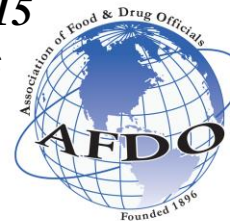




June 20-24, 2015
Indianapolis



Regulatory Genomics and Beyond:

How Whole Genome Sequencing is Augmenting FDA's Role in Foodborne Outbreak Investigations

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Director
Division of Microbiology
Center for Food Safety & Applied Nutrition
U.S. Food & Drug Administration
College Park, Maryland 20740

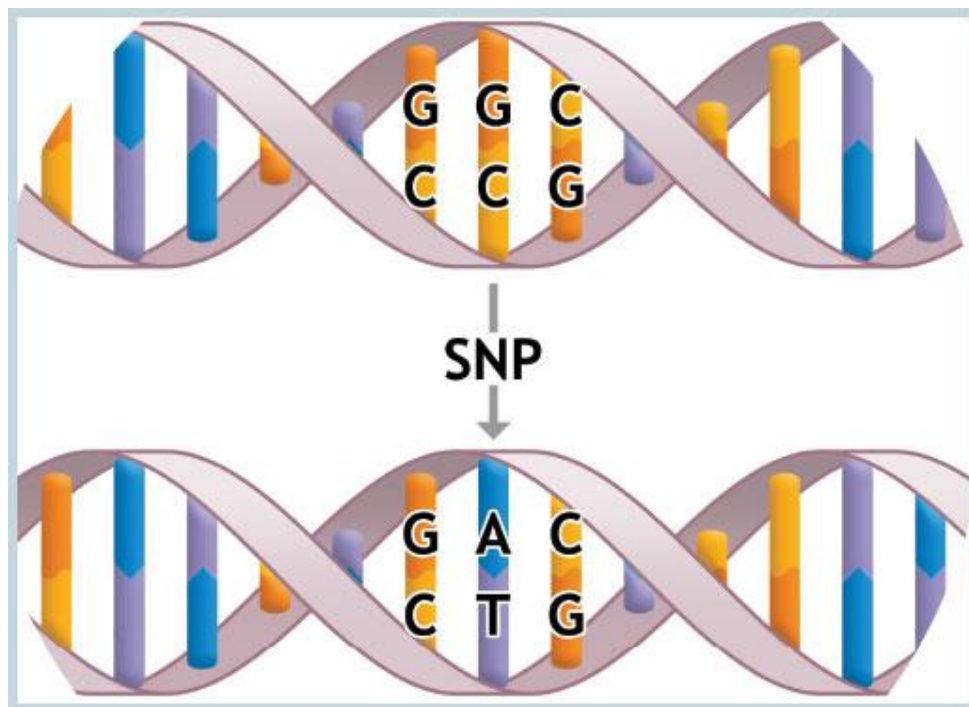


PFGE v/s WGS

- WGS is high resolution
 - 3-5 million data points are collected for each isolate
- WGS analyses are statistically robust
 - Unlike PFGE patterns, WGS data can be analyzed in its evolutionary context. Accurate and stable genetic changes within pathogen genomes enable us to pin point specific common sources of outbreak strains (farms, processing plants, food types, and geographic regions).
 - **Source Tracking is Key Application**

Background: CFSAN SNP Pipeline

Single Nucleotide Polymorphism



Reference

Food or
Environmental
Isolate

<http://www.ibbl.lu/wp-content/uploads/2012/07/SNPs.jpg>

Circa 2009 IN or OUT?

FOODBORNE OUTBREAK INVESTIGATION: WGS analysis of foodborne salmonellae case study

This investigation focused on *Salmonella* Montevideo samples associated with red and black pepper used in the production of Italian-style spiced meats in a New England processing facility. This manufacturer was implicated in a major salmonellosis outbreak that affected more than 272 people in 44 states and the District of Columbia.

15-20x shot gun sequencing
35 pure culture isolates
from patients, foods and
Environmental samples.

Concatenate 40 variable genes for Phylogenetic analysis



N Engl J Med. 2011 Mar 10;364(10):981-2. doi: 10.1056/NEJMc1100443. Epub 2011 Feb 23.

Identification of a salmonellosis outbreak by means of molecular sequencing.

Lienau EK, Strain E, Wang C, Zheng J, Ottesen AR, Keys CE, Hammack TS, Musser SM, Brown EW, Allard MW, Cao G, Meng J, Stones R.

FDA WGS Application to Actual Food Contamination Events



Montevideo black and red pepper
 Senftenberg black and red pepper
 Enteritidis shell/liquid eggs
 Heidelberg ground turkey
 Heidelberg chicken broilers
 Heidelberg chicken livers
 Enteritidis custard
 Bareilly tuna scrape
 Tennessee peanut butter/peanut butter paste
 Typhimurium peanut butter
 Braenderup peanut butter/nut butter
 Tennessee cilantro
 Agona dry cereal
 Agona papaya
 Newport tomatoes
 Newport environmental
 Kentucky - Cerro dairy/dairy farms
 Anatum spices/pepper flakes
 Javiana cantaloupes
 Saintpaul hot peppers
 4,5,12: i –

Lmono cantaloupes
 Lmono queso cheese
 Lmono potato salad
 Lmono artisanal cheeses
 Lmono avocados
 Lmono ricotta
 Lmono celery/chix salad
 Lmono smoked fish
 Lmono other herbs
 Lmono peaches

