencing data can differ in their composition and quality. As a result, different laboratories compare different data and may generate different analysis results. To use NGS also for high throughput surveillance studies without the loss of quality we set up an automated and time- independent full walk-away process. This process was certified with DIN ISO 17025 in the last year and is the basis to generate comparable sequencing data of the same quality for any kind of species.

[13] Challenges and Opportunities for Establishing High Throughput Sequencing at the National Veterinary Research Institute, Poland

MAŁGORZATA OLEJNIK, DARIUSZ WASYL*
Department of Omics Analyses, National Veterinary Research Institute, Puławy, Poland

High Throughput Sequencing (HTS) technologies have been rapidly developed over the last decade proving their universal usefulness in genetic-based studies. Its most prominent application is whole genome sequencing (WGS) in outbreak and epidemiological surveys. Although outsourcing might be convenient, in-house sequencing capacity is needed for large scale studies, precisely in reference laboratories such as NVRI. Herewith milestones in setting up operational HTS laboratory are presented. Being a partner in the international ENGAGE[1] project (2016-2018; www.engage-europe.eu) gave a base for hands-on trainings, proficiency testing and gaining personnel competences. ENGAGE was also an incentive for the Ministry of Science and Higher Education (MoS) to grant resources[2] for equipment purchase for the newly created Department of Omics Analyses (2017). Usefulness of the implemented WGS was proved during the real-life scenario of multinational Salmonella Enteritidis outbreak related to Polish eggs. Timely response and support for the Ministry of Agriculture helped to convince national authorities on the advantages of WGS-based studies in food safety and protection of public health. Laboratory capacities have been also used in research projects such as EFFORT[3] (2014-2018, www.effort-agains-amr.eu) or One Health EJP[4] (2018-2022, www.onehealthejp.eu). Broad and effective usage of granted resources was the reason for further MoS donations to support the sustainability of special equipment (2018-2020)[5] and extension of research activities (2018-2019)[6]. Herein we show the establishment of High Throughput Sequencing laboratory that is capable of high-level research and reference testing in support for relevant national and regional authorities.

MoS co-funding donations: 3553/EFSA/2016/2[1]; 3173/7PR/2014/2[3]; 3932/H2020/2018/2[4]
MoS donations: 4477/E-180/R/2016[2]; 4477/E-180/SPUB/2018/1[5] 4477/E-180/S/2018-1[6]

[14] Whole Genome Sequencing – a Support Tool in *Salmonella* Reference Laboratory

MAGDALENA ZAJĄC[1], EWELINA KAMIŃSKA[1], MAGDALENA SKARŻYŃSKA[1], ALEKSANDRA GIZA[2], OLGA GOŁAWSKA[1], ŁUKASZ PRUSS[2], DARIUSZ WASYL[1,2]*

[1]Department of Microbiology, [2]Department of Omics Analyses, National Veterinary Research Institute, Puławy, Poland

Salmonella reference laboratory (1) continuously faces diagnostic and epidemiological challenges. Whole genome sequencing (WGS) is a great tool that allows to meet and overcome some of them. Here we show some examples in which WGS analysis with open CGE bioinformatics tools helped to answer vital diagnostic questions. Serovars Enteritidis, Infantis, Kentucky, and monophasic Typhimurium currently prevail in, respectively, laying hens, broilers, turkey, and pigs in Poland. WGS-based identification of sequence type (respectively, ST11, ST32, ST198, and ST34) confirms tested strains as part of the ongoing outbreaks or epidemics. Besides routine epidemiological investigations WGS supports and improves serotyping. The method fails to identify autoagglutinating strains, whereas WGS easily recognises them as the most common serovars, such as Enteritidis, Infantis, monophasic Typhimurium, or less frequent or exotic ones: Derby ST39, Brandenburg ST65, or Llandoff ST2321. Missing antigens might disturb efficient serotyping, but *Salmonella* 6,7:r:- and *Salmonella* 6,7:r:1,- were classified as Infantis ST32, whereas O:18 was identified in *Salmonella* IIIb -:l,v:z. Simultaneously, the strain represented novel *dna*N allele with closest match to ST1262. Serotyping of rare and exotic serovars can be confirmed (i.e. Corvallis, Mapo – undefined ST, Salford, *diarizonae* 50:z_{52}:z_{53}, 53:z_{10}:z_{35}, *houtenae* 48:g,z_{51}:-). WGS clearly demonstrates imperfection of KWLM scheme: we suppose serovar Bardo (8:e,h:1,2) does not exist and the strains belong to serovars Newport (6,8:e,h:1,2) ST166. In-depth analyses of *fliC* and *fljB* genes indicates reversed structure of flagellar antigens in KWLM listed serovar *diarizonae* 50:z:z_{52}. It is concluded that WGS improves quality and reliability of reference testing and may lead to scientifically relevant conclusions.

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[15] Food 3D Printing for Personalized Nutrition Based on Gut Microbiome

ANIRUDH AGARWAL
Research Associate, NAFTEC, Nanyang Technological University, Singapore

Personalized nutrition is on the rise in the food industry and people are increasingly more informed about nutrition and health. There is an increasing number of tracking devices and apps to track the level of activity and food intake over time to personalize diet and exercise.

Companies like GX Sciences and circle DNA offer DNA testing kits that take a cheek swab to determine nutritional requirement based on human DNA. 3D printing of food enables the precise deposition of the desired ratio and amounts of ingredients. This offers a way to customize every meal to every individual. A restaurant, Sushi Singularity, is opening in Tokyo in 2020 that provides 3D printed meals personalized to the nutritional requirements of the guest. The nutritional profiling is done using urine sampling a day in advance. We intend to use stool samples to analyse the gut microbiome using whole genome sequencing and develop customized 3D printed meals accordingly.

The 3D printed meals would adapt to one's microbiome results in 3 ways:

1. Changing the amounts of various pre-biotics – For guts with all essential bacteria
2. Adding needed pro-biotics – For guts with missing good bacteria in people with otherwise healthy immune systems
3. Metabolites – For guts lacking the correct bacteria and compromised or underdeveloped immune systems (eg babies, patients with poor/damaged immune systems)

[16] Characterization of Extended Spectrum Beta-Lactamase-Producing *Escherichia coli* Isolates from a Reservoir in Singapore

ZHONG YANG, PhD Student, NAFTEC, Nanyang Technological University, Singapore

Extended Spectrum Beta-Lactamase-Producing *Escherichia coli (E. coli)* is increasing detected from many sources including food, environment, clinic globally. The fast spreading of Extended Spectrum Beta-Lactamase-Producing bacteria and Extended Spectrum Beta-Lactamase (ESBL) genes has become a big challenge to public health. In this research, we characterized 9 ESBL-producing *E. coli* isolated from a reservoir in Singapore with both genotypic and phenotypic methods. Each of the cephalosporin resistant isolates is carrying at least 1 variant of $bla_{CTX\text{-}M}$ gene. The most common beta-lactamase gene is $bla_{CTX\text{-}M\text{-}15}$. And all the isolates were shown to carry at least two transferable vectors. We use Next-Generation-Sequencing and online analysis tools to investigate the relationship between beta-lactamase and beta-lactam resistance. In this way, we are providing reference information for controlling and tracking beta-lactam resistance from environmental water source.

GMI Working Group Outcomes

Following on GMI11 suggestions, GMI12 increased the amount of time dedicated to work group discussions with breakout sessions scheduled on the first and third day of the meeting, and included a reception fostering networking opportunities. A two day NGS training workshop was organized and preceded the three day GMI12 meeting. In striving for the inclusion, funding was raised for the attendance of developing country delegates, with selected individuals invited to share their experience of NGS used in their home countries. A special thanks go to the UN Food and Agriculture Organization (Regional Office for Asia and the Pacific), and the World Health Organization (HQ) for providing the funding to support participation of 27 scientists from developing countries.

At the GMI12, a one page Singapore Sequencing Statement was drafted for the intended viewership of all parties interested in public health and food safety i.e. scientists, politicians and consumers, aimed at promoting public debate and potential political action. Inputs from of all work groups and GMI12 participants, as well as all GMI members in general were considered for incorporation in the final version as exhibited on the next page.

Singapore Statement on Sequencing

June 2019

Recognizing that risks related to the spread of dangerous microorganisms in humans, plants, food, animals and environment, compounded by the growing threat of antimicrobial resistance (AMR), are a global concern.

• Recent Public health and One Health initiatives attempts to protect citizens from health risks posed by pathogenic microorganisms, which could cause as many as 18-19 million deaths annually including 10 million due to AMR by 2050 (more than present deaths from cancer);

• Novel developments in sequencing DNA from microorganisms is revolutionizing the detection and prevention of the spread of such microorganisms and AMR. Equal access and implementation of such new sequencing technology between countries can dramatically reduce the global burden of disease by enabling a novel, real-time surveillance of all animal and human diseases and food safety risks.

