Establishing a National Surveillance Network for Foodborne Pathogens Based on Whole Genome Sequencing

Steven Musser, Ph.D.

Deputy Center Director for Scientific Operations Center for Food Safety and Applied Nutrition, FDA

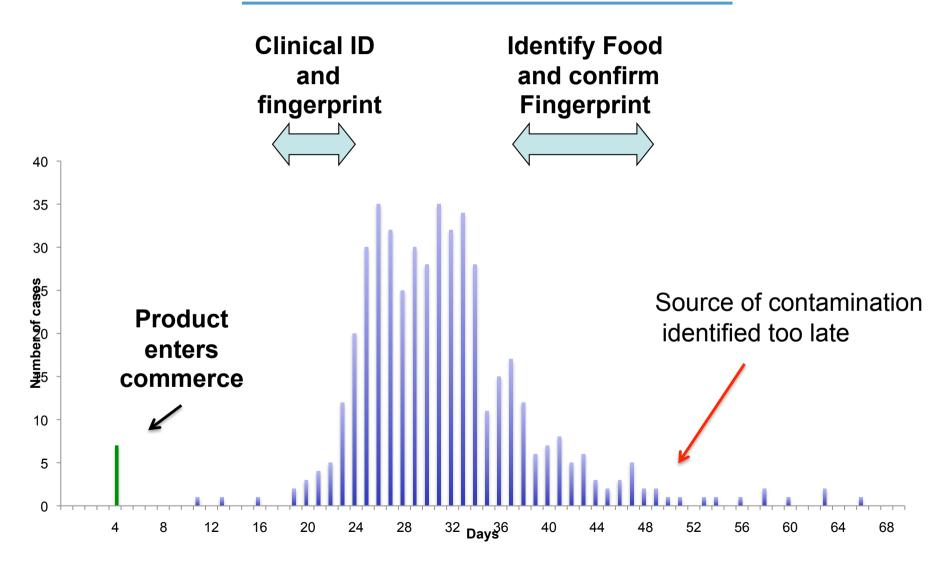
Next-Generation Sequencing for Food Pathogen Traceability
UCD Institute of Food and Health *in conjunction with* UCD Centre for Food Safety
and the Food Safety Authority of Ireland - March 24, 2014

Foodborne Illness in the US

- ★ Each year 9.4 million episodes of foodborne illness in the United States
- **★** 55,961 hospitalizations
- * 1,351 deaths
- * Salmonella spp. cause 11% of foodborne illnesses each year

(Scallan et al. 2011 Emerging Infectious Diseases • www.cdc.gov/eid).

The Public Health Need



Some perspective on the food supply

- Tracking and Tracing of food pathogens
 - Almost 200,000 registered food facilities (2/14)
 - -81,574 Domestic and 115,753 Foreign
 - More than 300 ports of entry
 - More than 130,000 importers and more than 11 million import lines/yr
 - In the US there are more than 2 million farms

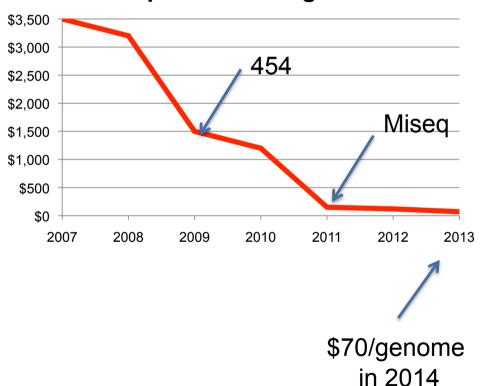


and possibly prevent them from occurring in the first place. NOTE: Countries are listed in alphabetical order and not by volume of export.

Is WGS a viable solution?

