



Microbial DNA Sequencing – New Global Potential for Public Health, Food Safety and Biosecurity

Dear Honourable Minister,

We are writing to you on behalf of the Global Microbial Identifier (GMI), an international consortium whose members include more than 250 scientists (<http://www.globalmicrobialidentifier.org/>). The range of members span public health, food safety and infectious disease scientists, health policy specialists, epidemiologists, veterinarians, and clinicians. GMI members work in more than 40 countries and are galvanized by a single focus: realizing a global genomic infrastructure and database for the analysis of microbial DNA¹ sequences to support rapid infectious disease surveillance, diagnostics, and prevention. We are writing to all nations of the world because Next Generation Sequencing (NGS) technologies are revolutionizing the field of microbiology and we have serious concerns as to whether the world will realize the full effects of this technology so that all countries may benefit equally. Indeed, the impact of introducing NGS technologies for microbial identification is comparable to the initiation of microbiological laboratory techniques by Pasteur 150 years ago.

NGS presents two important subtyping advantages: it is both universal and comprehensive. Most conventional diagnostic methods and subtyping tests are specific to a genus (e.g. *Salmonella*, *Ebolavirus*) and/or a species (e.g. *Salmonella enterica*, *Ebolavirus Zaire*). Further, these approaches are often part of a suite of time-consuming and individual microbiological tests aimed at answering a single aspect of the organism under question. In contrast, NGS can combine all of those analyses into a single workflow that can determine the Whole-Genome Sequence (WGS) of the infectious agent in an actionable timeframe (24-48 hours). WGS data is incredibly comprehensive: allowing for the complete identification of the genetic material (including plasmids) that includes clinically useful information, such as virulence markers, predicted antimicrobial resistance, and likely response to vaccines or other therapies. In the future, most likely a global WGS system will enable very specific and almost real-time identification of all microorganisms, thus the reference to a 'Global Microbial Identifier'.

¹ Note that microorganism here refers to virus, bacteria, fungi and protozoa

One global and standardized WGS platform is important for the fast identification, research and control of emerging and re-emerging infectious diseases when we face possible public health emergencies of international concern. In addition, the combination of microbial sequence data and associated sample data (metadata) that describes the isolate (year of collection, isolate source, geographical information, etc.) can then be used to: (1) to identify origins of outbreaks ; (2) to support epidemiological relationships between food, environmental, and clinical infectious samples; (3) to greatly enhance the traceability of a food, water, community, or healthcare-associated outbreak back to its source, and 4) to monitor and guide control measures. Additionally, WGS can be used to exclude suspected sources of infection (e.g. specific food commodities), which prevents economic damage that was previously unavoidable. All of this enables a significantly more targeted public health response as well as a judicious use of healthcare resources world-wide.

The success and impact of integrating genomic data with existing surveillance networks is well recognized, and includes the polio, influenza, and measles surveillance programs. Furthermore, there have been significant gains in improving food safety with WGS data, and these public projects (e.g. PulseNet and GenomeTrakr) have sequenced over 150,000 microbial isolates. At the same time the COMPARE project is building a multidisciplinary analytical framework and platform for the rapid identification of emerging infectious diseases and foodborne outbreaks. Most likely other similar projects will soon be under development in other regions.

The benefits of high-throughput sequencing go well beyond the public health sectors. NGS technologies are being adopted in applied agronomy and plant and animal health and will likely be used for the diagnosis of (quarantine) plant pests providing a generic tool for pest detection and identification as well as for animal disease control. Likewise the analysis of microorganisms of value in food production and in environmental hygiene is ongoing. All together, these sequencing initiatives are proof-of-concept that these approaches are now ready to transition into a truly global enterprise for the benefit of global public health utilizing the common platform of WGS data.

We submit that the global community should embrace these technical opportunities and consider building a global platform and inter-connected databases for microbial genomes that integrate national and international efforts related to combating all infectious diseases and analysing microorganisms in general. The use of genomic data during the recent Ebola and Zika virus outbreaks has underscored the importance for a shared international commitment and shared values and standards regarding the collection and use of this type of information. Again, this technology will not only improve outbreak response, but will also enable a revolutionizing capacity for mitigation of general communicable and foodborne disease risks.

Furthermore, a global genomic data-sharing system could be used to share information on drug susceptibility, virulence, assist in the development of new therapies and vaccines, and support biosafety and biosecurity. It could also play a pivotal role in addressing the rise of antimicrobial resistance in bacterial populations, a critical challenge identified by the United Nations in a recent (2016) resolution. Finally, such a system would also enable characterization of beneficial microorganisms (used in food production or environmental management).

We call on our governments to actively advocate for a global platform and inter-connection of genomic databases for all microorganisms, including pathogens, thus creating one harmonized and revolutionary tool supportive of the International Health Regulations and global public health.

We recognize that developing a shared global WGS platform and database is a daunting endeavour and not without challenges. For example, one of the greatest concerns is data ownership and sharing genetic sequence data in light of international agreements such as the Nagoya Protocol. In order to move forward with implementing a global WGS network, we believe it is critical to have a global dialogue to address challenges and concerns such as those related to data sharing and compliance with international regulatory agreements.

To this end we are requesting your country's support to include sharing pathogen sequence data and the creation of a global WGS database system as an agenda item at the World Health Assembly, similar to the discussion on sharing influenza sequences and influenza preparedness in WHA64.5.

Please do not hesitate to contact us should you need further clarification about the ideas and issues referred here.

Sincerely yours,



Jorgen Schlundt, Ph.D.

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CC: Ministry of Agriculture
INFOSAN Contact Point