• Global sharing of sequencing results will allow for the early detection of emerging threat and rapid identification, investigation, and prevention of national, regional and global disease outbreaks.

Scientists, gathered at the 12th Meeting of the GMI (Global Microbial Identifier) in Singapore, urge all countries to consider the public, animal and plant health, food safety and economic benefits of introducing a global mechanism for the sharing and analysis of DNA sequences (www.globalmicrobialidentifier.org).

• The GMI initiative is a not-for-profit international consortium comprising scientists from over 55 countries collaborating and sharing sequencing data for microorganisms, enabling efficient global surveillance and a new understanding of the importance of microorganisms in general. Membership in GMI is entirely open and encouraged for everyone working in this field.

• GMI provides a framework for coordinating DNA data collection and analyses of microorganisms with the goal of open sharing of sequence data. GMI provides validation guidance for both the sequencing data collection and analyses, as well as capacity building efforts for developing countries

• In a fully realized global sequencing database (or interconnected databases), microorganisms can be rapidly characterized in context of their global diversity, controlling disease outbreaks, enacting food recalls, providing a resource for preventive controls, and tracking the spread of AMR.

• The use of sequencing methodologies revolutionizes our understanding and management of plant, animal, environmental, human health, and food safety. Optimal use is dependent on policies and the willingness and ability of countries to share genomic sequences across borders and in real-time.

Government and intergovernmental organizations must implement sequencing data sharing policies and mechanisms, ensuring equitable access and benefits to people worldwide, with the vision to improve global human health[1].

[1] Many countries are currently re-thinking laws and policies that address the management and conservation of biodiversity, as well as the protection of the public's health and the promotion of Open Science. GMI urges governments and intergovernmental organizations to use this window of opportunity to support and regulate global microbial DNA sequence data sharing.

Work Group 1: Political challenges, outreach and building a global network

As agreed at GMI11, the second letter was drafted (Annex 3), translated, and sent to the ministers of health and agriculture where the group either had connections or had received a positive response to the initial letter, reinforcing a need for sequencing technology implementation in the government regulatory setting. Among all the countries contacted i.e. Belgium, Botswana, China, Denmark, France, Germany, Greenland, Ireland, Italy, Israel, Ireland, Malaysia, the Netherlands, Singapore, South Africa, Spain, United Kingdom, USA, Canada, Mexico and New Zealand, full letters of response were received from the three latter countries (Annex 4).

Following GMI 12 Day 1 and Day 3 breakout discussions, key action items were set out as per below:

12th Global Microbial Identifier Meeting, Summary of Break-out Sessions, 14 June 2019
Work group 1: Political challenges, outreach and building a global network

1. Follow-up to the two Letters to countries – incl. G20 considerations
- promote GMI in other meetings, regional bodies, related initiatives i.e. one health, AMR (Everyone)
- identify and send letter to country focal points (Joergen Schlundt, Natasha Yang)
- sharing of relevant news/events between WG members (JS, Natasha)
- work with replied countries on action for global solution (JS)

2. GMI 13 (William Hsiao)
- discuss scope (pan-pathogens), correct nomenclature, update and revise previous work map
- less presentation talks, more WG discussions: promote collaboration between dev. and developing country participants
- keep track of developing country activities e.g. identify relevant "easy" journals for developing countries to publish in, count relevant publications, no. of machines available

3. Potential for a cost benefit analysis of WGS introduction from a global perspective
- engage with World Bank showing new vs old surveillance system (Eric Stevens, Luis Montesclaros)

4. Dev. Country capacity building
- provide a list of all diff training opportunities available for developing countries i.e. data analysis (Frank Aarestrup)
- consider regional centres for training e.g. universities/students (Adithya Acharya)

5. Data inclusion (suggest type of data for sharing, and top-down, bottom-up approach)
- linking data governance to novel and existing technical solutions (linking WG1 to WG2) (William Hsiao)

6. Contact to WHO/FAO/OIE about WGS and data-sharing action as relates to AMR (One Health) surveillance and solutions (GMI SC)

7. GMI federation
- Prepare one page document on concept of GMI federation scope where "small regional GMI's" can act on behalf of GMI (Mark Struelens, Mirko Rossi, Peter Gerner-Smidt)

8. List of good examples of what has already been down in countries in re to data sharing (Peter Ben Embarek)

9. Updates on ethical and legal guidance of data sharing (George Haringhuizen)

Work Group 2: Repository and storage of sequence and meta-data

Following the breakout discussions, WG2 prepared two summary slides with general and specific plans/recommendations as per below respectively:

Work group 2: Repository and storage of sequence and meta-data, 12 June 2019

Review the working group strategy to support emerging needs around data infrastructure

GMI community encouraged to come forward with further development needs

Understanding the rules of data ownership between jurisdictions
- GDPR - implications, how sequence data processing and sharing is impacted, i.e. sharing data/metadata globally
- Data de-identification (metagenomics – filtering human background, field describing if/what has been done)
- Classification of pathogens from metagenomes linked with clinical expertise

Methods for harmonizing metadata using ontologies, e.g. genomic epidemiology ontology
Breaking down certain metadata attributes, e.g. isolation_source
Tiered level of access to metadata (mark-up)
- Obfuscate contact info to avoid inadvertent info leaks

Service for serovar/serotype reanalysis of all Salmonella isolates

Issue of providing data/metadata:
- Are these based on the nature of the standards in place or due to general data sharing barriers that institutions face (mainly the latter)
- Can INSDC to work with journals to enforce domain specific minimum metadata standards

Methods for acknowledging and tracking contributions (like an impact factor, # sequences – get credit for generating and contributing seq data)
Methods for metadata curation in the INSDC:
- Crowd sourcing?
- Follow up when MDM info is missing prior to publication (difficult due to resources constraints)

Work group 2: Repository and storage of sequence and meta-data, 14 June 2019

Expanding WG2 focus to "Storage of sequence and metadata" (which will include repos, but also sharing between other partners)

Create an overview of what has been done, and how fulfills WG2 goals

System for documenting, updating and communicating so we don't have to start from scratch every meeting (people will know what the ongoing activities are)

Generate a list of general challenges with metadata and sequence storage
- Stoplight system → tagging what's been done

Core group who met throughout year (virtually) to increase accountability and continuity of activities
- Share slides, docs etc in a google folder → set up a virtual environment

Generate a list of resources, templates, ontologies, metadata standards

Create a community → Directory of who to contact for advice about topics within GMI group (names and fields of expertise)
- Message board for asking questions
  - Interpreting clinical meaning of data & metadata (e.g. SNPs and AMR)
  - prioritization of metagenomics hits, link to clinical

Evaluate what file formats are currently used, which file formats provide easier exchange

Work Group 3: Analytical approaches

Following Day 1 and 3 breakout discussions, WG3 has revised their sub-work groups to four subgroups, with the removal of "Expand benchmark datasets", "Metadata standards", and addition of WG3.4, "AMR and other resistance". The accomplishments and future plans of WG3 have been extracted from their summary slides as per below:

WG3.1 steering workgroup

WG3.1 has updated the GMI website under the WG3 tag with relevant information e.g. publications, useful for WG3 members. WG3.1 will continue to update the website.

WG 3.2 pipeline and metrics comparison

Accomplishments from last year:

- Standardized benchmarking workflow. Phylogenetic trees topologies comparison (Robinson-foulds, recall/precision) -> https://github.com/BU-ISCIII/openebench_gmi
- Integration with the Elixir OpenEbench platform. Should be ready in the next few weeks.

Goals 2019:

- Add vcf and distance matrix comparison to the standardized benchmarking workflow.
- Think about another benchmarking workflow like bacterial assembly, AMR, wgMLST, etc.
- Generate three simulated datasets from the same outbreak for validation.
- Add automated pipeline creation from bio.tools

WG 3.3. metagenomics

Accomplishments from 2018:

- Manuscript underway: Address data sharing and privacy issues for metagenomics datasets
- Manuscript underway: Environmental scan for wet- and dry-lab approaches for different application
- Manuscript published – overview of laboratory techniques for clinical foodborne samples
- Bait capture (e.g. CRISPR cas systems - FLASH), amplicon-bases systems, shotgun metagenomics, single cell sorting systems

Goals 2019:

- Publication list for current important metagenomics papers (wet and dry lab)
- Develop guidelines for building reference databases fit-for-purpose
- Research the possibility of creating a central database repository within an assigned DOI that can be referenced in publications
- Develop an SOP to perform validation of benchmark datasets
- identify minimum analytical metadata to include
- Join our GMI13 slack board and slack channel to get involved!!