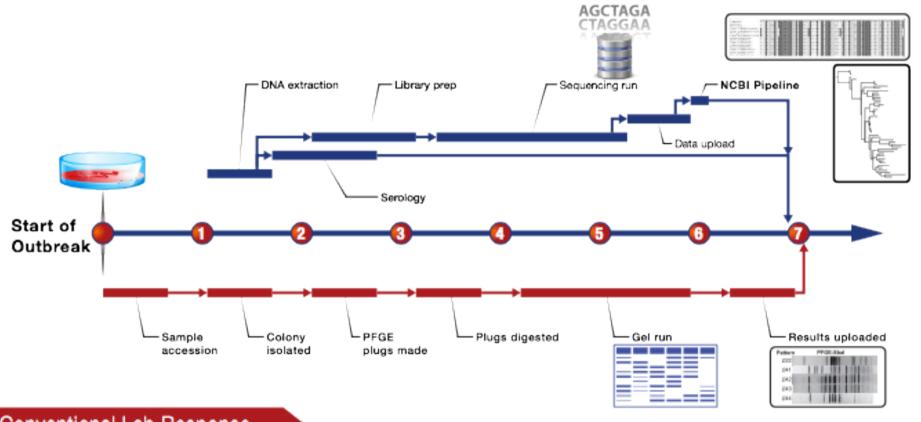
- Cost
- Increasing ease of operation
- Database longevity
- Sample prep
 - Identical for all pathogens
- Cost savings
 - Resistance, subtyping, virulence factors, more...
- New applications
 - tracking, regulatory/compliance actions, historical trends, more...

Cost per bacterial genome



Next-generation Lab Response vs. Conventional Lab Response

Next-Generation Lab Response









This from 1859, Darwin's, On the Origin of Species

 "It is obvious that the Galapagos Islands would be likely to receive colonists, whether by occasional means of transport or by formerly continuous land, from America; and the Cape de Verde Islands from Africa; and that such colonists would be liable to modification;— the principle of inheritance still betraying their original birthplace"



With WGS, we now have the potential to discern those birthplaces...

Can WGS fill a Public Health role?

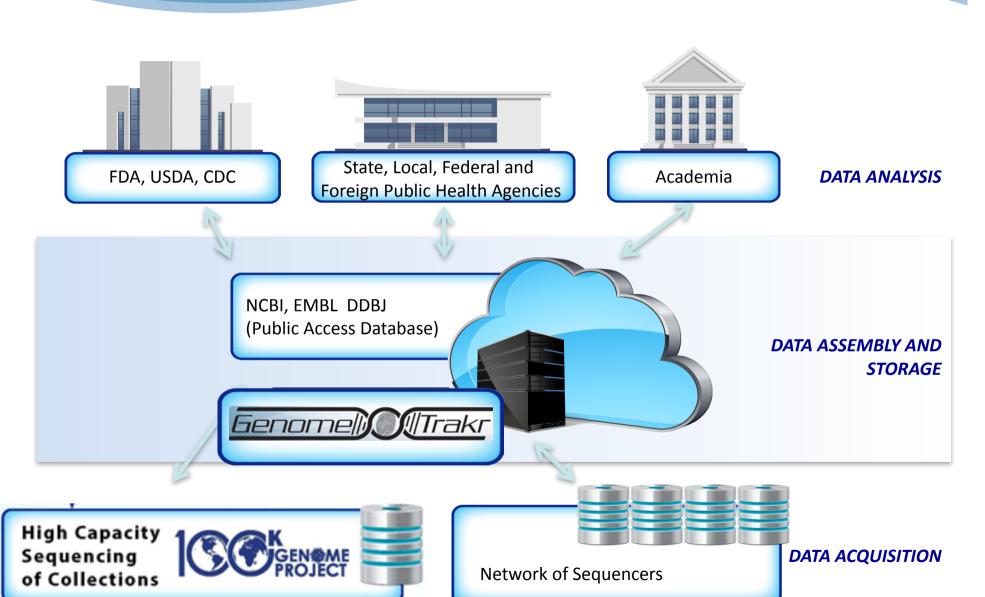
- If yes, then...
 - Initiate pilot study
 - Develop collaborations and partnerships
 - NCBI, States, CDC and other Federal partners
 - What infrastructure would be needed?
 - Support multiple sequencing platforms?
 - Multiple data formats
 - How reproducible are the data AND answers?
 - How would data be accessed and stored?
 - Public vs. private No data hoarding
 - Metadata

