9th Annual Workshop of the National Reference Laboratories for *E. coli* in the EU 20-21 October, 2014

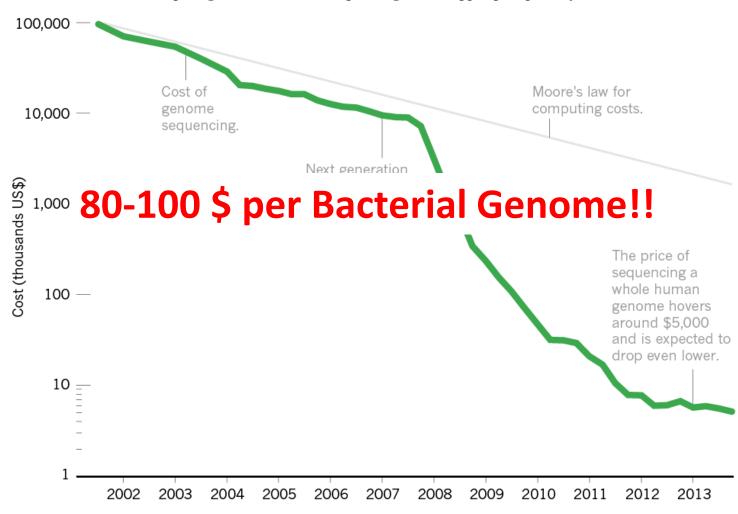
Session 2.

Next Generation Sequencing (NGS):

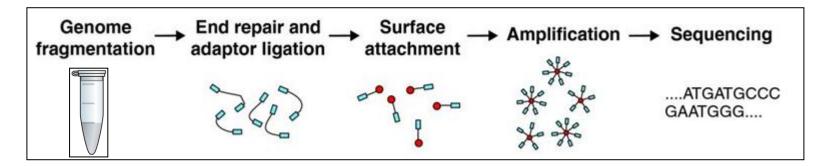
International initiatives and application in surveillance and outbreak investigations

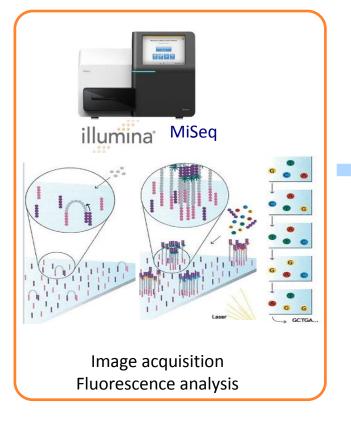
Falling fast

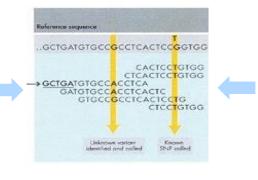
In the first few years after the end of the Human Genome Project, the cost of genome sequencing roughly followed Moore's law, which predicts exponential declines in computing costs. After 2007, sequencing costs dropped precipitously.