WG3.4. AMR and other resistance

Goals 2019:

- Develop benchmark datasets for evaluating AMR bioinformatic pipelines (phenotype, MIC prediction, etc)
- Identify and/or develop training resources (webinars, documentation, etc.)
- Framework for collaboration (partner countries/groups with sequencing capacity with those with isolates).
- Develop guidance for MTAs and MOUs
- Reach out to WHO (Global Antimicrobial Surveillance System), encourage collection and sharing of WGS data in addition to phenotypic data
- Identify and communicate with laboratories and research groups peforming AMR and sequencing

Work Group 4: Ring trials and quality assurance

Ring trials for bacteria:

WG4 is in the last phase of finalizing the results of the food proficiency test (PT) based on a salmon matrix (led by University of Bologna and FLI), as well as the 2016-2017 bacterial PT (led by members from Technical University of Denmark) whereby participants of the latter will soon receive grading for the reliability of their submitted results. The 2020 PT involving target species *E. coli, Salmonella, Campylobacter*, will proceed shortly and invites will be sent to previous participants, with new members welcome to participate by emailing Frank Aarestrup fmaa@food.dtu.dk. For clarity's sake, an overview of the past and present PT's will be listed, with the status of each made known.

Ring trials for viruses:

Previous ring trial (dry lab) results have been published while results for the wet lab are insufficient to draw conclusions. A new scenario based PT called "Skin Panel" has been developed whereby participants will be provided with inactivated material and/or datasets. Interested parties are welcome to participate by contacting Andreas Nitsche, nitschea@rki.de.

Concluding Remarks

The increased number of participants, sponsorships and media coverage at GMI 12 suggests increasing level of interest and support towards GMI's goals. As raised in GMI 11, and echoed in GMI12, there is a need to re-examine the mission and vision of the consortium in line with the evolution of sequencing over the past 8 years. This, in addition to the preparation of GMI 13 AND GMI 14 set to be in Vancouver and Barcelona respectively, are currently under way.

Annexes

Annex 1. Presenter Biographies

Frank Moller Aarestrup of the Danish Technical University has a research focus primarily targeted the association between use of antimicrobial agents to farm animals and the emergence and spread of antimicrobial resistance including the human health consequences. Professor Aarestrup obtained his PhD in veterinary microbiology in 1995. Recently, he has been engaged in creating online tools for bioinformatics analysis of single bacteria, as well as meta-genomic data. His research has contributed to the international standards for detection and monitoring of antimicrobial resistance in foodborne pathogens and had major influence on the ways antimicrobial agents are used worldwide. The global focus is also documented by the fact that the research has been conducted with more than 400 co- authors, in more than 135 institutions in more than 35 countries. Aarestrup is appointed head of the WHO and EU reference laboratories for antimicrobial resistance in foodborne pathogens.

Clara Amid is the Content Coordination and Submissions lead of the European Nucleotide Archive (ENA) at EMBL-EBI. She has a background in Molecular Genetics and has worked in the bioinformatics service environment in Germany and UK, gaining extensive experience in data coordination projects. She leads, from the content side, the ENA's Data Coordination activities around Microbial Collaborations and has been a member in the COMPARE project, where she has been involved in sample metadata standards development, as well as 'Data Hub' set up for data sharing and coordination of data flow into these. She is also involved in other microbial projects such as GMI and ZIKAlliance, but also various environmental projects. Members of Dr. Amid's team lead the ENA Helpdesk and Training activities and are involved in designing curation workflows and the biological rule-base used for content validation.

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.

Nathan Bachmann has completed a PhD in microbial genomics and bioinformatics at the University of Queensland. He then worked as a post-doc at the University of the Sunshine Coast on culture-independent genome sequencing of *Chlamydia pecorum* from swab samples collected from koalas. Nathan relocated to Center for Infectious Diseases and Microbiology (CIDM) at the Westmead Hospital, Sydney, Australia as part of the Tuberculosis Centre for Research Excellence.

Timothy Barkham studied Medicine and Clinical Microbiology at St. Thomas' Hospital in London, UK. He moved to Tan Tock Seng Hospital, Singapore, in 1999. He also works at the National University of Singapore. He steered the diagnostic laboratory response and preparation for various outbreaks including SARS, Dengue, Chikungunya, Influenza, MERS CoV and Zika Viruses. He played a leading role investigating the foodborne GBS outbreak in Singapore in 2015, and showed it was due to ST283. He hypothesised that ST283 in humans and fish was a South-East Asian regional problem, and initiated and formed the One Health collaboration that found that ST283 has been causing human and animal disease across SE Asia for decades. He is exploring GBS ST283 transmission in SE Asia, and the possibility of foodborne transmission of other GBS sequence types in Singapore.

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).

Maria Borowiak is a molecular biologist at the German Federal Institute for Risk Assessment. She currently works in the department biological safety as a specialist for the characterization of foodborne pathogens using WGS methods. Here, she is responsible for development, implementation and validation of WGS protocols. She is involved in national working groups focusing on harmonization and standardization of WGS methods for the characterization of bacterial strains.

Heather Carleton received her Master's in Public Health in Infectious Diseases in 2002 from University of California Berkeley and her PhD degree in Microbial Pathogenesis in 2012 from Yale University. She started at the Centers for Disease Control and Prevention in Atlanta, GA in the Enteric Diseases Laboratory Branch in the PulseNet team in 2012 and is currently Lead of the Bioinformatics and Metagenomics Team (BIOME). Dr. Carleton and her team work on development and validation of whole genome multilocus sequence typing schemes for enteric bacteria, real-time outbreak analyses, and development of culture-independent subtyping techniques for enteric bacteria directly from specimens.

Luca Cocolin: full professor of food microbiology, Department of Agricultural, Forest and Food Sciences, University of Torino, Italy. He is the author of more than 320 publications that relate to the microbiology of food, most of them (ca. 230) in international.

Executive Board Member of the International Committee on Food Microbiology and Hygiene (ICFMH). Member of the Leadership Team of the European Technology Platform Food for Life. Scientific responsible for the University of Torino in the EIT Food.

Editor in Chief of International Journal of Food Microbiology.

Expert in: (i) Development, optimization and application of molecular methods for the detection, quantification and characterization of foodborne pathogens; (ii) Study of the microbial ecology of fermented foods (mainly sausage, cheese and wine) by using culture independent and dependent methods; (iii) Bioprotection: molecular characterization of bacteriocin production and its study in vitro and in situ; (iv) Study of the human microbiome.

Alessandra De Cesare is Contract Professor of Food Safety and Food Inspection at the Department of Agricultural and Food Sciences at the University of Bologna in Italy. She obtained her MD in Molecular Biology and the PhD in Food Science. She has been and is currently involved in many national and EU projects dealing with genotyping of foodborne pathogenic bacteria to trace them back from their sources up to foods and humans; metagenomic investigations of both the gut of farm animals and the environment where they live as well as the foods of animal origin to find a way to drive and support positive interaction between them promoting the replacement of antibiotics; the definition of food safety criteria for specific biological hazard/food combinations to possibly decrease pathogenic bacteria in foods of animal origin in the framework of the microbiological risk assessment.

Paola Flórez de Sessions holds a PhD from Duke University where she helped elucidate the mechanism of action of an oncolytic virus called PVS-RIPO, which targets glioblastomas. She did postdoctoral studies at the Novartis Institute for Tropical Diseases in Singapore, where she was exposed and extremely interested in the world of bioinformatics. She then led the Genome Institute of Singapore (GIS) Efficient Rapid Microbial Sequencing (GERMS) Platform at GIS. The GERMS team offered and end-to-end solution, from project design to sample handling, sequencing strategies, cutting-edge analysis pipelines and comprehensive interpretation. GERMS specialized in small genomes: viral, bacterial, parasites and fungal entities and their genomic peculiarities for both industrial purposes as well and public health genomics. Currently, she is the technical services manager for Oxford Nanopore Technologies (ONT) in the Singapore satellite office and the Asia Pacific region, where she helps enable others to implement ONT technologies in their own labs.

Matthew Ellington is a research active clinical scientist with broad experience in HCAI organisms. He has 15 years experience at the clinical / research interface in reference and frontline clinical laboratories with a specific and consistent focus on the molecular epidemiology of antimicrobial resistance among "ESKAPEE" pathogens. Dr Ellington's expertise in investigating the factors underpinning antimicrobial resistance and supports his involvement with the European Committee on Antimicrobial Susceptibilty Testing (EUCAST) subcomittee on WGS for AST, as well as his recent appointment to the British Society for Antimicrobial Chemotherapy (BSAC) standing committee on antimicrobial susceptibility testing.