Metadata

- Simple but complete for each Strain
 - Clinical or environmental (specific source)
 - Environmental swab or type of food
 - Location as accurate as allowable
 - State, Region, Country
 - Submitter name Usually organization
 - Date of isolation

Network Requirements

- Well characterized strain sets
- A large database of sequences with accurate metadata
- A network of sequencing labs
- Analytical software
- Somewhere to store the data



FDA provides

- 1 Miseq system
- Sufficient reagents to sequence> 300 genomes per year
- Dedicated scientific staff
 (bioinformatics and/or laboratory support) through Oak Ridge Institute for Science and Education (ORISE)
- Bioinformatics and laboratory support, analysis pipeline

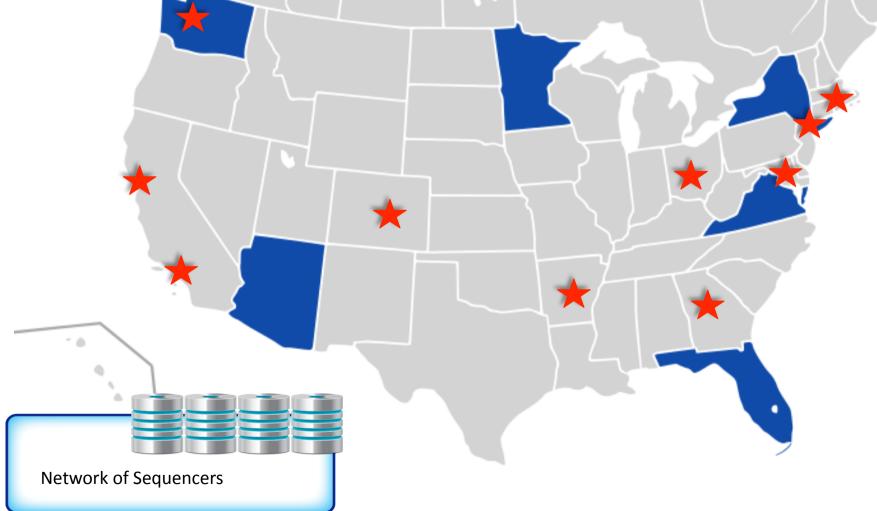
Network Lab provides

- Minimum ~300 genomes with metadata uploaded to NCBI per annum, minimum 20X coverage
- food and environmental related bacterial (prefer Salmonella) isolates

Cost to FDA ≈ \$200k/lab

7 state health depts.





FDA-State Desktop Pilot called GenomeTrakr

http://www.ncbi.nlm.nih.gov/bioproject/183844

Food and Drug Administration, Center for Food Safety and Applied Nutrition: GenomeTrakr Project

Accession: PRJNA183844 ID: 183844

Currently encompasses whole genome sequencing of cultured pathogens as part of a surveillance project for the rapid detection of outbreaks of foodborne illnesses

Project Type: Umbrella project (Subtype: Disease)

Relevance: Agricultural, Medical, Industrial, Environmental

Project Data:

Resource Name	Number of Links	
Sequence data		
Nucleotide (total)	31172	
WGS master	194	
Genomic DNA	30978	
SRA Experiments	437	
Protein Sequences	901056	
Publications		
PubMed	12	
PMC	9	
OTHER DATASETS		
BioSample	1104	
GEO DataSets	1	