Cronobacter infant formula

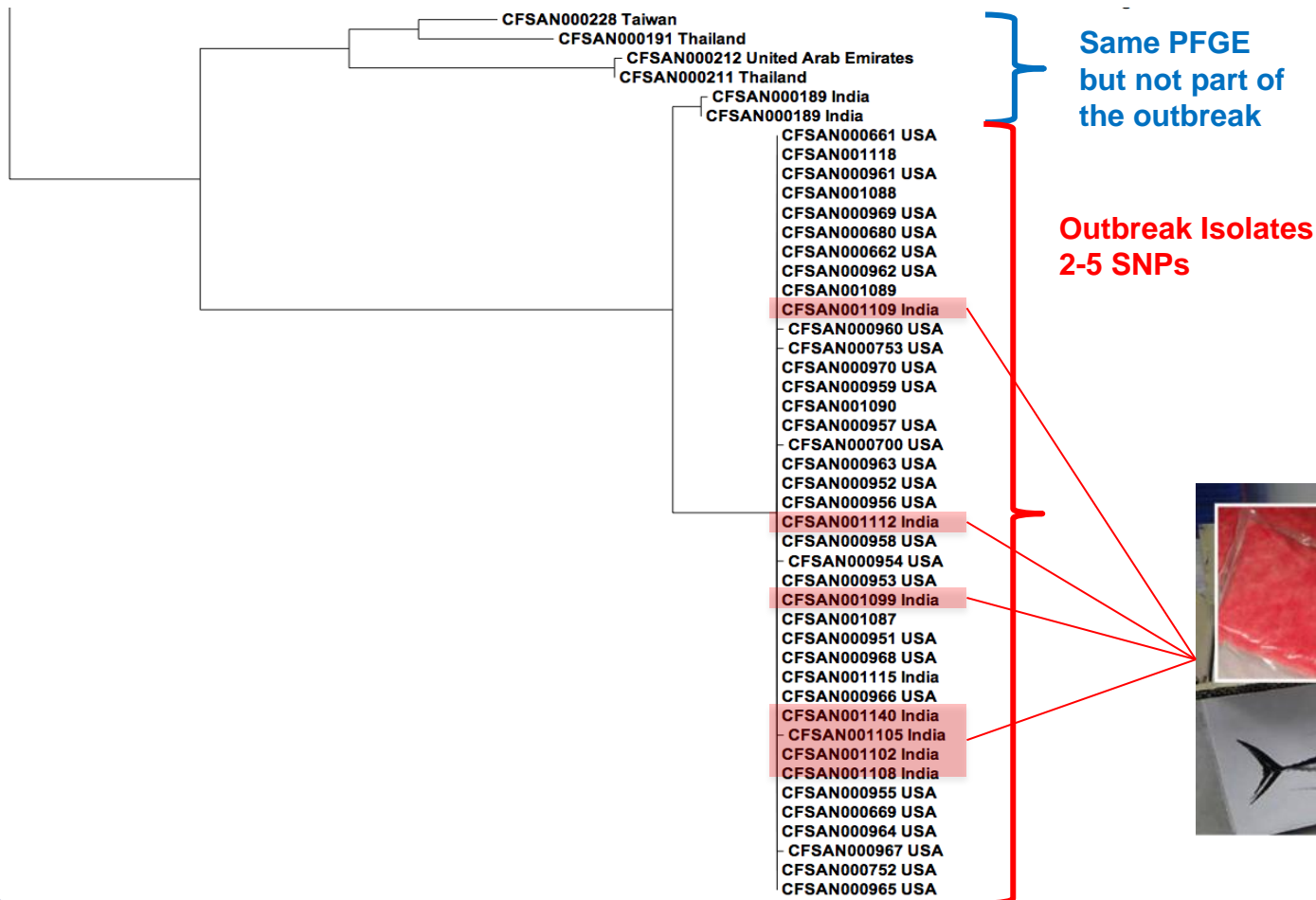
V para oysters

EcO157:H7 lettuce

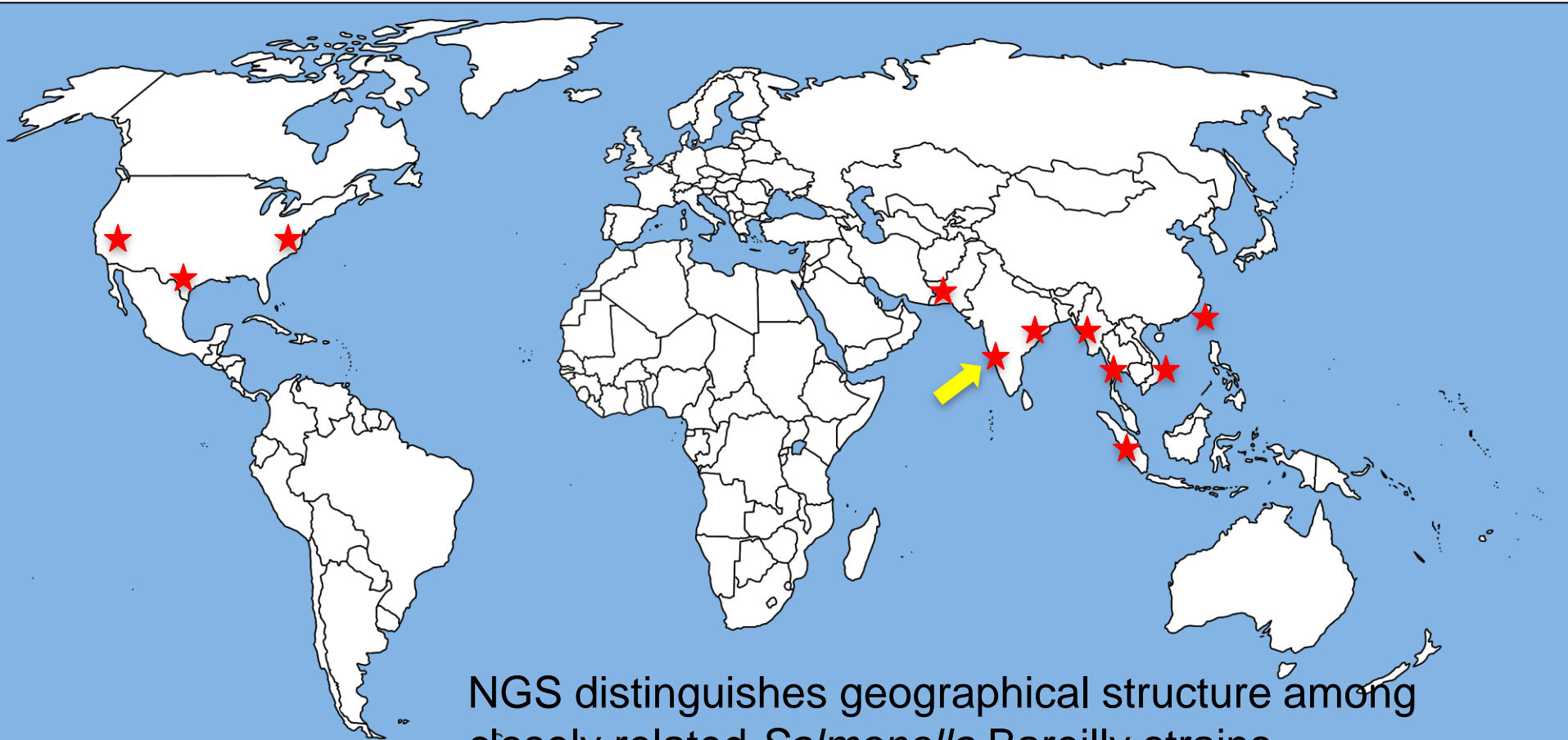
STEC beef

