

Global Microbial Identifier: A Revolution Against Infectious Diseases

The challenge of infections

About 22% of all deaths are caused by infectious diseases. Treatment and control are often hampered by delayed diagnosis and lack of current data.

The solution we propose

A global microbial identifier that can revolutionize and vastly improve identification of pathogens from their whole genome sequences and link this information to resistance profiles, transmission routes and optimal treatment plans.

Information analysis is key

Establishing an international genomic sequence database is a necessity for the global fight against infectious diseases in humans and animals.

The benefits for society

The proposed global microbial identifier will enable early identification and optimal treatment, prevent epidemics and reduce the socioeconomic burden of disease. In addition, knowledge will be shared on a global scale.



The Global Microbial Identifier system is backed by over 300 scientists from more than 30 countries and has been conceptualized through 4 international expert meetings.

Rapid diagnosis => improving health

Action: A sample taken during examination allows near-instant identification of the pathogen and its resistance profile



Proposed research: A simple workflow must be established worldwide for doctors to obtain DNA sequences and interpret the output

Benefits: Improved health, food safety, animal health and prevention of global epidemics

Whole genomes => improving competition

Action: High-tech DNA sequencers establish the pathogens whole genome DNA or RNA sequence



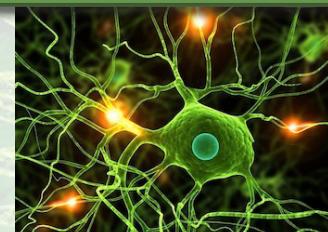
Proposed research: DNA sequencing techniques must be developed and refined to deliver in minimal time and at minimal cost

Benefits: High-tech capability accessible to all, creating opportunities for innovative and competitive industries



Medical research => building knowledge

Action: Scientists generate knowledge on pathogens and share it in the global database



Proposed research: Medical and veterinary research on pathogens and their antibiotic resistance profiles enabling efficient treatment

Benefits: Centres of excellence capable of breakthrough understanding of pathogens and the prevention of transmission of disease

Information analysis => sharing wisdom

Action: Genomic and medical data are analysed and shared in real-time for immediate access



Proposed research: Creation of easily accessible global databases with whole genome sequences linked to medical data

Benefits: Generates expertise in analysis and handling of information, knowledge transfer and capacity building

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1. Rapid diagnosis

We need a revolution....

SARS, avian flu, influenza and salmonellosis are all human infections originating from animals and with a global epidemiology. Add to this the recurring challenges imposed by food and water-borne infections and antibiotic-resistant bacteria. Therefore rapid detection and identification of microorganisms - enabling timely response - are crucial to control global, regional and local spread of disease in humans, among animals and through food.

The current methods for identification are, however, based on culture techniques developed by Pasteur in the 1880's. They are often slow, requiring weeks for characterisation, so treatment and preventive measures are delayed. In the worst case, this can lead to local infectious diseases developing into major public health emergencies.

.... and a prompt answer

The proposed global microbial identifier will allow health care professionals at the point of care to acquire comprehensive information about the pathogen within hours or a few days. For all pathogens – virus and bacteria - the system will provide treatment potential as well as spatial and temporal data of similar infections that can be used to detect an emerging outbreak and its origin.



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Case: Germany 2011

- A food-borne outbreak of E. coli strain O104 spreads to 16 countries. More than 3,800 gets seriously ill and 53 die
- EU fruit and vegetable producers declare damages of over 225 million euros
- Faster identification of the strain's specific pathogenicity and the origin of the outbreak would have allowed health care professionals and officials to act earlier
- That might have reduced the outbreak's economic and health consequences

Major impact on global health

Our proposal will enable major leaps in infectious disease detection, not the least for developing countries. It provides better control over global, regional and local epidemics, thereby relieving society of huge socioeconomic burdens.

As the system is not limited to human infections, it can also be used to monitor food-borne diseases or infectious diseases in domestic animals or even crops. In this way, the system can also lead to improvements in food safety and animal health.

