Global Microbial Identifier

REPORT OF THE 8TH GMI MEETING, 11-13 MAY 2015

Meeting Report from the 8th GMI Meeting, 11-13th May 2015

Beijing, Peoples Republic of China

Welcome from the meeting hosts

Delegates were welcomed to Beijing on behalf of the local hosts and organizers by Jianguo Xu, China CDC and Junshi Chen, China CFSA.

Welcome from the GMI Steering Committee

Acknowledgement and appreciation to the hosts were given by the Chair of the GMI Steering Committee, Jorgen Schlundt, for accepting to host and fund this important GMI meeting, part of a series of such international meetings over the previous 4-year period.

Through initiative from the Chinese hosts, the GMI Steering Committee has accepted a new format for the GMI meeting, enabling a more general Day 1, focusing on sharing of experience as well as building local capacity to enable a broader understanding of the new potential of NGS developments. This to be followed by the traditional 2-day GMI meeting focused on activities in the five working Groups. This new format seemed to work very well in Beijing and enabled information exchange to a broad audience, resulting in a total participation (Day 1) of more than 400 scientists, regulators and industry representatives. This new format will thusbe repeated at GMI9 in Rome 2016.

Keynote address

Building a Global Genomic Network for Pathogen Trace back and Outbreak Detection in Food Safety

Steve Musser, Food and Drug Administration, USA

Next-generation whole-genome sequencing (WGS) is now widely used as a high-resolution molecular epidemiologic tool for assisting in the investigation of foodborne outbreak events and for the tracking of complicated and genetically homogenous bacterial strains. To further enhance the unique capabilities of WGS, the GenomeTrakr network was established as a means of linking a distributed network of laboratories utilizing whole genome sequencing for pathogen identification and outbreak investigations. The network consists of public health, government and university laboratories throughout the world that collect and share genomic data from foodborne pathogens. The data, which are housed in public databases at the National Center for Biotechnology Information (NCBI), can be accessed by researchers and public health officials for real time comparison and analysis that promises to speed foodborne illness outbreak investigations and reduce foodborne illnesses and deaths**.** Over the last two years, the network has contributed more than 20,000 pathogen genomes to the public database at NCBI, and this number is expected to grow to more than 40,000 by the end of 2015. The Genometrakr databases are now routinely used to supplement and focus the investigation of foodborne outbreaks.

http://www.fda.gov/Food/FoodScienceResearch/WholeGenomeSequencingProgramWGS/ucm363134.htm

Day 1: Development and Use of Next Generation Sequencing in Food Safety and Disease Surveillance

Sharing of experience from China, USA, Canada, EU, Denmark and Germany

Marking a new departure in GMI meetings, GMI8 was initiated with a one-day information sharing meeting, enabling local and international participants to get an overview of the recent developments in the use of next generation sequencing in disease surveillance and food safety, as well as in research in general.

The program is included in this report at page 10.

Day 2-3 Working Group Progress

WG 1: Political challenges, outreach and building a global network.

Rapporteurs: Jorgen Schlundt and Stephanie Defibaugh-Chávez

Working Group 1 is developing a long-term plan to shape political level involvement in GMI discussions at the global, regional and national level.

General achievements since GMI7:

The website and newsletter systems are functioning, the Steering Committee is active and functioning and participation now covers most continents. The GMI Charter has been developed and adopted There seems to be a global interest in international GMI meetings. Contact to the Global Alliance for Genomics and Health has been established. Meeting venues for the upcoming two global meetings have been proposed: GMI9 accepted in principle by the Steering Committee (May 2016, Rome), GMI10 could be in Mexico (May 2017).

Ongoing activities:

- Engaging FAO/WHO/OIE,
- Increasing involvement of developing countries,
- Engaging industry,
- Outreach and Promotion. Three papers in draft: 'Open data sharing' (Haringhuizen et al paper), 'Legal entity' (Schlundt et al paper), 'Landscape analysis' (excerpts from Gates paper).
- Considerations of Funding potential.