...Numerous other taxa

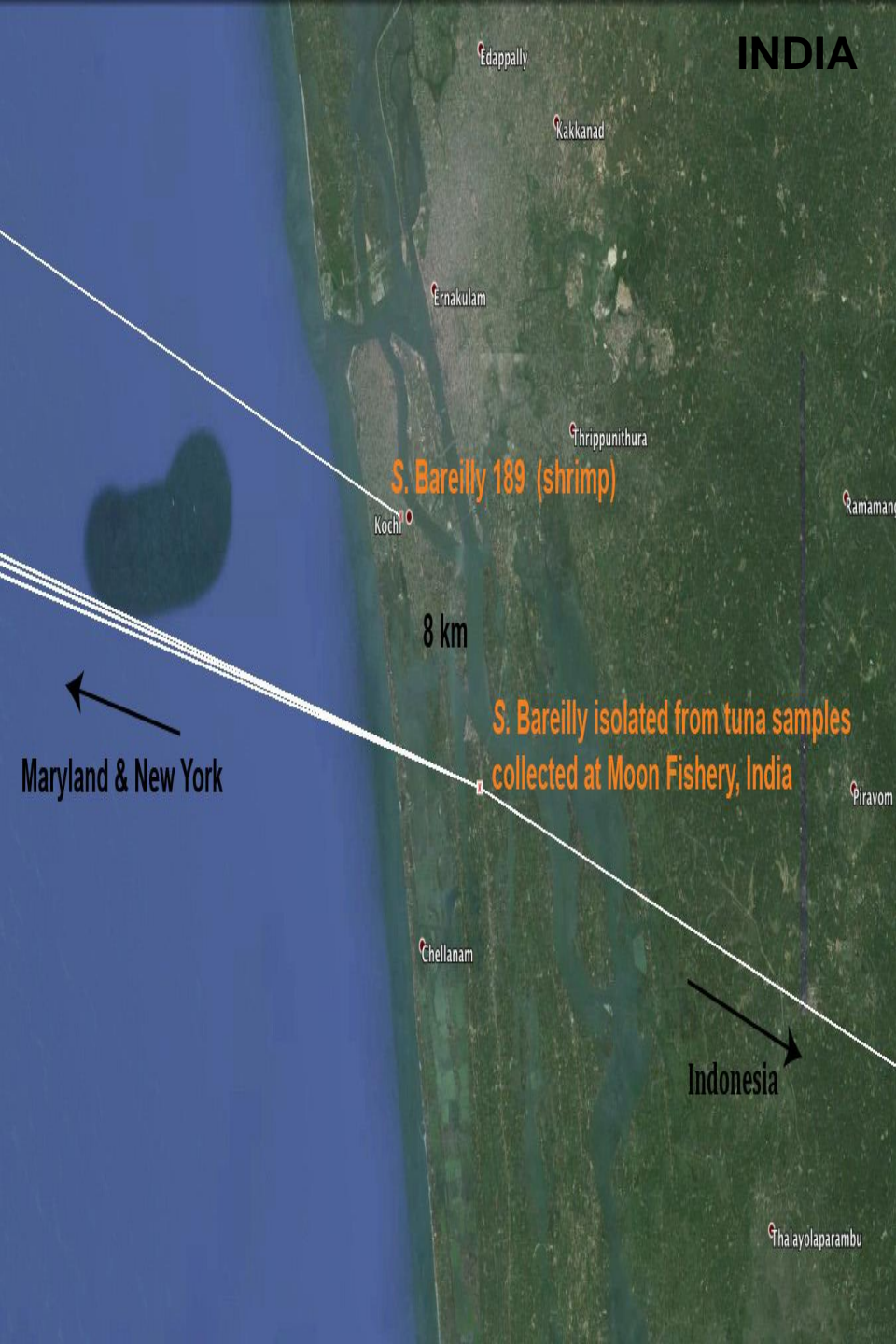
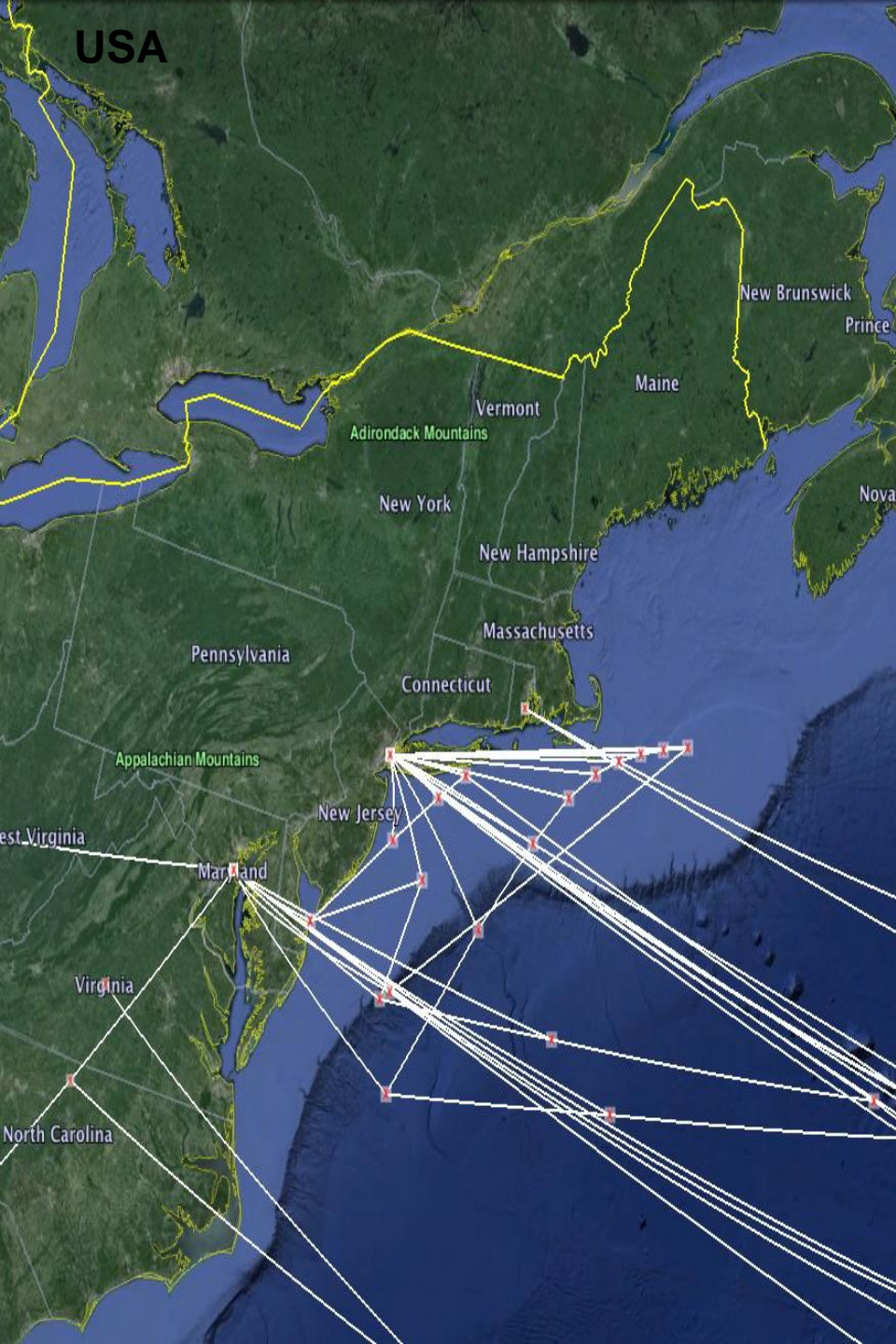
SNP phylogeny for S. Bareilly strains