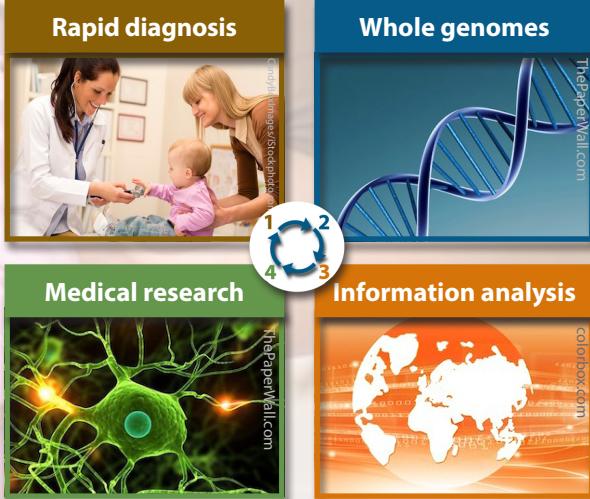
User-friendly, simple and automated

The rapid microbial identification system we propose must be so user friendly and simple to use that the point of care professional can easily process a sample and readily understand the output.

After sampling the pathogen, all subsequent manipulation - e.g. DNA extraction - should ideally be automated. In larger clinical settings, whole genome sequencing can be performed in-house while the general practitioner might transfer the sample to a shared facility. Either way, the workflow must be efficient and simple.

The system must be able to automatically evaluate the generated information and interpret the results, so the health care professional can act immediately. Ideally, it should provide warnings when clusters of disease are occurring in time or space.

Global microbial identifier outline



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2. Whole genomes

Cost goes down - Capacity goes up

The cost of whole genome sequencing is in free fall and currently drops by a factor of 10 every second year. At the same time, capacity is skyrocketing and a whole bacterial genome can now be sequenced in a few hours. In addition, developments in ease of use and price of the necessary equipment are rapidly making it broadly available. Thus, it is likely that whole genome sequencing will soon be within reach for every lab.

A leapfrog into the future: linking mobiles and health

Implementation of new technologies can boost development in poorer countries - like mobile phones leapfrogged traditional landline technology in Africa and effectively brought people in contact with each other and the internet.

The same can happen for health care where current diagnostic methods are diverse and require a lot of training. Whole genome sequencing is a simple one-size-fits-all tool for diagnosis of all infectious diseases, and it holds the potential to dramatically improve public health in developing countries.



The time is right to unite forces and get more competitive

The diverse diagnostic techniques of today require a broad range of highly specialized staff for each group of pathogens. This is simply not an efficient way for society to utilize their expertise. The simple and universally agreed-on approach that we propose allows the experts to unite their forces and focus on a common task so society can get more competitive.

Technological progress and market forces are currently driving widespread deployment of genomic sequencing technologies for routine diagnostic testing. Thus, at present, there is a window of opportunity to develop a system built on common data format, ontology and nomenclature that can power a strong and competitive industry.



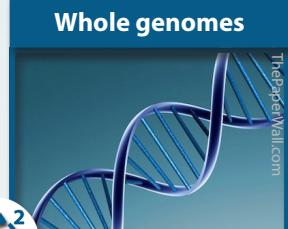
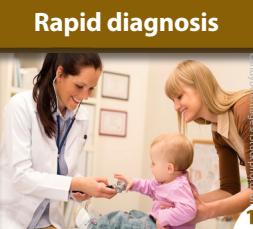
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Raising the bar to new standards

The whole genome sequence of a bacterium, virus or parasite uniquely defines its specific strain and can be linked in a global database to all known information about it. With only an internet connection and a few standardized tools, this will provide all health care professionals on the globe with an instrument to make a precise diagnosis and offer the best treatment in the fastest time.

This is in sharp contrast to current diagnostic techniques that use culturing and subtyping. They are inherently slow, require specialized training and only provide limited information on e.g. resistance or virulence. These limitations not only lead to increased costs and serious delays but also ignore the vast multitude of traits possessed by each pathogen. Traits that can be used to understand their identity, pathogenicity, transmission and optimal treatment.

Global microbial identifier outline



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3. Information analysis

Access to a world of information

The capacity to exchange and manage large data volumes over web-based systems has increased dramatically in recent years, enabling the potential creation of a global database of whole genome sequences of all relevant microbial strains and their associated medical data.

A global system to aggregate, share, mine and translate genomic data in real-time to address global and clinical medical challenges is therefore a realistic goal. The system will provide a direct, user-friendly interface to the database for end-users in health services, industry, academia and government - e.g. clinicians, veterinarians, epidemiologists and officials.