Project Type Genome sequencing Highest level of assembly: SRA or Trace No data links Total			Number of Projects 1 4 5
BioProject accession	Assembly level	Name	Title
PRJNA183847		GenomeTrakr Project: Arizona State Public Health Laboratory	GenomeTrakr Project: Arizona State Public Health Laboratory (Arizona State Public Health)
PRJNA183848	-	GenomeTrakr Project: Florida Department of Health	GenomeTrakr Project: Florida Department of Health (Florida Department of Health)
PRJNA186035	SRA or Trace	GenomeTrakr Project: Food and Drug Administration, Center for Food Safety and Applied Nutrition	GenomeTrakr Project: Food and Drug Administration, Center for Food Safety and Applied Nutrition (Center for Food Safety and)
PRJNA183850	-	GenomeTrakr Project: New York State Dept. of Health, Wadsworth Center	GenomeTrakr Project: New York State Dept. of Health, Wadsworth Center (New York State Dept. of Health)
PRJNA183851	-	GenomeTrakr Project: Washington State Department of Health Public Health Laboratory	GenomeTrakr Project: Washington State Department of Health Public Health Laboratory (Washington State Department)

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

Expanding the network

Partners with sequencers

State Partners

United Kingdom - FSA

Canada – CFIA and PHAC

Argentina - WHO

Taiwan

6 States have requested funding

Organizations/Countries joining

the network

Partners with isolates

Ireland

Mexico

Turkey

Columbia

Chile

Brazil

Thailand

Ethiopia

APHL

WHO

USDA

GMI

Italy

Germany

Denmark

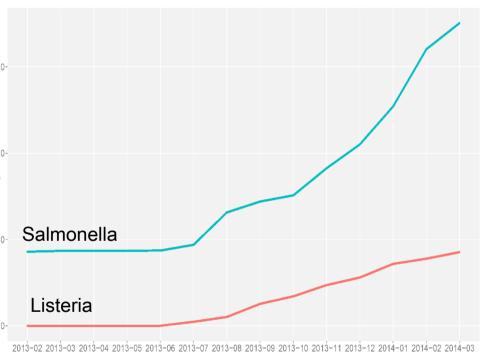
Australia

Spain



Now What?

- NGS clearly defines foodborne outbreaks more than 15 different examples
- NGS network is reliable, efficient and can provide very good location specificity of outbreaks
- We have sequenced about 2900 Salmonella, more than 900 Listeria, and closed 100 genomes. Our current rate is about 500 sequences a month.
- The need for increased number of well characterized environmental (food, water, facility, etc.) sequences may outweigh need for extensive clinical isolates
- Many requests for information or help from other public health labs



Needs/concerns

- Network security issues
 - Sequencers
 - Software
- Improved informatics and software development
 - Widely available commercial solutions
 - Custom solutions
 - Automated identification of AMR, virulence markers, etc
- Cloud computing and access to HPC
- Data presentation to different groups
 - Physicians
 - Epidemiologists
 - Researchers

FDA -CFSAN

Marc Allard Rebecca Bell

Eric Brown Andrea Ottesen James Pettengill

Ruth Timme Jie Zheng Charlie Wang

Christine Keys Cong Li

Errol Strain Yan Luo

Mark Mammel Darcy Hanes

FDA Division of Field Sciences Rebecca Dreisch

NYPH Bill Wolfgang Kimberly Musser and colleagues

MPH Alvina Chu and colleagues

FDH Anita Wright Judy Johnson

ADPH Victor Waddell Dave Engelthaller Paul Keim

WDH Brian Hyatt Chen Li William Glover

CDC John Besser, Eija Trees, Duncan MacCannell and colleagues

National Institutes of Health

David Lipman (NCBI) Martin Shumway (NCBI)
Tatiana Tatusova (NCBI) William Klimke (NCBI)

Illumina

Lisa Alves Susan Knowles Omayma Al-Awar and colleagues CLC Bio David Michaels Cecilia Boysen and colleagues



Questions