Suggestions for focus:

WG1 has been lagging behind the stipulated workplan most of the last period. WG1 needs to focus on finalizing the seminal 3 papers (mentioned above) for further potential discussion at GMI9, and for potential inclusion in the FAO/WHO process. WG1 should support FAO/WHO fund-raising for NGS expert meetings. WG1 should take advantage of a potential link to WP12 in the new EU COMPARE projects, focusing on NGS constraints.

It is anticipated that FAO/WHO (in potential collaboration with OIE) will be developing further the planning of (a series of) Expert Meetings on NGS. It is important for Member States to initiate discussions in the inter-governmental bodies, for OIE it seems likely that a resolution, including mentioning of NGS is to be adopted in 2015. These discussions should be broad in scope, and should include issues related to standard setting in the area, potentially building on the existing framework for GMI standards. The work in FAO/WHO needs a formal basis in some sort of official request for discussion coming from one or several Member States. This

approach could be based in the Expert Meeting process, or could be initiated in parallel. A process to reach out to selected Member States with a view of initiating work towards achieving a final WHO Resolution could be initiated by WG1.

Consideration should be given to link NGS issues to a One Health focus and to ongoing AMR action, and in this process it is important to involve both Health and Agriculture constituents. Likewise, a potential initiation process through the Codex Alimentarius Commission could be considered.

It was suggested to develop two documents: a) A potential 'strawman' resolution text (see Appendix 1), and b) A short technical paper, with a simple cross-sector scope, potentially lifting topics from the landscape document and targeted Reg. Agencies, Academia, Industry, Health sector and Labs.

Several upcoming meetings, where GMI would be part of the discussions were mentioned:

- IAFP (Int. Ass. For Food Protection), Des Moines, USA, Aug 2015 will include a debate section on 'Is Shoe Leather Epidemiology Dead in the Age of Whole Genome Sequencing?' (sic!) as well as several sessions on NGS and Whole Genome sequencing with significant participation of GMI Members.
- The first ASM (American Society for Microbiology) Conference on Next Gen Sequencing, Washington DC, USA, September 2015, will include presentation of GMI, and GMI Members are significantly involved in the Planning Committee.
- Global Food Safety and Technology Forum (Hong Kong, SAR China, Feb 2016) will have plenary presentation of NGS/GMI and has participation of GMI Members in the planning committee.
- GFSI (Global Food Safety Initiative) Global Conference, Berlin, Germany, March 2016 will include a section on 'Big Data' including consideration of NGS developments –GMI Members participate in the planning committee.

It was suggested to investigate potential outreach to relevant major Industries: Unilever, Nestle, Pepsico, S-Safe (Food Industries umbrella organization), as well as potential Feed Industry companies.

Steering Committee Members need to provide more strategic input, further discuss the value of bringing in other sectors, including epidemiology-focused researchers (human and veterinary). It was suggested to actively seek participation of funding focused members in the Steering Committee. Funding potential to be sought from: Gates, Rockefeller, COMPARE (?), National Agencies or Institutions.

It was suggested to initiate the preparation of an 'Open data-sharing' paper which would cover a selection of the most important/contentious issues to be discussed in relevant detail, and include a description of the infrastructure problems in building open-source systems with data-confidentiality capacity. The paper would benefit from input from developing countries presently using NGS.

WG2: Repository and storage of sequence and metadata

Rapporteur: Bill Klimke

Working Group 2 strives towards developing a format to capture ”Minimum Data for Matching (MDM)”, consisting of reads and minimum metadata.

The MDM should be deposited and made globally and universally accessible as soon as available. The MDM may or may not be accompanied by assemblies and/or annotation and/or additional metadata. If not provided with initial submission, these may be added later by the submitter, or by some agreed upon third party. Ideally, any MDM provided for purposes of searching the GMI databases should immediately also become a deposit available for searching by later submitters.

Any matches from the MDM search should be reported to the searcher and to the relevant GMI Participants. The data layer is provided by The International Nucleotide Sequence Database Collaboration INSDC and is therefore both international and public.