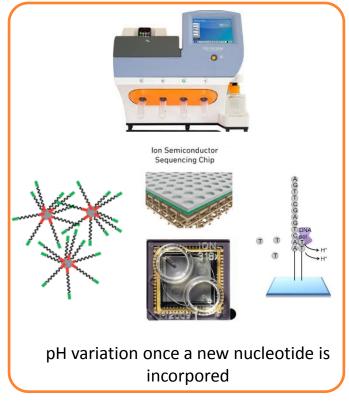
Next generation sequencing



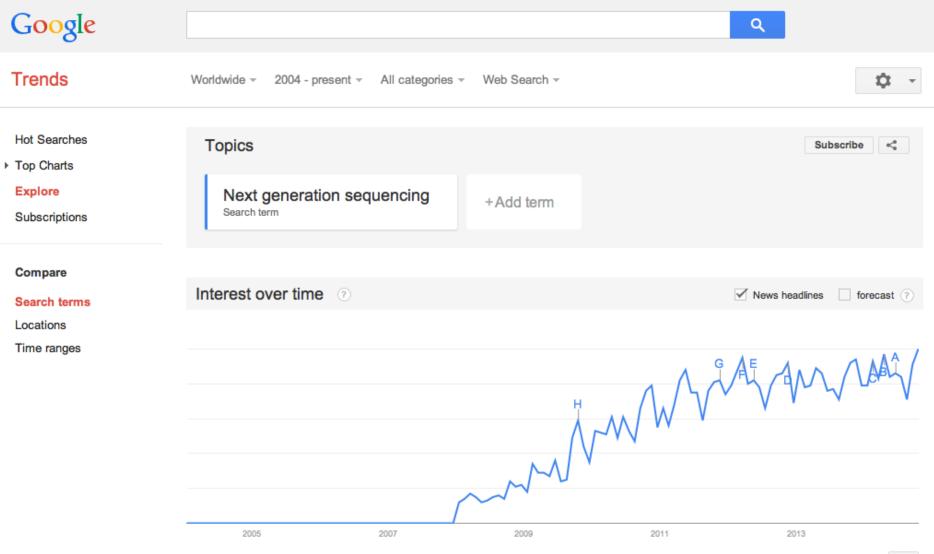




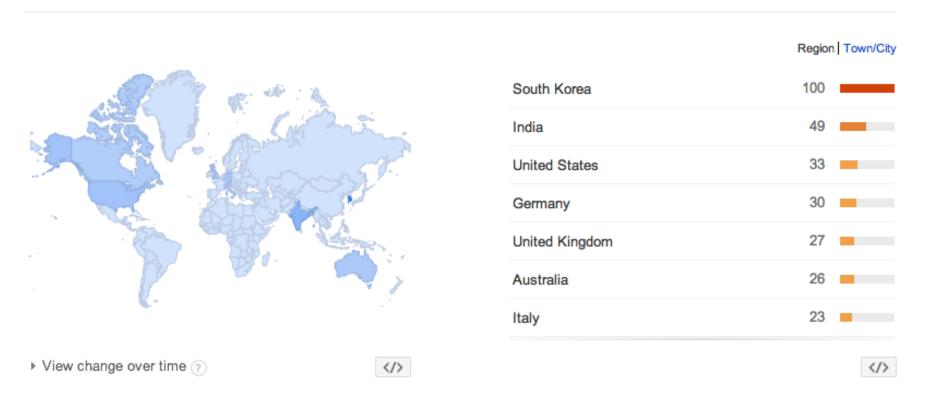
Short Reads 200bp-400bp



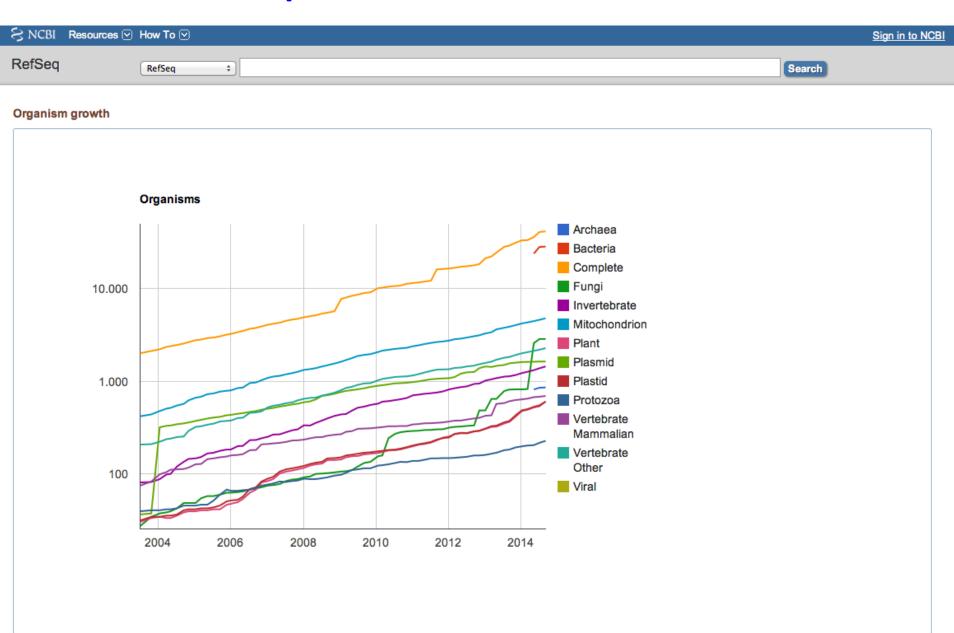
NGS: A growing interest



NGS: Regional interest



Sequence data at NCBI







100K Genome Project

QUICKLINKS

3/3



100K Foodborne Pathogen Genome Project

Food safety, which is a very complex series of events, is the responsibility agriculture, public health, and medicine that requires bold and revolutionary efforts to ensure. The 100K Pathogen Genome Project is a landmark consortium that addresses the persistent food safety concerns by engaging world-wide partners to create a publicly available genetic database of the most common foodborne disease causing microbes. As our food supply becomes a global industry food safety becomes a worldwide mandate. This project will revolutionize the methods used in agriculture by bringing a new paradigm to public health to empower precise and robust molecular testing in the food chain – from the farm to the kitchen table.