PFGE identical in red



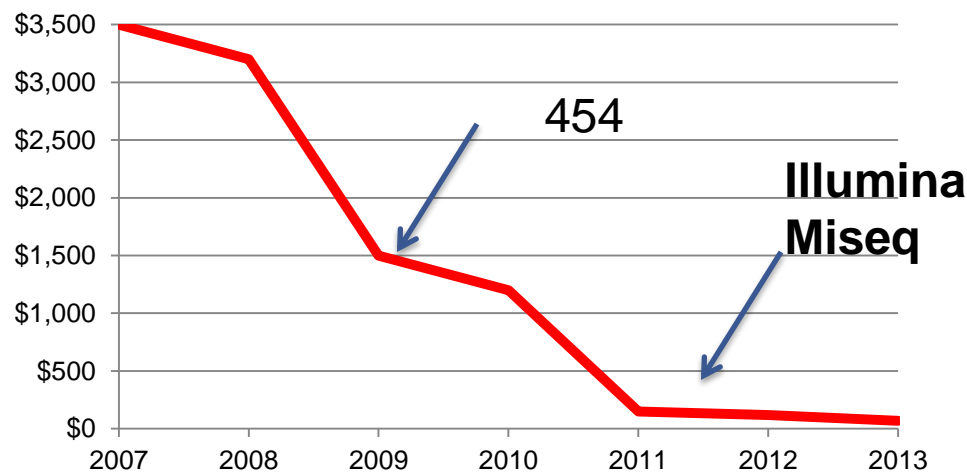
NGS distinguishes geographical structure among closely related *Salmonella* Bareilly strains



Is WGS a viable solution?

- Cost
- Increasing ease of operation
- Database longevity
- Comparable times to conventional pipelines
- 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



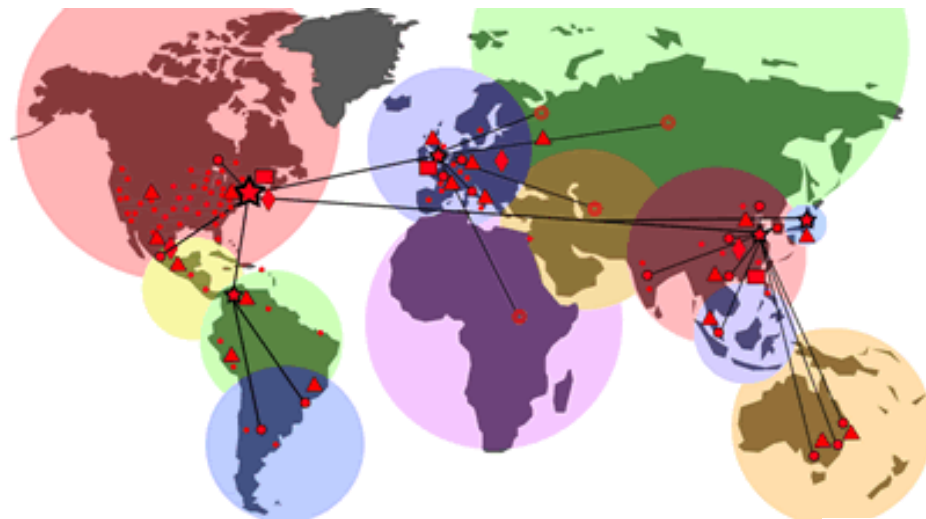
\$70/genome
in 2014

\$40/genome
in 2015 w/
Illumina NextSeq Technology

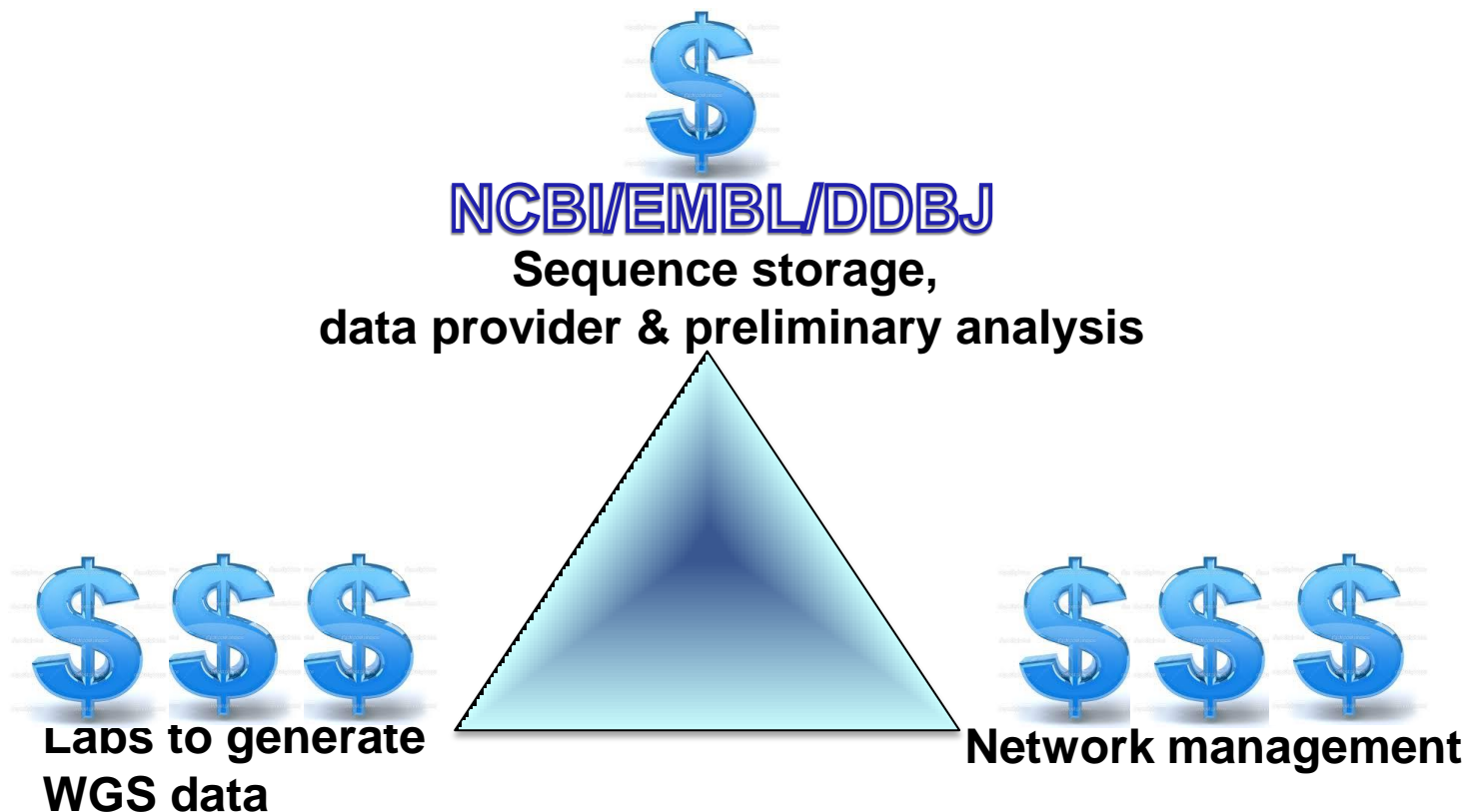
Illumina NextSeq Technology

Why Develop a WGS based Network?