Yasmina Jaufeerally Fakim;

BSc Biochemistry, UK; MSc Immunology UK; PhD Molecular Genetics: University of Mauritius
Position: Professor Biotechnology at the University of Mauritius
Area of expertise: Genomics and Bioinformatics;
Research interest: Microbial genomics, gene evolution, genome analysis.
Previous PI and current co-PI for H3ABioNet node, member of several H3ABioNet working groups

Maria Hoffmann is a Genomics Research Microbiologist in the Division of Microbiology in the Office of Regulatory Science, Center for Food Safety and Nutrition (CFSAN), Food and Drug Administration (FDA). She received her master degree in Food Chemistry from the University of Hamburg in 2007 and her Ph.D. in Microbial Evolution/Systematics/Population Genetics from the University of Hamburg in 2012. She has over 10 years of experience in the field of public health microbiology, foodborne infectious diseases and the evolution and genetics of human foodborne pathogens. Dr. Hoffmann serves as a subject matter expert on long read sequence technology to completely close bacterial genomes and their plasmids. In addition, since 2011 she has been working on next generation molecular genetic detection, identification, and traceback technologies to study and survey foodborne pathogens in produce. Her research goals are to improve the ability to predict and apply key phenotypic and genomic characteristics of recurring isolates from food industry and farms to ultimately assist in preventive controls.

Renaud Jonquieres is Senior Vice President for Merieux Nutrisciences, a world leader in Food safety and Quality services. Based in Singapore, he is part of the company executive committee and leads the Middle-East Africa Asia-Pacific region. Renaud holds a Master of Science in Food Science and Engineering from AgroParisTech France and a PhD in Fundamental Microbiology from Pasteur Institute and University Paris 7 France. Having held various management positions based in Europe, USA and Asia for R&D, Strategy, Sales & Marketing, Renaud comes with more than 20 years' experience in the fields of Biotechnology, Food Safety and In Vitro Diagnostics. Renaud has expertise in bringing bio-science innovations to the market place.

William (Bill) Klimke is the NCBI Pathogen Detection Team Leader at the National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health, and Department of Health and Human Services. William Klimke received his Ph.D from the University of Alberta in 2002, and has been at NCBI since that time. He has been involved with RefSeq microbial genomes, various annotation projects to improve functional annotation, and has helped to create the NCBI Protein Clusters database. Dr. Klimke's has received numerous awards for his work on the Pathogen Detection pipeline.

Natalie Knox is Head of the Computational Biology Unit within the Bioinformatics Section at the Public Health Agency of Canada's National Microbiology Laboratory in Winnipeg, Canada. Dr. Knox provides leadership and guidance on the development, application, and deployment of genomics and bioinformatics technology to modernize bacterial disease surveillance and outbreak response, and transmission analysis into frontline public health activities. Other areas of expertise include genomic epidemiology, pathogenomics, metagenomics, and clinical microbiology. She is involved in numerous research programs including the applicability of metagenomics as a culture-independent diagnostic test. Dr. Knox also contributes to the development of novel comparative bacterial genomic pipelines for outbreak investigations and leads several large-scale bacterial whole-genome and metagenomics sequencing projects.

Pimlapas Leekitcharoenphon (Shinny) is a researcher with expertise on whole genome sequencing (WGS) and epidemiology, evolution in bacterial genomes and population structure of foodborne pathogens such as *Salmonella*, *E.coli*, *Campylobacter* and *Listeria*. She has extensive experience in applying WGS in food safety and public health protection with the main focus on antimicrobial resistance. Some of her current projects include WGS analysis within the EU Reference Laboratory for AMR, the EU Horizon 2020 COMPARE project on source attribution using machine learning, and the Novo Nordisk Foundation project on AMR. In addition, she facilitated and conducted international bioinformatics training courses in WGS data analysis including online courses on WGS analysis and metagenomics in COURSERA.

Tapfumanei Mashe One Health Research Scientist,, Deputy National AMR Coordinator, Ministry of Health and Child Care, Zimbabwe.

Tapfumanei Mashe is a One Health Research Scientist who coordinates laboratory activities of the Advisory Group on Integrated Surveillance of Antimicrobial Resistance (AGISAR) and Global ESBL Tricycle projects in Zimbabwe which is funded by the World Health Organization. As a member of the Zimbabwe AMR R&D as well as Surveillance TWG he is involved in implementation of the Zimbabwe AMR NAP. He also has vast experience working with enteric pathogens. He has also spoken on AMR at numerous conferences including the Second Ministerial Conference on Antimicrobial Resistance, 12th Meeting on Global Microbial Identifier, 11th International Conference on Typhoid and other invasive Salmonelloses, the 59th Colloquium of the Institute of Tropical Medicine and 4th International Conference on Prevention and Infection Control.

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).

Kalliopi Rantsiou has a BSc in Biology, University of Athens, GR and a PhD in Food Science, University of California, Davis, USA. Dr Rantsiou was a research fellow at the Faculty of Agriculture, University of Udine, IT, and a scientific expert on microbial risks in food, Hellenic Food Authority, GR. She is now Associate Professor at the Department of Agricultural, Forest and Food Sciences, University of Turin, IT. Her research interests include molecular biology of foodborne pathogens and the use of culture independent methods to study the microbiota of foods. She is co-author of more than 80 papers, a member of the Editorial Board of the *International Journal of Food Microbiology* and Heliyon, Academic Editor of PLOS ONE*, co*-Editor of the *Italian Journal of Food Science* and *ad hoc* reviewer for major food microbiology scientific journals.

Bernhard Renard serves as director and professor and head of the bioinformatics unit at Robert Koch Institute, the German national public health institute. He is further professor at the department of mathematics and computer science at Freie University Berlin and faculty member at the International Max Planck Research School on Biology and Computing in Berlin, Germany. A

biostatistician and computer scientist by training, Bernhard earned a PhD in interdisciplinary informatics from University of Heidelberg. After being a long-term visitor at the Proteomics Center at Children's Hospital Boston/Harvard Medical School and the Seminar for Statistics at ETH Zurich and after being part of a team pioneering fully individualized cancer vaccines in industry, Bernhard joint Robert Koch Institute to develop and apply bioinformatics.

Mirko Rossi: Doctor in Veterinary Medicine with a PhD in Epidemiology and control of Zoonoses from University of Bologna, he received the title of Docent in Zoonotic Bacteriology from the University of Helsinki in 2015. From 2013 to 2018 he was appointed as associate professor at the University of Helsinki researching on genomic epidemiology of Campylobacter and other food-borne pathogens. Moreover, he was coordinator of the project INNUENDO co-founded by the European Food Safety Authority (EFSA). Currently he is scientific officer at EFSA, Unit Biological Hazards and Contaminants.

Robert Schlaberg, MD, Dr Med, MPH, is a medical director at ARUP Laboratories, an assistant professor of Pathology at the University of Utah, and a co-founder of IDbyDNA Inc. He completed his Clinical Pathology residency and Master of Public Health training at Columbia University, and a Medical Microbiology fellowship at ARUP Laboratories. His research is focused on next-generation sequencing-based infectious disease diagnostics and is supported in part by the Bill & Melinda Gates Foundation. He has co-developed Taxonomer, an ultrafast, user-friendly, web-based metagenomics data analysis tool, and a diagnostic version (TaxonomerDx) with the goal of facilitating adoption of metagenomic testing in routine diagnostic practice. He is board-certified in Clinical Pathology and Medical Microbiology by the American Board of Pathology. He is a member of the College of American Pathologists' Microbiology Resource Committee and Standard Committee.

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.

Anthony Smith: I am currently employed as a Principal Medical Scientist at the Centre for Enteric Diseases, National Institute for Communicable Diseases, Johannesburg, South Africa. I have a 29-year employment history with this institution. In May 1996, I obtained my PhD in molecular microbiology from the University of the Witwatersrand; I currently hold a joint appointment (Senior Research Officer) with this university through the Faculty of Health Sciences. I have a 'C2' rating with the National Research Foundation of South Africa; a rating category for established researchers with a sustained recent record of productivity in their field of study. I am the coordinator for PulseNet Africa and a member of the PulseNet International steering committee. My everyday activities include surveillance and epidemiology of enteric bacterial pathogens in South Africa and southern Africa. My list of published work can be found at the link:
https://www.ncbi.nlm.nih.gov/myncbi/browse/collection/48299923/?sort=date&direction=descending

Marc Struelens (MD, PhD, FSHEA, FESCMID) is Chief Microbiologist and Head of Microbiology Coordination Section at ECDC. He is also Professor of Medical Microbiology at Université Libre de Bruxelles, Belgium. After a research fellowship at the International Centre for Diarrhoeal Diseases Research, Bangladesh in 1981-84, Marc led an academic career in clinical microbiology and control of infectious diseases at Erasme University Hospital from 1985 to 2009. He is a former President of the European Society of Clinical Microbiology and Infectious Diseases. At ECDC, he is leading cross-disease integration of molecular and genomic methods into European surveillance and alert systems. His team is collaborating with National Microbiology Focal Points on shared commitment to EU common approaches in public health microbiology. They monitor convergence across EU towards implementing critical laboratory capabilities for epidemic preparedness and advanced surveillance of communicable diseases and antimicrobial resistance.