Dr. Weimer will discuss the 100K Genome Project as part of the Food Labs Conference, taking place March 19-20, 2013. For information on the conference, please go here.

Despite efforts to reduce foodborne illness, outbreaks from Salmonella, Campylobacter, enteropathogenic E. coli, Listeria monocytogenes, Vibrio, and Shigella continue to occur worldwide. The recent E. coli O104:H4 outbreaks in Europe highlights the need for this approach as it was determined that genetic exchange led to a chimeric genome that was far more pathogenic than either of the other two organisms. In spite of extensive efforts to increase regulation and develop early warning diagnostics for improved public health monitoring definitive foodborne illness interventions remains elusive in large part due to the lack of sufficient information about microbial diversity. The 100K pathogen genome sequencing project will use next generation sequencing approaches to enable new diagnostic and public health approaches for use in novel solutions in the management of foodborne disease to facilitate improved public health.

Continual genetic evolution of pathogens is hindering our ability to consistently detect and mitigate these organisms in food, the environment, and livestock, which interfere with our preparedness to defend the food supply. This project will sequence 100,000 genomes of important pathogens to increase food security.



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Global Microbial Identifier

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infrastructure.

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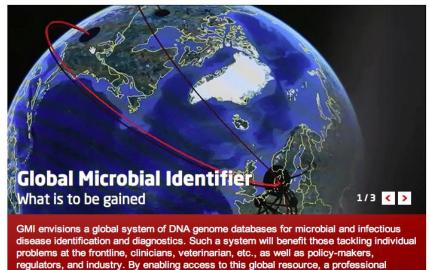
CONTACT



Updated GMI7 programme

For full details of the event and the preliminary programme, please visit www.fera.co.uk/events/GMI2014

Q



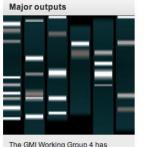
response on health threats will be within reach of all countries with basic laboratory













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Projects and collaborations

PulseNet's evaluation of NGS as a potential tool for surveillance and outbreak investigations has many projects and collaborators, shown below.

| Projects | Collaborations | |
|--|---|--|
| Sequence strains from recent and historical outbreaks as well as strains not associated with outbreaks both in house and with collaborators | CDC internal partners, FDA, device manufacturers, academic institutions such as UC Davis in the 100K Foodborne Pathogens Project | |
| Evaluate molecular subtyping schemes based on whole genome sequencing that provide the best clustering | Partners from universities, PulseNet participants in the states, PulseNet International and other public health laboratories abroad | |
| Determine what genetic cues (sequences) from clinical samples such as stool can be used to identify and cluster bacteria causing foodborne illness | | |
| Develop standardized laboratory and data analysis workflows | International partners for developing standards for whole genome sequencing and analysis, such as the Global Microbial Identifier initiative and bioinformatics software manufacturing partners | |

Many groups are producing genome sequences, including CDC's <u>Enteric Diseases Laboratory Branch</u>, the <u>CDC Biotechnology Core Facility</u>, collaborative projects with device manufacturers, and collaborative projects with federal agencies and academic institutions.

Standardization





« Food products – Microbiology »

ISO/TC 34/SC 9

Doc. Number:

Date:

N 1676

2014-08-27

Assistant:

Your contact:

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Gwénola Hardouin

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US Proposal for Standardization of Whole-Genome Sequencing (WGS) for Food Microbial Typing and Genomic Characterizations of foodborne microorganisms



European Food Safety Authority Committed to ensuring that Europe's food is safe



NEWS & EVENTS

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EFSA Scientific Colloquium N°20: Whole Genome Sequencing of food-borne pathogens for public health protection

News Story - Parma, 16 June 2014

About 90 leading scientists, representatives of international and European organisations and national food safety authorities gathered in Parma, Italy, to discuss the use of the whole genome sequencing of foodborne pathogens for the protection of public health. EFSA's 20th Scientific Colloquium on whole genome sequencing (WGS) took place on 16-17 June.



 Scientific Committee and Emerging Risks Unit

EU financed a 20 M€ Project in the PHC7 call





MEETING REPORT

Expert Group on

Introduction of next generation typing methods for **Food- and Waterborne Diseases**

Terms of Reference, version 1.0, 24 July 2014

technical consultation on harnessing mics for epidemiological surveillance

Preparedness in the *E. coli* network

- The EU RL carries out research involving the use of NGS and is involved in the most of the mentioned initiatives
- Quite a few NRL already have access to the technology

- A training course on the use of open source Bioinformatics has been included in the 2015 Workprogram (planned next summer)
- Standard modules will be deployed for the training program of the EU RL VTEC