May 1st, 2015 Update:
There are 17 Bioprojects labeled with the GMI keyword including many that are from active collaborations of NCBI with federal, national, and state public health agencies. These projects connect to 36 924 samples, 17 480 of which are for clinical/host-associated isolates, and 18 872 are food/environmental/other samples isolates. These submissions are integrated via the NCBI Pathogen Detection system and analysis reports are made daily when new data are submitted. Major contributors include CDC, FDA, USDA-FSIS, and state public health laboratories in the US. International collaborators include Public Health England which has submitted thousands of samples and the first successful deposition of data from Argentina as part of the GenomeTrakr network occurred in April, 2015. The total number of samples submitted to NCBI using the GMI minimal metadata template is 60 845 samples (including those from active collaborations described above) and those submitted to ENA are 101 samples. Both NCBI and ENA have put together webpages describing how to submit GMI data and are working on harmonizing the metadata templates for data exchange.

WGS objectives were reviewed at GMI8:

1. Completed objectives:

    a. Creation of a mailing list of GMI users (potential and currant)
    b. Inform GMI submitters of how to submit data at EBI and NCBI, and help them through technical hurdle.

The email list was created and the first item included instructions on how to submit data:

WG2: Repository and storage of sequence and metadata

Pathogen genome-scale sequence data submissions
If you wish to contact NCBI or ENA directly about submissions:

NCBI:
pd-help@ncbi.nlm.nih.gov

ENA:
datasubs@ebi.ac.uk.

NCBI Submissions
Information on how to submit

http://www.ncbi.nlm.nih.gov/projects/pathogens/submit

The submission page:
http://submit.ncbi.nlm.nih.gov
The Pathogen system at NCBI requires three basic elements:

- *At least one BioProject that describes the project or initiative (the BioProject only needs to be created once).*
- *For each pathogen sequenced, submission of a Biosample record that lists the isolate metadata – submission is via a downloadable template – (Pathogen affecting public health) that is used to describe the sample including differentiation of isolates from clinical vs. environmental/food/other sources as well as information on when and where the isolate was obtained. The template definitions can be viewed here: https://submit.ncbi.nlm.nih.gov/biosample/template/?package=Pathogen.combined.1.0&action=definition*
- *For each pathogen, submission of the raw sequence data to SRA.*

For information on submitting assembled genomes or antimicrobial susceptibility information, please see the submission instructions linked above.

ENA Submissions
http://www.ebi.ac.uk/ena/submit/pathogen-surveillance

This page provides instructions for submitters of genome-scale pathogen sequence data to the European Nucleotide Archive (ENA). It includes a minimal checklist of sample metadata information to be reported associated with sequence data generated in high-throughput genome-scale pathogen surveys or research studies in clinical, organismal and environmental samples. On this page submitters will find links to instructions for different categories of submission, as follows:

- Project registration
- Submission of reads and samples
- Genome assembly submissions of clinical, organismal and environmental samples

Both interactive and programmatic tools (Webin) are available to aid in the submission of data to ENA.

2. In-progress objectives:

c. Poll the mailing list on where they are having difficulties in submission, either technically, or socially/politically. GMI would like to know what are the objections to the GMI concept as a core model?

There is a survey for attendees to fill out and the results will be compiled at a future date:

A brief survey to gather feedback from potential submitters on the legal, technical, or political hurdles to the release of data to the public archives.
https://www.surveymonkey.com/s/LPYL2MS

d. Find out from the GMI community what data errors are impacting their analyses and educate said community on how they can help the archives to clean up the errors
e. Continue to improve submissions and make it easier to do so. Inform the group established in point one when new submission capabilities become available. This point is currently ongoing.
f. EBI/NCBI will work out the translations of metadata fields between the two systems and report back to the community. Publish paper on the standard. How to use it and