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.

Ruth Timme is a Research Microbiologist at the FDA's Office of Regulatory Science. She received her Ph.D. in 2006 in Plant Biology at The University of Texas at Austin. Her research background is focused mainly on utilizing comparative genomics and phylogenetics methods to answer evolutionary questions. At the FDA she coordinates the GenomeTrakr lab network and works to validate phylogenomic methods used for foodborne pathogen surveillance.

Rory Welsh is a microbiologist and molecular epidemiology fellow in the Mycotic Diseases Branch at the Centers for Disease Control and Prevention in Atlanta, Georgia. He and a team of researchers at the CDC have been combating the emerging multidrug-resistant pathogenic yeast *Candida auris*, and have been at the forefront of tracking *Candida auris* in the United States and abroad. He conceived, developed, and validated the discovery of a low cost and effective enrichment broth procedure for the isolation of *C. auris*, which has since become a key tool in controlling the spread

of *C. auris*. He obtained his undergraduate degree from University of Georgia in Microbiology and PhD in Microbiology from Oregon State University in 2015 where he studied the role of bacterial predators in host-associated microbiomes.

Jianguo Xu is the director of State Key Laboratory for Infectious Diseases Prevention and Control (China CDC); Chairman, division of Capacity building, State Key Project for Aids, Infectious Hepatitis and other major infectious disease, National Health and Family Planning Commission China; Member of consulting committee, Division of Medical Sciences, National Natural Science Foundation; Member, steering committee, China Association of Medicine. Member of Chinese Academy of Engineering. DR. Xu's team conducted the etiological investigations of outbreaks in China caused by Escherichia coli O157:H7 in 1999, by Streptococcus suis sequence type 7 2005, by Anaplasma phagocytophilum in 2006, by Neisseria meningitides sequence type 4821 complex in 2005. Recently, his team identified the emerging new serotype of Shigella flexneri Xv, the cytotoxic and aggregative Citrobacter freundiiin and Streptococcus lutetiensis as potential enteric pathogen. He found that some outbreaks occurred in China in last ten years could be prevented by changing the social and personal behaviour. His current research field is new pathogen discovery

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.

Annex 2. List of Participants

No.	Name	Organisation	Country
1	Abdul Ahad	National Institute of Health Islamabad Pakistan	Pakistan
2	Abiola Obisesan	Afe Babalola University Ado-Ekiti	Nigeria
3	Adithya Narayan Acharya	DY PATIL SCHOOL OF BIOTECHNOLOGY AND BIOINFORMATICS	India
4	Aditya Bandla	NUS	Singapore
5	Aditya Bandla	SCELSE	Singapore
6	Alessandra De Cesare	University of Bologna	Italy
7	Amaladoss Anburaj	Temasek Polytechnic	Singapore
8	Andrea Thürmer	Robert Koch-Institute	Germany
9	Andreas Nitsche	Robert Koch Institute	Germany
10	Ang Beng Seng	Skymech	Singapore
11	Ang Poh Nee	SCELSE	Singapore
12	Anirudh Agarwal	SCBE	Singapore
13	Anjali Bansal Gupta	SCELSE	Singapore
14	Anni Vainio	National Institute for Health and Welfare	Finland
15	Anthony Smith	National Institute for Communicable Diseases	South Africa
16	Armand Sanchez	Universitat Autònoma de Barcelona	Spain
17	Ashlyne Chen	Illumina SG	Singapore
18	Aung Kyaw Thu	Singapore Food Agency	Myanmar
19	Ayuba Sunday Buru	Kaduna State University, Kaduna, Nigeria	Nigeria
20	Balasubramanian Ganesan	Mars Inc.	USA
21	Bernhard Renard	Robert Koch Institute	Germany
22	BHARATULA LAKSHMI DEEPIKA	SCBE	Singapore
23	Bimal Kumar Dahal	Department of Food Technology and Quality Control, Kathmandu, Nepal	Nepal
24	Borowiak, Maria	German Federal Institute for Risk Assessment	Germany
25	CANDELIERE FRANCESCO	University of Modena and Reggio Emilia	Italy
26	Cara Lim	Illumina	Singapore
27	Carol Hull-Jackson		Barbados
28	Cassie Elizabeth Heinle	SCELSE	Singapore
29	Celine Nadon	Public Health Agency of Canada	Canada
30	Chalida Rangsiwutisak	King Mongkut's University of Technology Thonburi (KMUTT), Thailand	Thailand
31	Chanditha Hapuarachchi	National Environment Agency	Singapore
32	CHANGARAMVALLY MADATHUMMAL MUFEEDA	SBS	Singapore
33	Chen Gang	SPMS / CBC Div	Singapore
34	Chen Liwei	SCBE	Singapore
35	Chi Yeun Cheung		
36	Ching Biyun	National Parks Board	Singapore
37	Ching Ging Ng	DSO National Laboratories	Singapore
38	Chng You Rong	National Parks Board	Singapore
39	CHONG KIAN LONG KELVIN	IGS	Singapore
40	Chong Zhi Soon	SBS	Singapore
41	Chongtao Ge	Mars Global Food Safety Center	China
42	Chow Mei Lun	CEE	Singapore
43	Citra Prasetyawati	Freelancer	Indonesia
44	CK Ren		Singapore
45	Clara Amid	European Bioinformatics Institute (EMBL-EBI), Cambridge CB10 1SD	UK
46	Claudia Jaeckel	German Federal Institute for Risk Assessment	Germany
47	CORDEVANT, Chris	ANSES	France
48	Damian	Veredus Laboratories Pte Ltd	Singapore
49	Dariusz WASYL	National Veterinary Research Institute	Poland
50	Dave Ow	Bioprocessing Technology Institute A*STAR	Singapore
51	Dave Siak-Wei Ow	Bioprocessing Technology Institute, A*STAR	Singapore
52	David Phang	Veredus Labs	Singapore
53	Delphine Cao	Singapore General Hospital	Singapore
54	Dirk Höper	Friedrich-Loeffler-Institut	Germany
55	Don Lee	Thermo Fisher Scientific	Singapore
56	Duccio Cavalieri	University of Florence	
57	Dwi Wahyudha Wira	Universitas Padjadjaran	Indonesia
58	Edgar Schreiber	Thermo Fisher Scientific	Singapore
59	Efri Mardawati	Universitas Padjadjaran	Indonesia
60	Elizabeth Lim	DSO National Laboratories	Singapore
61	Emma Griffiths	University of British Columbia, Canada	Canada
62	Eric Stevens	US FDA	USA
63	ERNEST BONAH	FOOD AND DRUGS AUTHORITY	Ghana
64	Errol Strain	US FDA	USA
65	Fang You	National University of Singapore	Singapore
66	Faruk Dube	National Veterinary Institute, Sweden	Sweden
67	Frank M. Aarestrup	DTU National Food Institute	Denmark
68	GAN SEO HWEE LINDA		Singapore
69	Geoffry Smith	ILSI - International Life Sciences Institute	Singapore
70	Gregory Armstrong	US Centers for Disease Control and Prevention	USA
71	Gu Xiaoqiong	SMART postdoctoral associate	Singapore
72	GUO SIYAO	SCBE, NTU	Singapore