- Tracking and Tracing of food pathogens
 - Insufficient resolution of current tools
 - matching clinical to environmental
 - Faster identification of the food involved in the outbreak
 - Limited number of investigators vs. facilities and import lines
 - Global travel
 - Global food supply



Key elements of a national/international WGS network



GenomeTrakr Strategy

- Develop a distributed sequencing based network, rather than centralized model
- Provide sequence and minimal metadata in a publicly accessible database
 - Partner with NCBI for storage and serving data
 - Cost prohibitive for FDA to establish its own high capacity data site
 - Industry (food, pharma, and methods development), academia, hospitals, clinical public health laboratories, and other government agencies have access to data for individual needs (ie, BioFire Test Film – economic development, job creation)

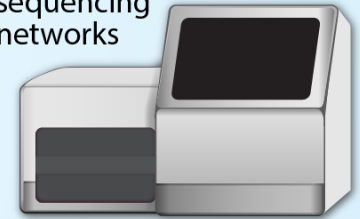
Basic Data Flow for Global WGS Public Access Databases

DATA ACQUISITION

Sequence and upload genomic and geographic data



Other distributed
sequencing
networks

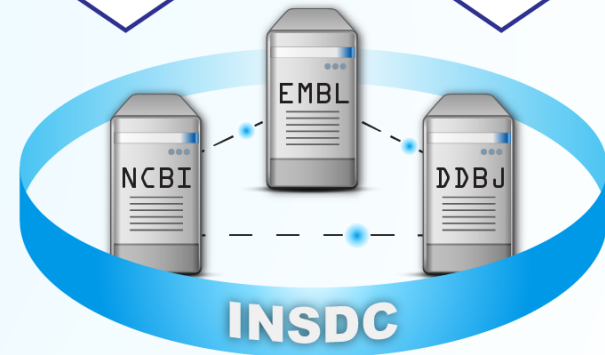


DATA ASSEMBLY, ANALYSIS, AND STORAGE

International Nucleotide Sequence Database Collaboration (INSDC)

Shared Public Access Databases

- NCBI – National Center for Biotechnology Information
- EMBL – European Molecular Biology Laboratory
- DDBJ – DNA Databank of Japan

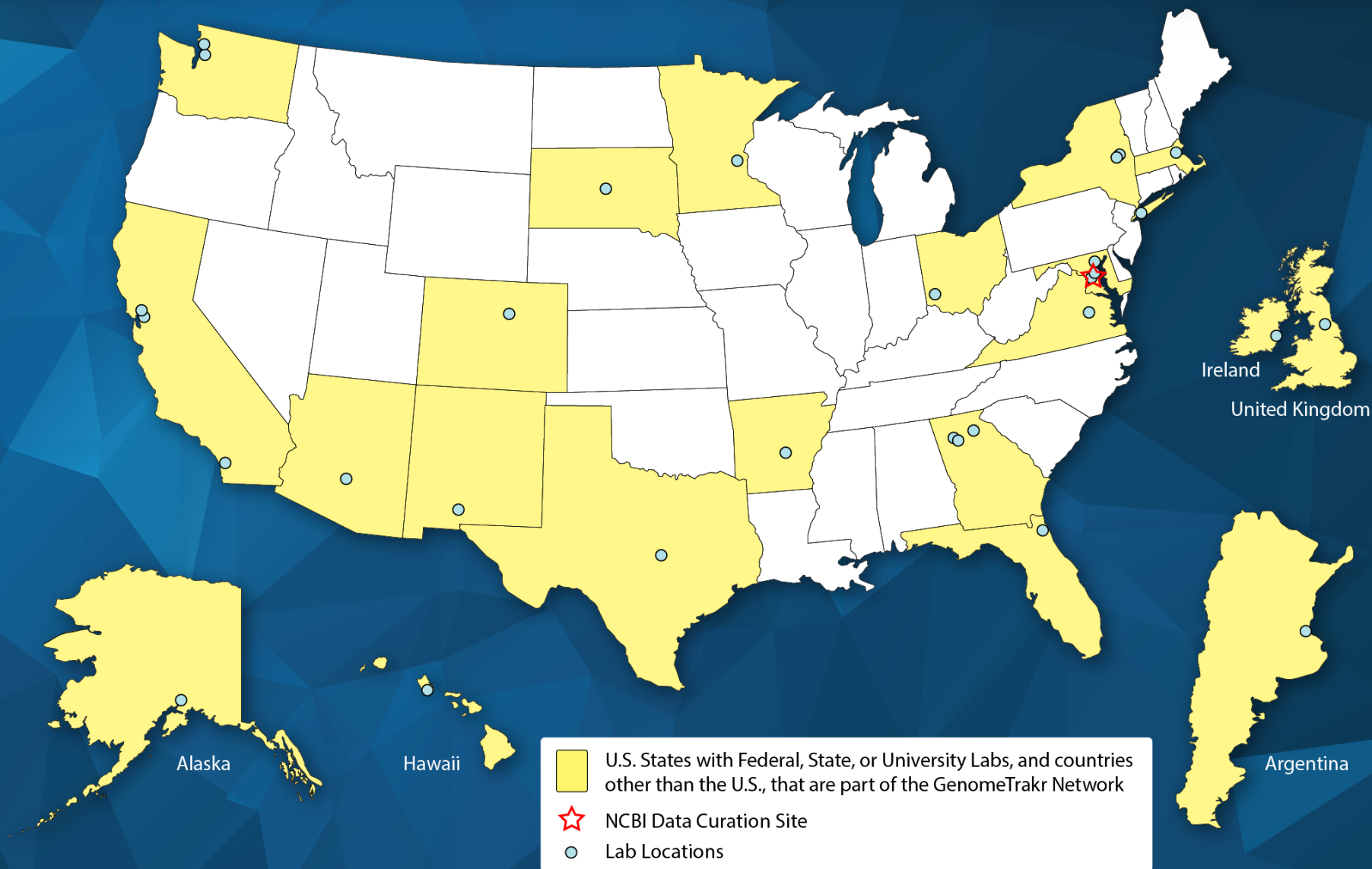


PUBLIC HEALTH APPLICATION AND INTERPRETATION OF DATA

- Find clinical links
- Identify clusters
- Conduct traceback
- Develop rapid methods
- Develop culture independent tests
- Develop new analytical software