what it can do (EBI/NCBI). On the GMI site describe the standard, and point to the archive descriptions and implementations (with version – at NCBI/EBI)
g. Put together a publication on the standard, how to use it, and what it can do.
h. Educate the community on how to access the submitted data (search, retrieval, find samples and sequences collected in 2014, for example). Inform them that some data is protected/not submitted and end users will likely need to contact the submitter in order to access the protected data.
i. Determine who is willing to contribute under the GMI concept and label their data with the GMI keyword (current contributors can be found at: https://www.ncbi.nlm.nih.gov/bioproject/?term=GMI[keyword])
j. Contact these subgroups and determine what optional fields they feel are useful to add to the template in order to fill out the spec for a proposal to GSC (ex: ST = sequence type)
k. Contact these submitters to get feedback on what reporting information they would like to receive – ex: programmatic way to retrieve the analysis results without having to go to the website/ftp and download them (GMI Reporting Std.)

3. Objectives not started:

l. API to retrieve compliant data.

4. New objectives:

m. Encourage or educate other microbial communities to submit data in order to address the issue that GMI is not strictly related to bacterial pathogens for food safety
n. NCBI already has capability to accept antimicrobial susceptibility phenotypic testing data, work with ENA to do the same

NCBI has an addition to the pathogen template to capture phenotypic date:
http://www.ncbi.nlm.nih.gov/biosample/docs/antibiogram/
Biosamples that have been submitted with antimicrobial susceptibility data can be retrieved via this search filter:
http://www.ncbi.nlm.nih.gov/biosample/?term=antibiogram%5bfilter%5d

WG3: Analytical approaches

Rapporteur: Ruth Timme and *Piotr Wojtek Dabrowski,*

Sub-WG3 topics

1. Wiki creation – seeded with survey results
2. Pipeline comparison needs
3. Benchmark datasets

WG3.1

Reach out to SeqAnswers – 2mos. Wojtek, dabrowskiw@rki.de
Sub-pages

1. Populate with results of survey
2. benchmark datasets (each with a subpage summary)
3. metric summary for each type of tool, Wojtek, dabrowskiw@rki.de

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WG3.2 Pipeline comparison (suggested result formats, etc)

SUMMARY: There are important analysis steps performed either by single tools or as steps by larger pipelines. The most important of these steps have been written down. Then, PoCs for each of these steps were defined. These PoCs will define metrics that could be used to objectively describe the quality of the results of their respective tools/pipeline steps. Within 2-3 months after GMI 8, the PoCs will reconvene to discuss the defined metrics. Then, they will have another 4-5 months to calculate these metrics for several tools (with a priority on the tools mentioned in the survey). At the end of this period, they will again reconvene to discuss the results and potentially necessary changes to the metrics. In the last months leading up to GMI9, metrics will be calculated for further tools or previously calculated metrics will be recalculated using the updated definitions. By GMI9, the calculated metrics should be introduced into the tool's respective pages on the wiki (seqanswers.com?).
In parallel, the authors of tools which perform especially poorly on the defined metrics will be contacted in order to potentially redefine these metrics or at least give the authors a chance to update their tools.
Finally, a publication will be drafted including the defined metrics and the results obtained from benchmarking tools using the datasets provided by WG 3.1. This publication can – once finalized and submitted – used to convince tool authors to keep the results of their benchmarks up to date on their respective seqanswers wiki pages whenever they release new versions to take maintenance load off GMI.

1. Defined tool types:
    a. Mapping: Wojtek, dabrowskiw@rki.de
        i. Identification of correct reference from raw data, Martin, mcft@cbs.dtu.dk
    b. SNP calling, Ruiting, r.lan@unsw.edu.au and Sophie, s.octavia@unsw.edu.au
    c. Tree calculation, Johan, johan_goris@applied-maths.com
        i. Clone/outbreak identification, Johan, johan_goris@applies-maths.com
    d. Assembly, Ruiting, r.lan@unsw.edu.au and Sophie, s.octavia@unsw.edu.au
    e. Annotation
        i. MLST/Resistance genes/Virulence genes, Shinny, pile@food.dtu.uk, Junning, junning_wang@zetabio.com, Eija, eih9@cdc.gov
        ii. Functional annotation/Gene annotation, Wojtek, dabrowskiw@rki.de
        iii. Core genome, Eija, eih9@cdc.gov
2. Action plan:
    a. Literature research/Metrics definition by defined PoCs
        i. Reconvene in 2-3 months to discuss results
    b. Testing of first tools (most-used tools from survey) tools/calculation of agreed-upon metrics by PoCs