73	Hannah Phoon	National Public Health Laboratory, Ministry of Health Malaysia	Malaysia
74	He Yan	South China University of Technology	China
75	Heather Carleton	US Centers for Disease Control	USA
76	Hettiarachchige Ilmini Thejanee Perera	University of Colombo, Sri Lanka	Sri Lanka
77	Hu Chengcheng	SCBE, NTU	Singapore
78	Indira Basu	Auckland City Hospital, New Zealand	New Zealand
79	Isabel Cuesta	Institute of Health Carlos III (ISCIII)	Spain
80	Jacelyn Lau	QIAGEN	Singapore
81	James Pettengill	FDA/CFSAN	USA
82	Janine Michel	Robert Koch Institute	Germany
83	Jasmine ng	dso national laboratories	Singapore
84	Jean Teh Pui Yi	SCBE	Singapore
85	Jeffrey Koh	QIAGEN	Singapore
86	Jens Andre Hammerl	German Federal Institute for Risk Assessment	Germany
87	Jiang Changde, Donald	Singapore Food Agency	Singapore
88	Jianguo Xu	Chinese Center for Disease Control and Prevention	China
89	Jiraporn Jirakkakul	King Mongkut's University of Technology Thonburi, Thailand	Thailand
90	Jittisak Senachak	National Center for Genetic Engineering and Biotechnology	Thailand
91	Jocelyn Jin	NCID	Singapore
92	Jocelyn JIN	National Centre for Infectious Diseases	Singapore
93	Joergen Schlundt	SCBE	Singapore
94	Jolene Gien	Singapore General Hospital	Singapore
95	Jong Li Ching	Thermo Scientific Microbiology Pte Ltd	Singapore
96	Judith Wong	National Environment Agency	Singapore
97	Jyoti Acharya	Central Department of Microbiology	Nepal
98	Kadamb Patel	temasek polytechnic	Singapore
99	Kaitlyn Soh	Illumina	Singapore
100	Kalliopi Rantsiou	University of Turin, Italy	Italy
101	Kanthida Kusonmano	King Mongkut's University of Technology Thonburi	Thailand
102	Kelly Hoon	Illumina	Singapore
103	Kenneth Goh	Singapore General Hospital	Singapore
104	Khalid Abdallah Mohammed Enan	Department of Virology Central Laboratory- The Ministry of Higher Education and Scientific Research	Sudan
105	Kian Chew Lim	Illumina Inc	Singapore
106	Kiat	King Mongkut's University of Technology Thonburi (KMUTT), Thailand	Thailand
107	Kiattiyot Laeman	King Mongkut's University of Technology Thonburi (KMUTT), Thailand	Thailand
108	Kim Hie Lim	ASE	Singapore
109	Ko Kwan Ki Karrie	Singapore General Hospital	Singapore
110	Koh Susie	DSO National Laboratories	Singapore
111	Koh Yanqing	SCELSE	Singapore
112	Kritchai Pooncharoen	Phayao university, Thailand	Thailand
113	Krithika Arumugam	Nanyang Technological University	Singapore
114	Ku Chee Seng		Singapore
115	Kutmutia Shruti Ketan	SCELSE	Singapore
116	Lai Ghee Hwee	SCELSE	Singapore
117	Lakshmi Chandrasekaran	SCBE	Singapore
118	Lakshmi V Madabusi	Thermo Fisher Scientific	Singapore
119	Larissa Murr		Germany
120	Lawrence Goodridge	University of Guelph	Canada
121	Lee Katz	Centers for Disease Control and Prevention	USA
122	LEE LI XIAN MEGAN	LKCMedicine	Singapore
123	Lengsea Eng	Calmette Hospital	Cambodia
124	Leo Yi Ning, Justina	Singapore Food Agency	Singapore
125	Li Jia'En, Jasmine	Singapore Food Agency	Singapore
126	Liljana Petrovska-Holmes	Animal and Plant Health Agency, Weybridge, UK	UK
127	Lim Jiali	DSO National Laboratories	Singapore
128	Lim Jiali	DSO National Laboratories	Singapore
129	LIM JIN HENG	SPMS	Singapore
130	Lim Liting	NUS	Singapore
131	Liping Xie		China
132	LIU RAN	ILLUMINA China	China
133	Liu Xianghui	SCELSE	Singapore
134	LOH JIN PHANG JIMMY	DSO NATIONAL LABORATORIES	Singapore
135	Lourdes Simental	Inoquotech	Mexico
136	Luca Simone Cocolin	University of Torino-DISAFA	Italy
137	M V KRANTHI KUMAR	Bioserve-A ReproCELL group	India
138	Maddalena Rossi	Department of Life Sciences, University of Modana and Reggio Emilia	Italy
139	Mandar Godge	Temasek Polytechnic	Singapore
140	Marc Struelens	European Centre for Disease Prevention and Control (ECDC)	Belgium
141	Maria Hoffmann	FDA	USA
142	MARK CHAN BOON PHO	LKCMedicine	Singapore
143	Matiur Rahman	National food Safety Laboratory,Institute of Public Health	Bangladesh
144	Mazlina	Bti	Singapore
145	Melissa Meow	Temasek Polytechnic	Singapore
146	Michelle Ang	NPHL	Singapore
147	Mindia Adinda Sari	SCELSE NUS	Singapore

148	Mirko Rossi	European Food Safety Authority	Finland
149	MISTOU	ANSES	France
150	mjalrgrj	CDC	USA
151	Mohamed Ijas	Colombo Municipal Council (Veterinary Dept.)	Sri Lanka
152	Mohammad Ridhuan Mohd Ali	Institute for Medical Research (IMR), Malaysia	Malaysia
153	Monia BOUKTIF	Ntional Agency of Sanitary and Environmental Control of the PRoducts (Ministry of health)	Tunisia
154	Montesclaros, Jose Ma. Luis	NTS	Philippines
155	Montree Wutthi-in	Systems Biology and Bioinformatics (KMUTT)	Thailand
156	Mwesige Theophilus	Ministry of Agriculture, Animal Industry & Fisheries	Uganda
157	Nagmeldin Abdalla	Sudanese Standards and Metrology Organization	Sudan
158	Natalie Becker	Federal Office for Consumer Protection and Food Safety	Germany
159	Natalie Knox	Public Health Agency of Canada	Canada
160	Natasha Yang	Nanyang Technological University	Singapore
161	Nathan Bachmann	Centre for Infectious Diseases and Microbiology	Australia
162	Niranjan Nagarajan	Genome Institute Singapore	Singapore
163	Ng Lee Ching	National Environment Agency	Singapore
164	Ng Oon Tek	Tan Tock Sing Hospital	Singapore
165	Ng Sock Hoon	DSO National Lab	Singapore
166	Nguyen Anh Chien		Singapore
167	Noikaseumsy Sithivong	national Center for Laboratory and Epidemiology	Lao PDR
168	Noor Haza Fazlin Hashim	National Hydraulic Research Institute Malaysia (NAHRIM)	Malaysia
169	Nurdyana Abdul Rahman	Singapore General Hospital	Singapore
170	October Sessions	National University of Singapore	Singapore
171	Olayinka Osuolale	Elizade University	
172	Olga Francino	Universitat. Autonoma Barcelona	Spain
173	Omkar Kulkarni	SCELSE NUS	Singapore
174	ONG HONG MING GLENDON	SCBE	Singapore
175	Ong Kar Hui	Singapore Food Agency	Singapore
176	Ong Twee Hee, Rick	SSHSPH, NUS	Singapore
177	Padmini Ramachandran	Centers for Disease Control and Prevention	USA
178	Pan Chaozhi	CEE	Singapore
179	Pantakan Puengrang	King Mongkut's University of Technology Thonburi	Thailand
180	Paola de Sessions	Oxford Nanopore Technologies	Singapore
181	Pei Yun Hon	National Centre for Infectious Disease	Singapore
182	Peter Ben Embarek	World Health Organization	Switzerland
183	Peter Gerner-Smidt	US CDC	USA
184	Peter Preiser	Nanyang Technological University	Singapore
185	PICHAHPUK UTHAIPAISANWONG	King Mongkut's University of Technology Thonburi	Thailand
186	Piengchan Sonthayanon	Mahidol University	Thailand
187	Pimlapas Leekitcharoenphon	DTU	Denmark
188	Poh Leong Soon	CEE	Singapore
189	Pongpun Sawatwong	U.S. Centers for Disease Control and Prevention Southest Asia Regional Office	USA
190	Pramod Kumar	AIIMS, New Delhi	India
191	Prasobsook Paenkaew	King Mongkut's University of Technology Thonburi	Thailand
192	Prof. Dr. Farooq Ahmad Gujar	MAE, NTU, Singaore	Singapore
193	Prof. Dr. Sajjad Hussain	MAE, NTU, Singaore	Singapore
194	Ramona GUTIERREZ	National Centre for Infectious Diseases	Singapore
195	Rebecca Lindsey	CDC	USA
196	Rekha	ntuitive	Singapore
197	Remedios F. Micu *(absent)*	National Meat Inspection Service	Philippines
198	Renaud JONQUIERES	Merieux Nutrisciences	Singapore
199	Richard J Sugrue	SBS	Singapore
200	Rikky Wenang Purbojati	SCELSE	Singapore
201	Rivoal	Anses	France
202	Robert Schlaberg	University of Utah	USA
203	Rory Welsh	Mycotic Diseases Branch, U.S. Centers for Disease Control and Prevention	USA
204	RR		
205	Ruth E Timme	US Food and Drug Administration	USA
206	Santi maneewatcharangsri	Faculty of Tropical Medicine, Mahidol University	Thailand
207	Sara Monzon	Institute of Health Carlos 7777	Spain
208	Sathish Arivalan	National Environment Agency	Singapore
209	Saw Nay Min Min Thaw	SCELSE	Singapore
210	Seow Lee Ghee	SCBE	Singapore
211	Shabbir M Moochhala	MSE	Singapore
212	Sharmili d/o Kuppan	National Public Health Laboratory	Malaysia
213	Shruti Pavagadhi		
214	SINSINBAR GAURAV	MSE	Singapore
215	Songsak Wattanachaisaereekul	King Mongkut's University of Technology Thonburi	Thailand
216	Souvia Rahimah	Universitas Padjadjaran	Indonesia
217	SPENCE SAMUEL DAVID	ASE	UK
218	Sri Harminda Pahm Hartantyo	Singapore Food Agency	Singapore
219	Stephanie Defibaugh-Chavez	USDA-FSIS	USA
220	Stephan Schuster	Nanyang Technological University	Singapore