The database interface will allow retrieval of both simple and extremely complex information - from identification of a single pathogen to national and international health surveillance and outbreak investigation. Moreover, it will allow upload of novel information - like clinical or epidemiological data acquired through research or field observations.

All new and existing information in the database will be analyzed and integrated continuously, so the system will always provide the end-users with the most competent and up-to-date answers.



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Maintaining the integrity of systems that protect us from cross-border health threats, that detect and respond to outbreaks, pandemics and emerging diseases is of concern to all nations.

Dr. Margaret Chan,
WHO Director-General



Privacy and respect have high priority

Sharing pathogen sequences in an international context may be sensitive, and this issue must be addressed in order to engage the relevant stakeholders. This includes reluctance of governments to share data when there are competing interests such as trade and tourism; the need to protect individual patients' privacy rights; and reluctance of researchers to share data before publication.

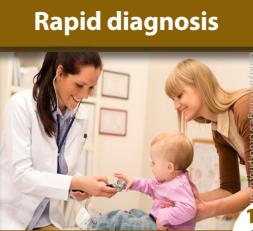
Standards should be developed by scientists, health workers and relevant agencies like the World Health Organization to ensure an all-inclusive, non-exclusive database that can be easily accessed by all stakeholders. Moreover, the database should be both backward and forward compatible so all current, historic and future data can be inserted into it.

Knowledge for everyone

By enabling access to the global database that we propose, a professional response to novel and known health threats will be within reach of all countries with basic laboratory infrastructure. This will have major benefits for local, national, regional and global public health as well as for food safety and animal welfare.

In addition, the necessary global cooperation for the efficient development of this system will provide unique opportunities for capacity building and knowledge transfer between research groups, public health and animal health institutes around the world.

Global microbial identifier outline



Rapid diagnosis



Whole genomes



Medical research



Information analysis

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4. Medical research

Antibiotic resistant bacteria

When Alexander Fleming discovered the first antibiotic in 1928, humanity got an extremely powerful weapon against bacterial infections. Unfortunately, many pathogenic bacteria have since become resistant to antibiotics, resulting in a public health crisis.

Infections by antibiotic resistant bacteria are a growing and often fatal problem that frequently occur and spread through hospitals or animal production systems. The system we propose will make it easier to monitor development and spread of antibiotic resistance and this can ultimately save lives.



A multi resistant pathogen growing in the presence of five different antibiotics.

Building new knowledge

Making huge amounts of research data as well as any related genome sequences readily available to all researchers will strengthen the scientific community and lead to substantial knowledge building. This can provide the foundation for centres of excellence that advance our understanding of not only pathogens but also of related microbial, cellular, biochemical and genetic phenomena.



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A war we can win

Scientists around the world are making tremendous progress in the continuous war against infectious diseases, and while the number of deaths caused by them is still staggering, it is actually falling: from 32% of all global deaths in 1993, to 26% in 2002, and down to a low of 22% in 2008.

To make further advances in the war against infectious microorganisms we need to understand the genetic and biochemical basis for their pathogenicity, transmission etc. Such efforts will be greatly supported by linking medical and genomic data of pathogens on a massive scale as we propose.

Another important means to reduce the consequences of infectious diseases is to improve surveillance of outbreaks. This is especially important during humanitarian emergencies where present systems may be underperforming, disrupted or non-existent.

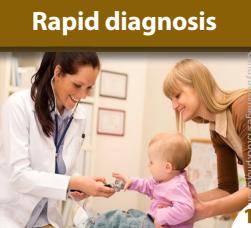
The global microbial identifier will provide a much improved means to detect and monitor outbreaks. Such a system might have reduced the consequences of the cholera outbreak that began in Haiti after the earthquake in 2010 and killed more than 7,900 people.

Making data available

Regardless of how much progress scientists make in the fight against infectious diseases, we can only take full advantage of it when scientific breakthroughs are efficiently communicated and made available to other scientists and health care professionals.

Our proposed system will allow every scientist with an online connection to share new results in the global database so the knowledge instantly becomes available for all colleagues and interested parties - no matter where they are and no matter what scientific journals they can access.

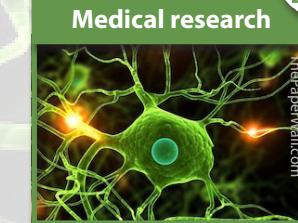
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