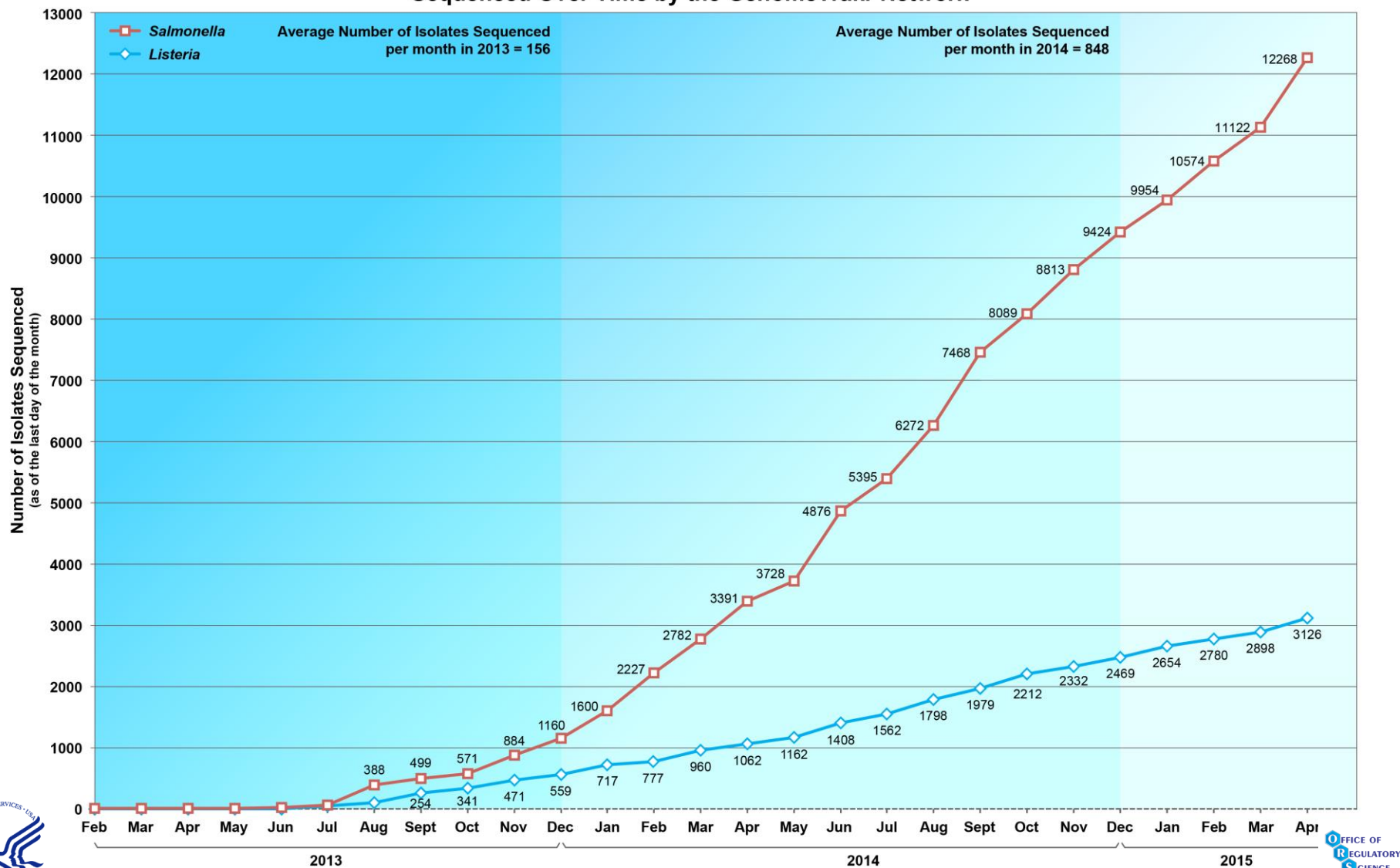


GenomeTrakr Labs





Cumulative Number of *Salmonella* and *Listeria* Isolates Sequenced Over Time by the GenomeTrakr Network







Real-time Integration of WGS into FDA regulatory workflow



DEPARTMENT OF HEALTH AND HUMAN SERVICES

Food and Drug Administration
Silver Spring, MD 20993

March 11, 2014

[REDACTED] t

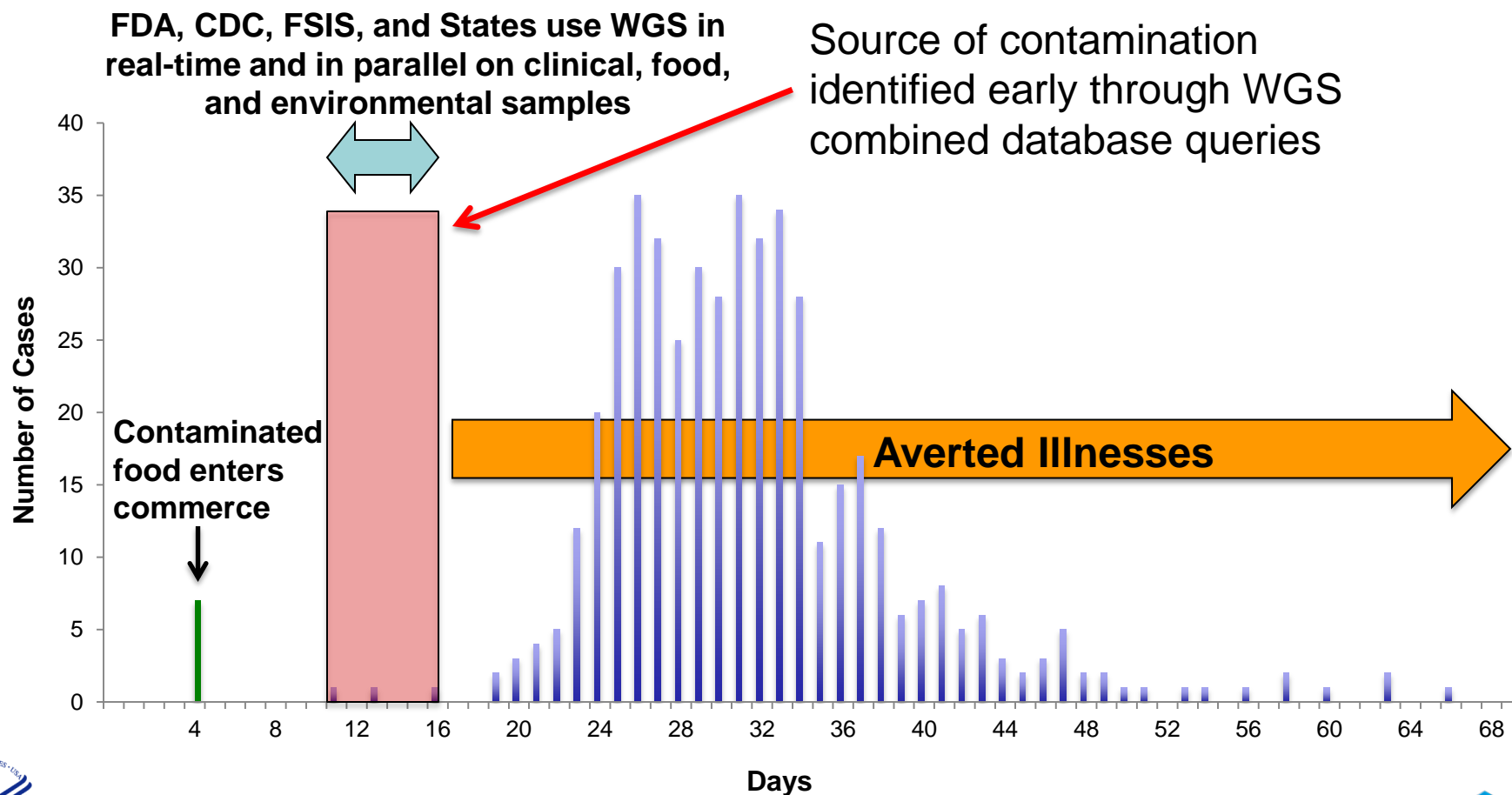
Roos Foods Inc.
251 Roos Lane
Kenton, DE 19955