221	Sudarat Dulsawat	King Mongkut's University of Technology Thonburi	Thailand
222	surampudi venkata suresh kumar	Bioserve Biotechnologies private limited	India
223	Surya pavan Yenamandra	National Environmental Institute	India
224	Suthasinee Rattanachan	Systems Biology and Bioinformatics	Thailand
225	Swaine Chen	Genome Institute Singapore	Singapore
226	Tan Chuan Hao	MSE	Singapore
227	Tan Wei Ling	SFA	Singapore
228	TAN YI JING	TAN TOCK SENG HOSPITAL	Singapore
229	TANG PEI YI, PEGGY	SBS	Singapore
230	Taru Lienemann	National Food Authority	Finland
	Tapfumanei Mashe	National Microbiology Reference Laboratory	Zimbabwe
231	Terry Loo	Illumina Singapore Pte Ltd	Singapore
232	Thomas Neo	Illumina	Singapore
233	Tien Wei Ping	National Environment Agency	Singapore
234	Ting Peijun		Singapore
235	Timothy Barkham	National University of Singapore	Singapore
236	Trang Dahlen		USA
237	Tri Yuliana	Padjadjaran University, Bandung, Indonesia	Indonesia
238	Vanja Cnops	NTU	Singapore
239	Vernadette S. Sanidad	National Meat Inspection Service	Philippines
240	Vidya N Chamundeswari	NTU	Singapore
241	Wang Dongling	DSO National Laboratories	Singapore
242	Wang Hao	CEE	Singapore
243	Wang Lin	SPMS / PAP Div	Singapore
244	WEE SOON KEONG	LKCMedicine	Singapore
245	WEERARATHNA VIDANAGE POORNA	CEE	Singapore
246	William Hsiao	University of British Columbia	Canada
247	Xiaoyan Yin	Illumina	Singapore
248	Xu Yalei	SCBE	Singapore
249	Yam jing yu	Tan tock seng hospital	Singapore
250	Yap Peng Huat Eric	LKCMedicine	Singapore
251	Yasmina Fakim	University of Mauritius	Mauritius
252	YIMING LIANG		China
253	Yue Ying Tan	Illumina Singapore	Singapore
254	yunus effendi	Al Azhar Indonesia University	Indonesia
255	Zatil Afrah	Research Center for Chemistry - Indonesian Institute of Sciences	Indonesia
256	ZHANG YU		China
257	Zheng Jinxuan Amanda	Tan Tock Seng Hospital	Singapore
258	ZHONG YANG	SCBE	Singapore
259	Zwe Ye Htut	National University of Singapore	Singapore
260	Zuwei Qian	Pacific Biosciences Inc.	Singapore
261	Warren Bach	K.K. Oxford Nano Tech	Japan
262	Mari Miyamoto	K.K. Oxford Nano Tech	Japan
263	Wilawan Thongda	BIOTEC	Thailand

Annex 3. Second GMI letter

XXX
Minister of Health/Agriculture
Country

April 2019

Microbial DNA Sequencing – future international discussions

Dear Honourable Minister,

We are writing to you on behalf of the Global Microbial Identifier (GMI), an international consortium created and supported by more than 250 public health, food safety and infectious disease scientists, health policy specialists, epidemiologists, veterinarians, clinicians and microbiologists (http://www.globalmicrobialidentifier.org/).

We wrote to Your Ministry, as well as to national Ministries functioning in similar roles in 183 countries, in November 2017 about the revolutionizing new potential of Next Generation Sequencing (NGS) technologies, and our concerns as to whether the world will realize the full effects of this technology so that all countries may benefit. We submit that the global community should embrace these technical opportunities and consider building a global platform to exchange microbial genomic information. Such a global genomic data-sharing system at the disposal of the international community will provide to the "One Health" holistic approach an unparalleled tool to effectively increase the fight against human and animal infectious diseases. It will assist in the development of new therapies and vaccines, supporting biosafety and biosecurity. It will also play a pivotal role in addressing the major threat that the spread of antimicrobial resistance poses to human and animal health, a critical challenge identified in a Political Declaration of the High-Level Meeting of the General Assembly of the United Nations (2016) (A/RES/71/3). NGS technologies could also be used for source attribution of diseases, as well as an effective means for continuous measurement of the efficacy of public policies in combatting diseases, driving biosafety policies in a more efficient way.

Following our Letter of November 2017, we have received positive response from several countries in support of discussing a global WGS database system as an agenda item at the World Health Assembly (WHA). We have therefore chosen to continue the discussion with this 2nd letter to a number of countries (26 in all) from which we have indications of interest for this issue.

At the latest GMI11 Meeting in Geneva in May 2018, a suggestion was tabled to reach out to WHO Member States that have potential interest in this issue with a view of moving such discussions onto the agenda of the WHA. This could be done by initiating a draft WHA Resolution text, with the involvement of a group of positive countries. In Denmark, our contact point is Technical University of Denmark, National Food Institute.

We are therefore kindly requesting your country's support to include the creation of a global WGS database system and sharing of pathogen sequence data as an agenda item at the 73rd WHA to be held in May 2020.

WHA resolution texts are usually drafted by countries, sometimes in collaboration with the WHO Secretariat; it would be interesting to have an indication whether your country:

a) would be interested in and supportive to the initiative to draft a resolution text in this area
b) would be interested in participating in the drafting of such text and could provide names and functions of potential contributors
c) would be interested in supporting such text when drafted

The GMI community obviously has no place in WHA deliberations, and thus the movement of this issue would lie squarely with Member States. GMI is taking the initiative of these two letters in support of such action, realizing that real action and negotiation will have to be undertaken by interested countries.

Sincerely yours,

Joergen Schlundt, Ph.D., D.V.M
Head, GMI Steering Committee, on behalf of over 250 Scientists and Physicians of the Global Microbial Identifier,
www.globalmicrobialidentifier.org
Michael Fam Chair Professor, Nanyang Technological University, Singapore

Annex 4. Country responses to the second GMI letter

The second GMI letter was sent to Ministries of Health and Agriculture during the period of April 2019: Belgium, Botswana, China, Denmark, France, Germany, Greenland, Ireland, Italy, Israel, Ireland, Malaysia, the Netherlands, Singapore, South Africa, Spain, United Kingdom, USA, Canada, Mexico and New Zealand. While Denmark was unable to provide a response due to the upcoming elections, full letters of response were received from Canada, Mexico and New Zealand.

Hon Damien O'Connor

MP for West Coast-Tasman
Minister of Agriculture
Minister for Biosecurity
Minister for Food Safety
Minister for Rural Communities
Minister of State for Trade and Export Growth

MIN19-0327

10 MAY 2019

Natasha Yang
natashayang@ntu.edu.sg

Dear Natasha

Thank you for your correspondence of 9 April 2019 regarding future international discussions around Microbial DNA Sequencing.

I appreciate your desire for New Zealand to be able to benefit from DNA sequencing technologies, and the information that they generate. I agree that the global spread of antimicrobial resistance (AMR) is of significant concern and that the management and use of AMR related data, such as that generated by sequencing, has the potential to help inform this and other issues (e.g. foodborne illness).

While I understand the potential of a global database, I am also aware of the concerns raised with respect to use of metadata, confidentiality and privacy.

For further discussion on this matter, I suggest you communicate directly with MPI officials (science@mpi.govt.nz), and with Dr Brent Gilpen, a Science Leader at the Institute of Environmental Science and Research, who I understand is heavily involved in this area.

I have also asked MPI to forward your letter to relevant officials in the Ministry of Health and the Ministry of Business, Innovation, and Employment, to ensure they are aware of your consortium and intentions.