        i. Reconvene in another 4-5 months to discuss results/necessary modifications of metrics
    c. If necessary retesting of tools with updated metrics by PoCs, upload of results to Wiki
        i. Done by GMI 9
    d. Contact authors of "bad" tools & prepare manuscript about datasets and benchmark metrics/results
        i. To be started by GMI 9

WG3.3 - Benchmark datasets

SUMMARY: WG3 has identified the need for well-curated public benchmark datasets for validating various phylogenomic pipelines. A diverse set of datasets would cover taxonomic breadth, outbreak type, and more targeted testing, like re-sequencing studies and experimental evolution. We also see a need for simulated datasets where the true tree and location of variable sites are known. These datasets can be provided via a standard table on the wiki site containing the public accession numbers (metadata and sequence data), epi data, and any other relevant data for the dataset. WG3 thinks that making these datasets available is a reasonable goal for GMI9.

a. Re-Sequencing
    i. Montevideo re-seq dataset (ruth.timme@fda.hhs.gov) – 2 months
    ii. Staph re-sequencing (lund@cbs.dtu.dk) – 4 months
    iii. S. Typhimurium re-sequencing (lund@cbs.dtu.dk) – 4 months
b. Multiple outbreaks
    i. Leekitcharoenphon et al. Se. enterica (lund@cbs.dtu.dk)
c. Taxonomic diversity
    i. Sal. Bareilly (FDA) – ruth.timme@fda.hhs.gov, 2 month
    ii. L. mono (FDA/CDC) – ruth.timme@fda.hhs.gov/Eija 2 month
    iii. STEC (CDC) – ruth.timme@fda.hhs.gov / Eija? – 2 months
    iv. EHEC (German E.coli outbreak) – (rkmo@food.dtu.dk), 2 months
d. Known phylogeny:
    i. Experimental evolution E.coli dataset. Not public yet. Will test tree-reconstruction. (lund@cbs.dtu.dk)
    ii. Simulated datasets (TreeToReads) (ruth.timme@fda.hhs.gov) – GMI9
e. Table describing each dataset – ruth.timme@fda.hhs.gov – 2 months
    i. Taxon ID
    ii. SRA accession
    iii. BioSample ID (or equiv)
    iv. Epi data
        1. 0: non outbreak
        2. 1 – n, OB
    v. Data quality
    vi. Publication
    vii. Link to summary info

GMI8 - WG3 email list

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YABI – webservice – Australian pipeline.

WG4: Ring trials and quality assurance

Rapporteur: Rene Hendriksen

WG4 made progress on many fronts at GMI8– in particular the details behind the full rollout of the Bacterial PT and the initiation of a Virus PT. Below is a summary of what was discussed and decided:

Participation in the full rollout of the PT:

- We only have enough material for 100 participants
- If < 100 register we will accept all registrants but if not we will hold a phone call to determine how best to select participants. If > 100 register – phone call to determine who will participate
- Weekly updates will be issued of the number of registrants to determine what steps need to be taken, if any, to increase the number of registrations within the 30 day window that registration is open.