ORDER: Suspension of Food Facility Registration Notice of Opportunity for Hearing

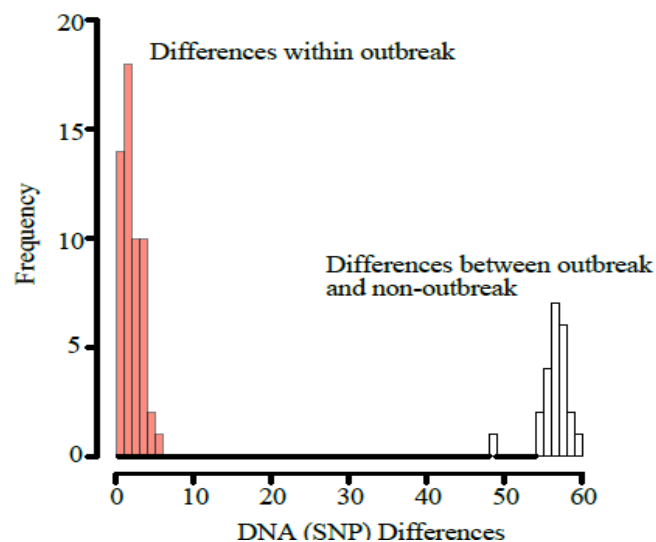
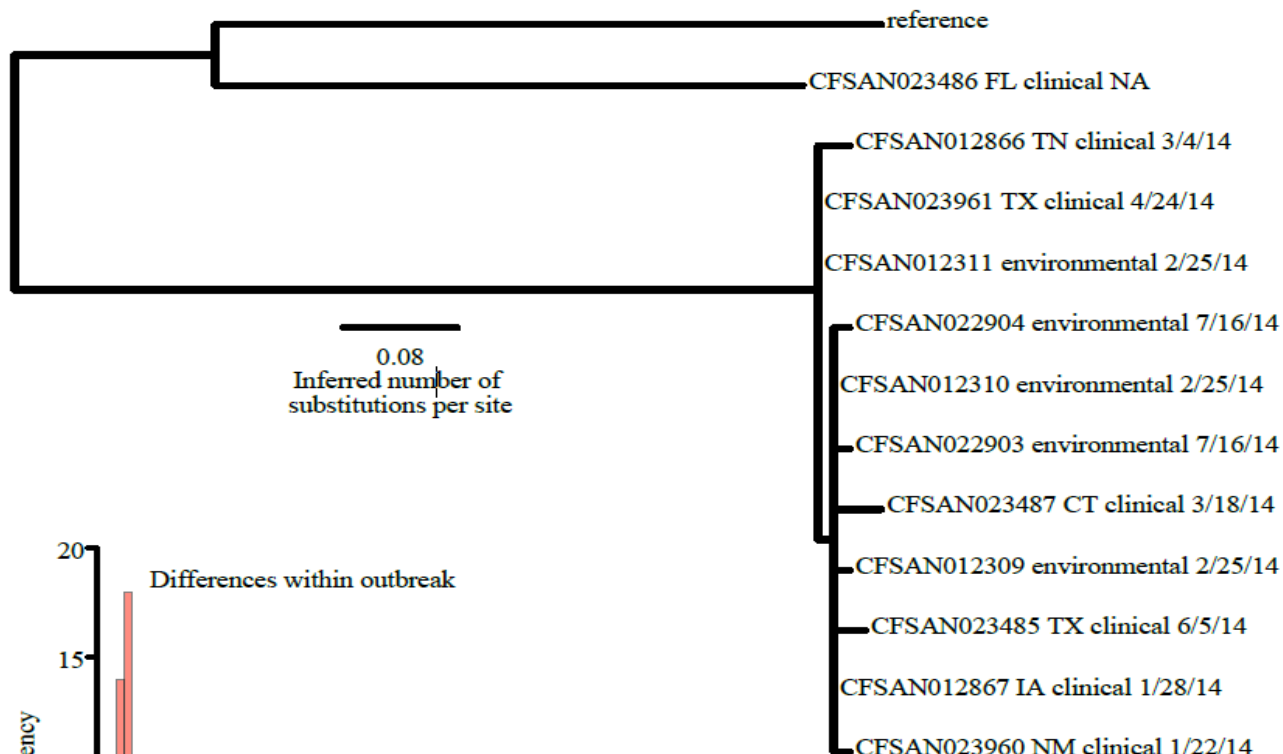
[REDACTED]

The U.S. Food and Drug Administration (FDA) hereby issues this Order to suspend the registration of your food facility, Roos Foods, Inc. (Roos), located at 251 Roos Lane, Kenton, DE 19955. Your food facility was registered with FDA pursuant to section 415(a) of the Federal Food, Drug, and Cosmetic Act (FD&C Act) (21 U.S.C. 350d(a)) on June 4, 2013. Section 415(b)(1) of the FD&C Act provides, in relevant part, that if FDA determines that a food manufactured, processed, packed, received, or held by a facility registered under section 415 has a reasonable probability of causing serious adverse health consequences or death to humans or animals, FDA may by order suspend the registration of a facility (1) that created, caused, or was otherwise responsible for such reasonable probability; or (2) that knew of, or had reason to know of, such reasonable probability, and packed, received, or held such food.