Yours sincerely

Hon Damien O'Connor
Minister for Food Safety, Biosecurity and Agriculture

+64 4 817 8715 Private Bag 18041, Parliament Buildings, Wellington 6160, New Zealand d.oconnor@ministers.govt.nz beehive.govt.nz

N° de Oficio B00. 820 /2019

Ciudad de México, a 03 MAY 2019

DR. JOERGEN SCHLUNDT
COMITÉ DIRECTIVO DEL GLOBAL MICROBIAL IDENTIFIER (GMI).
PRESENTE

El Servicio Nacional de Sanidad, Inocuidad y Calidad Agroalimentaria (SENASICA), agradece la invitación a participar en el consorcio del *Global Microbial Identifier*, toda vez que coincide plenamente con la visión de que la Secuenciación de Genoma Completo es una herramienta robusta y poderosa para la toma informada de decisiones en materia de inocuidad alimentaria, así como en todos los aspectos del enfoque "Una Salud".

En los últimos años el SENASICA ha implementado la Secuenciación de Genoma Completo (WGS, por sus siglas en inglés), como parte de la estrategia para la toma de decisiones con bases técnicas y científicas, en el marco del cumplimiento de la legislación en materia de inocuidad agroalimentaria. La información de dicha técnica, aunada a los análisis bioinformáticos asociados, ha permitido resolver controversias comerciales con países socios, refrendando nuestro carácter de institución encargada de vigilar la inocuidad de los alimentos. Asimismo, se ha sistematizado el uso de dichos recursos tecnológicos para la búsqueda de genes de resistencia a antimicrobianos en las secuencias de genoma completo de bacterias de interés agroalimentario. Con todos los datos de genomas completos generados a la fecha, el SENASICA está construyendo una base de datos que facilite el acceso a la información.

Por lo anterior, es para nosotros de gran interés el apoyar la iniciativa de desarrollo de una base de datos global de Secuenciación de Genoma Completo, que permita el intercambio oportuno de información y con ello la toma acertada de decisiones por las autoridades correspondientes.

AVM/MGZN/CFHP

Boulevard Adolfo Ruiz Cortines 5010, P-9, Col. Insurgentes Cuicuilco, CP. 04530, Coyoacán, CDMX
Tel. 01 (55) 5905.1000 Ext. 51005, 51100 gestion@senasica.gob.mx www.gob.mx/senasica

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Ciudad de México, a 03 MAY 2019

En ese sentido, el SENASICA desea manifestar su interés en apoyar la iniciativa para redactar un texto de resolución en esta área, en colaboración con la Secretaría de la Organización Mundial de la Salud y que a su vez este sea un punto a tratar en la agenda de la 73a Asamblea Mundial de Salud (WHA, por sus siglas en inglés) a celebrarse en mayo de 2020.

Le comento que fungirán como punto de contacto para dar atención a este tema, la Directora General de Inocuidad Agroalimentaria, Acuícola y Pesquera, QFB Amada Vélez Méndez a quien puede contactar en el correo electrónico amada.velez@senasica.gob.mx, y/o al teléfono +52 (55) 5905-1000 ext. 51502, así como la Directora del Centro Nacional de Referencia de Plaguicidas y Contaminantes, Mayrén Cristina Zamora Nava, correo electrónico mayren.zamora@senasica.gob.mx, teléfono +52 (55) 5905-1000 ext. 53035.

Esperando poder contribuir desde el área de nuestra competencia a la imperiosa tarea de compartir información en el ámbito global, quedamos atentos a su amable respuesta.

Sin más por el momento, reciba un cordial saludo.

ATENTAMENTE
EL DIRECTOR EN JEFE

SADER SENASICA
DIRECCIÓN EN JEFE
08 MAY 2019
DESPACHADO

DR. FRANCISCO JAVIER TRUJILLO ARRIAGA

C.c.p. DR. VÍCTOR MANUEL VILLALOBOS ARÁMBULA, SECRETARIO DE AGRICULTURA Y DESARROLLO RURAL.- Presente.
QFB AMADA VÉLEZ MÉNDEZ, DIRECTORA GENERAL DE INOCUIDAD AGROALIMENTARIA, ACUÍCOLA Y PESQUERA.- Presente.
QA MAYRÉN CRISTINA ZAMORA NAVA, DIRECTORA DEL CENTRO NACIONAL DE REFERENCIA DE PLAGUICIDAS Y CONTAMINANTES.- Presente.

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Boulevard Adolfo Ruiz Cortines 5010, P-9, Col. Insurgentes Cuicuilco, CP. 04530, Coyoacán, CDMX
Tel. 01 (55) 5905.1000 Ext. 51005, 51100 gestion@senasica.gob.mx www.gob.mx/senasica

Courtesy translation.

DR. JOERGEN SCHLUNDT
GLOBAL MICROBIAL IDENTIFIER
STEERING COMMITTEE.

The National Service of Health, Safety and Agri-Food Quality (SENASICA) of Mexico appreciates the invitation to be part of the Global Microbial Identifier Consortium as we fully agree with the point of view that Whole Genome Sequencing is a powerful and useful tool for the decision-making on food safety, as well as on all aspects of the "One Health" approach.

In recent years, SENASICA has implemented the Whole Genome Sequencing (WGS) as part of the making decisions strategy with technical and scientific bases in the framework of compliance with the legislation on food safety. The information of this technique, together with the associated bioinformatic analyzes, has allowed resolving commercial controversies with Mexican partner countries, endorsing our character of responsible for monitoring food safety. Likewise, the use of such technological resources for the search of antimicrobial resistance genes in the bacterial genomes of agri-food interest has been systematized. With all the data of whole genomes generated until now, SENASICA is building a database that facilitates information management.

Therefore, we have a great interest in support the initiative to develop a global database of whole genome sequences that allow the timely exchange of information and the concomitant correct decision-making by the corresponding authorities.

In this sense, SENASICA wishes to express interest in supporting the initiative to draft a resolution text in this area, in collaboration with the World Health Organization Secretariat and that this in turn it into a point to be discussed in the 73rd World Health Assembly agenda, to be held in May 2020. We hope to contribute from our competence area to the imperative task of sharing information in the global arena.

The staff that will act as contact to give attention to this theme are the General Director of Agrifood, Aquaculture and Fisheries Safety QFB Amada Vélez Méndez by e-mail amada.velez@senasica.gob.mx, and / or at the telephone number +52 (55) 5905-1000 ext. 51501, as well as the Director of the National Reference Center for Pesticides and Contaminants, QA Mayrén

Cristina Zamora Nava by e-mail mayren.zamora@senasica.gob.mx and / or at the telephone number +52 (55) 5905-1000 ext. 53035.

Hoping to contribute from the area of our competence to the imperative task of sharing information in the global field, we remain attentive to your kind response.

Kind regards.

Minister
of Agriculture and
Agri-Food

Ministre
de l'Agriculture et de
l'Agroalimentaire

Ottawa, Canada K1A 0C5

JUL 07 2019

Quote: 251370

Dr. Joergen Schlundt
Head
Global Microbial Steering Committee
c/o Dr. Natasha Yang
natashayang@ntu.edu.sg

Dear Dr. Schlundt:

Thank you for your letter regarding the potential for a whole genome sequencing (WGS) database sharing project to be included on the agenda of the 73rd World Health Assembly in May 2020.

Antimicrobial resistance (AMR) has been identified by the World Health Organization as one of the biggest threats to global health, food security, and development today. As a party to the Convention on Biological Diversity, Canada has endorsed a decision in the context of the 13th Conference of Parties of the Convention on Biological Diversity to avoid the overuse, and unnecessary routine use, of antibiotic and antimicrobial agents. Agriculture and Agri-Food Canada (AAFC) is conducting ongoing work on AMR by using a genomics-based approach to develop greater understanding of how food production contributes to the development of AMR and exploring strategies to reduce AMR in food production systems.

Canada is committed to promoting the One Health integrated approach to the management of ecosystems in order to minimize unnecessary disturbance to natural systems and avoid or mitigate the potential emergence of new pathogens and other contaminants. The Government has agreed that the One Health holistic approach combined with next generation sequencing will be instrumental to fight human, animal, and plant diseases.

The Canadian Food Inspection Agency (CFIA) is publishing food safety genomics data on publicly available platforms such as the National Centre for Biotechnology Information, in line with the open data/science initiatives like the Global Microbial Identifier. This was used in ad hoc instances and CFIA is now working on establishing a process to pursue this initiative on a routine basis and routinely shares information with the US Food and Drug Administration (FDA). Accordingly, AAFC supports the inclusion of global WGS database system on the agenda at the World Health Assembly to be held in May 2020.

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I trust that this information will be of assistance to you. Again, thank you for writing to me on this matter.

Sincerely,

The Honourable Marie-Claude Bibeau, PC, MP