Workload for full rollout:

- FDA/PHE will handle the dry lab analyses
- DTU will handle the wet lab analyses
- Applied Maths (Katleen Vranckx) will handle wgMLST for S. aureus
- Forum will be managed by Isabella and Jorge

Discussion of new isolates that will be part of subsequent PTs:

- 6 new isolates and fastq datasets will be sent out each rollout – ideally each year
- Determine list/priority isolates in future phone call

Virus PT:

- Building on the momentum from GMI7and experience of the bacterial PT a pilot virus PT will launch by end of year (2015), Andreas Nitsche (Robert Koch Institute, Germany) will take the lead on this subgroup
- 4 in silico datasets already created – clinical/plant/strawberry/simulated
- Will also include a 'purified' RNA virus to test ability to isolate/sequence DNA
- Determined results to be reported by participants

The future/potential new directions

- Benchmarking dataset to evaluate analyses pipelines. We will likely have a short joint meeting with WG3 to determine how best to proceed with the analysis of fastq datasets/pipeline evaluation.
- The question of whether to provide a more epi/outbreak like scenario for the dry lab was raised – also to be discussed with WG3
- Other organisms (e.g., – parasites, fungi, etc) that might be of interest to conduct a PT with were also discussed
- We will evaluate the communication stream within the working group to ensure all members are aware and involved if s/he would like to be so.

WG5: Pilot Projects

PPWG did not meet at GMI-8, and a motion was made to retire the group in favor of a new effort to focus on communication and outreach. An authoritative decision regarding the group's future direction could be handled by GMI's steering committee. PPWG was created during discussions at the GMI-5 meeting in Copenhagen, 27-28 Feb 2013, with immediate goals to establish a governance structure, define how the PPWG will communicate internally and with other GMI WGs, to define the purpose and nature of a pilot project within the context of GMI, and to proffer ideas for suitable pilot projects. The PPWG discussed projects with partners in developing countries and a project focusing on data analysis of a common dataset. They also identified existing or planned pilot projects including a whole genome sequence (WGS) based real time prospective surveillance project for *Listeria monocytogenes* (*Lm*) in case-patients and food/environmental samples, and a multistate S*almonella* mock exercise, both in the USA. PPWG discussions were extended at the GMI-6 meeting, in Davis, California, 9-10 September 2013, where a multinational effort to develop a whole genome MLST scheme was identified as a suitable project.

A number of activities were spawned or inspired by the PPWG. Three international projects were initiated to solicit participation by less-developed countries. Danish Technical University initiated a project with a research institute in Tanzania to share next generation sequencing (NGS) equipment and expertise to spur technical development in that country. FDA-CFSAN initiated a project in collaboration with Pan American Health Organization, and the Infectious Disease Institute – ANLIS "Dr. Carlos G. Malbran" a component institution of the Argentine public health infrastructure. The Malbran Institute is an important leader in the region, partnering with the World Health Organization and PulseNet to coordinate international projects, and also collaborates with the Wellcome Trust to develop training sessions on Genomics and Epidemiological Surveillance of Bacterial Pathogens (the next session is planned for 17-22 April 2016 in Buenos Aires). The FDA-Malbran project began in 2013 and has included transfer of an Illumina Miseq and ancillary equipment to the Malbran Institute laboratory in Buenos Aires in November 2014, two training sessions in the USA and Argentina to transfer FDA methods and experience in December 2014 and April 2015, and the electronic transfer of draft quality WGS data from Verotoxin E. coli and Salmonella of South American origin to the public International Nucleotide Sequence Database Collaboration (INSDC) sequence database (BioProjects PRJNA282762 and PRJNA271293). Data from the collaboration were presented at an International meeting on Shiga toxin *E. coli* in September 2015. FDA is also collaborating with the International Congress on Pathogens at the Human-Animal Interface (ICOPHAI) to provide over 1000 draft quality WGS Salmonella sequences from veterinary sources collected in Africa, Asia, South and North America to the public INSDC database (BioProject PRJNA275961).

Pilot projects to evaluate the utility of WGS have been developed in the USA, England, Denmark, and Canada, although not necessarily as a GMI project. A GMI-initiated international pilot project to develop a whole genome MLST scheme for the foodborne pathogen Listeria monocytogenes (Lm) is nearing completion. At the GMI-7 meeting 11-12 September 2014 in York, a team led by the Pasteur Institute reported on a scheme containing 1748 genes present in ~98% of Lm strains, and a common nomenclature is under discussion.

Overall, a number of pilot projects involving NGS technology, some of which have been influenced by the GMI's PPWG, have been initiated around the globe.

Acknowledgements

The 8th GMI meeting was organized by many staff, with particular thanks owed to; China CDC:

The meeting report was compiled by Jørgen Schlundt on behalf of the GMI Steering committee.

Appendix 1

Potential text for Potential draft WHO Resolution re. NGS capacity and global development

New global microbiological identification and surveillance capacities

Having considered relevant reports; ….

Recognizing WHO's role in the identification, surveillance and control of human pathogens;

Recalling resolutions……;

Recognizing that delayed diagnosis and lack of current data often hampers treatment and control of infectious and foodborne diseases, especially but not only in developing countries;

Aware that identification and diagnosis of a wide range of infectious and foodborne bacteria, viruses and parasites often require methods tailored to the specific analysis;

Noting that the recent advances in genomic sequencing technologies have drastically reduced the cost associated with use of these methods for identification and diagnostic purposes, and that these technologies offer a faster, standardized method for identification of all bacteria, virus and parasites;

Emphasizing the fact that the rapidly developing capacity in all parts of the world of exchange of large bodies of data via broad-band internet enables real-time sharing of microbiological and epidemiological data across borders;

1. URGES Member States:[1]
    (1) to collaborate with the Secretariat in developing and implementing a draft global action plan to increase political awareness, engagement and leadership in order to promote adoption of whole genome sequencing as a standardized laboratory method for identification and global surveillance of bacterial and viral organisms;
    (2) to mobilize human and financial resources in order to implement plans and strategies to implement a global data sharing platform of whole genome sequences;
    (3) to develop a plan for adoption of sequencing technologies on a global scale and ensure access to all relevant sectors, in particular health and agriculture, including animal husbandry, and to promote sharing of such information so that national, regional and global entities can access it from a global data sharing platform;
    (4) to leverage technical resources available in member states that have already adopted these methodologies to develop a standardized work-flow for diagnostic and surveillance of infectious and foodborne diseases

2. REQUESTS the Director-General:
    (1) to ensure that all relevant parts of the Organization, at headquarters, regional and country levels, are actively engaged and coordinated in promoting adoption of genomic sequencing technologies for diagnostic and surveillance of

[1] And, where appropriate, regional economic integration organizations.

infectious and foodborne diseases and implementation of a global data sharing platform for this sequence data;

(2) to set aside adequate resources for the work in the Secretariat, in line with the Twelfth General Programme of Work, 2014–2019;

(3) to strengthen the tripartite collaboration between FAO, OIE and WHO for development of this global genomic data sharing initiative in the spirit of the "One Health" approach;

(4) to explore with the United Nations Secretary-General options for a high-level initiative, including a high-level meeting, to increase political awareness, engagement and leadership on genomic sequencing for global diagnostic and surveillance purposes;

(5) to develop a draft global action plan to promote adoption of whole genome sequencing as a standardized laboratory method for identification and global surveillance of bacterial and viral organisms, and which addresses the need to ensure that all countries, especially low- and middle-income countries, have the capacity to implement such a system, and to ask member states to:

   (a) to commit to a comprehensive, financed national plan;
   (b) to strengthen surveillance and laboratory capacity;
   (c) to enhance surveillance of infectious and foodborne diseases;
   (d) to foster innovation and research and development for new tools for analysis of genomic sequencing data;
   (e) to apply a multisectoral approach to inform the drafting of the global action plan, by consulting Member States[2] as well as other relevant stakeholders, especially other multilateral stakeholders, such as FAO and OIE, taking into account the need to manage potential conflicts of interest;
   (f) to submit to the ……XXth…. World Health Assembly, through the Executive Board at its …YYYth …session, a draft global action plan to promote adoption of whole genome sequencing as a standardized laboratory method for identification and global surveillance of bacterial and viral organisms, together with a summary report on progress made in implementing the other aspects of this resolution.

[2] And, where applicable, regional economic integration organizations.