Timeline for Foodborne Illness Investigation Using Whole Genome Sequencing



S. Braenderup





Health and Economic Impact of Active WGS-based Surveillance

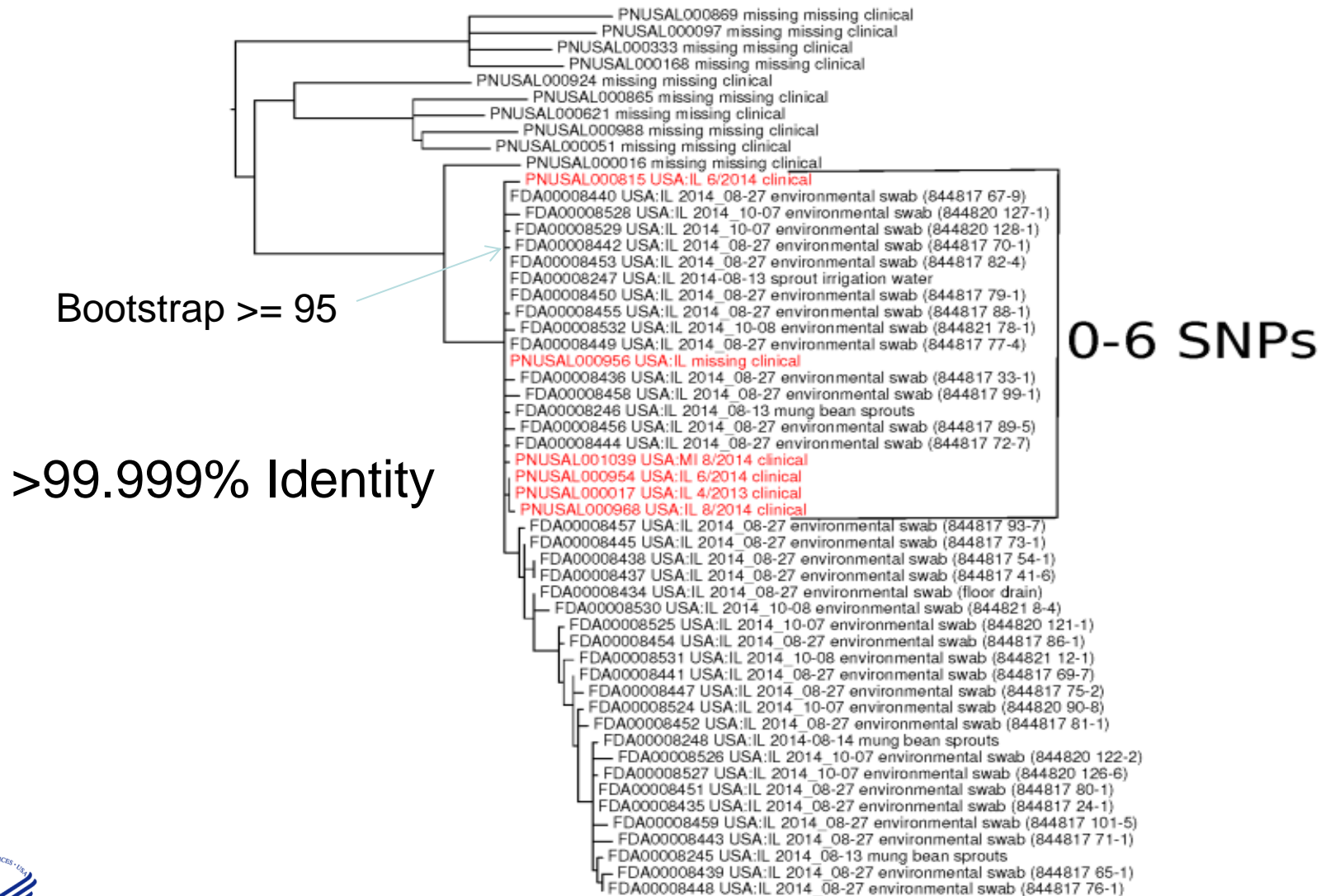
Comparison of 2 related contamination events.

- ☐ **Similar facilities – broad domestic distribution.**
- ☐ **Nut butter 1: 42 cases and 10 hospitalizations with as many as 1,260 illnesses unreported (Fall 2012)**
- ☐ **Nut butter 2: – 4 confirmed cases, 1 hospitalization (Summer 2014)**
- ☐ **WGS informed investigation prevented significant illness and hospitalizations**
 - **lower illness rate and treatment cost (\$14,000 per hospitalization and \$445 physician visit) + fraction of loss of productivity, long-term and chronic onset complications associated with Salmonella infection**

Example: *L. mono* in sprouts



1. Food and environmental samples collected as part of a routine inspection at a sprout facility
 - *L. mono* detected in 3 swabs
2. WGS analysis showed these isolates to be a match to recent clinical isolates sequenced as part of the CDC Real-Time Listeria project
3. Re-inspection of the facility found additional positive environmental *L. mono* positives
4. WGS analysis showed that the original food/environmental isolates, re-inspection environmental isolates, and clinical isolates from this period to be a match.

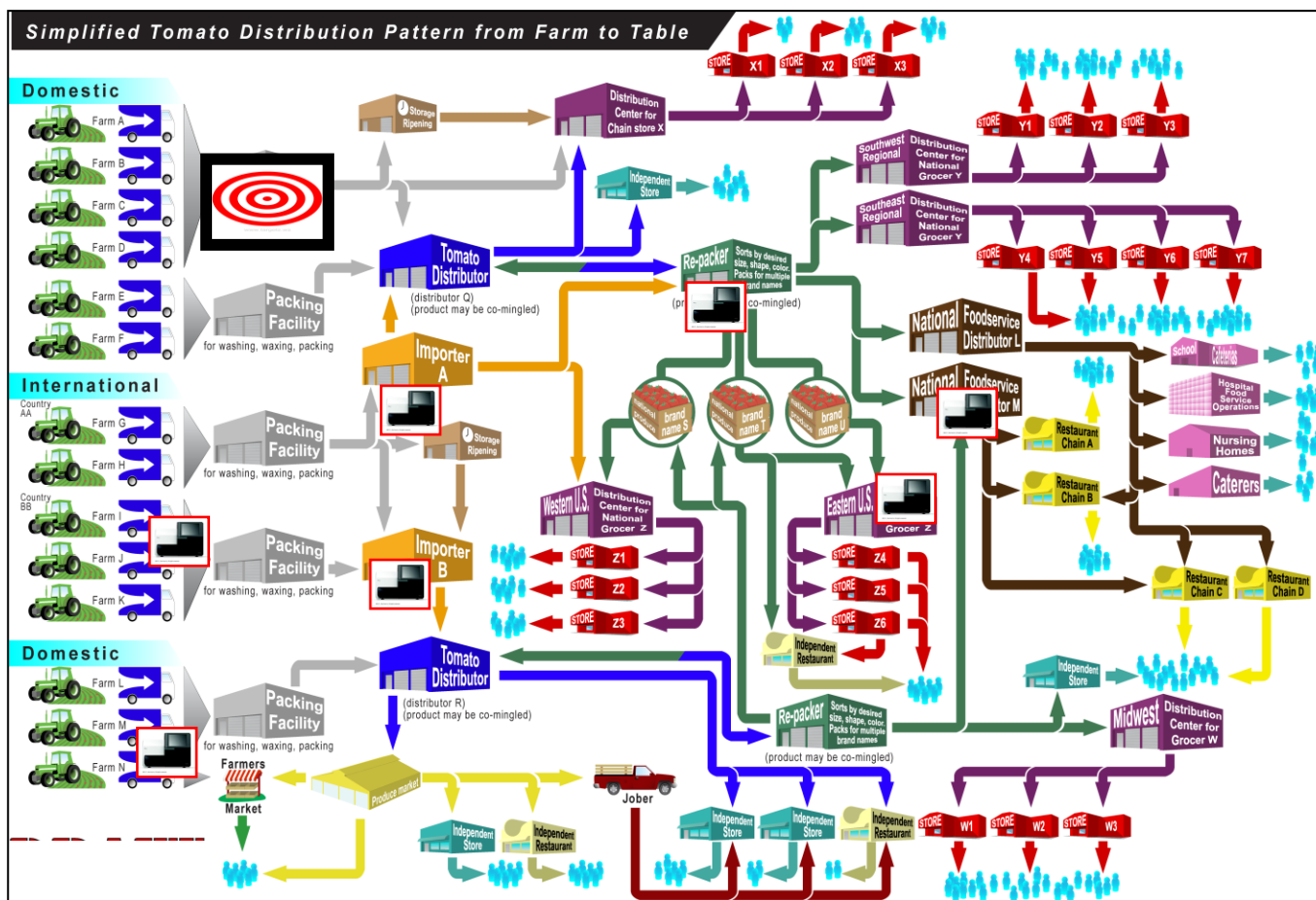


Current Status

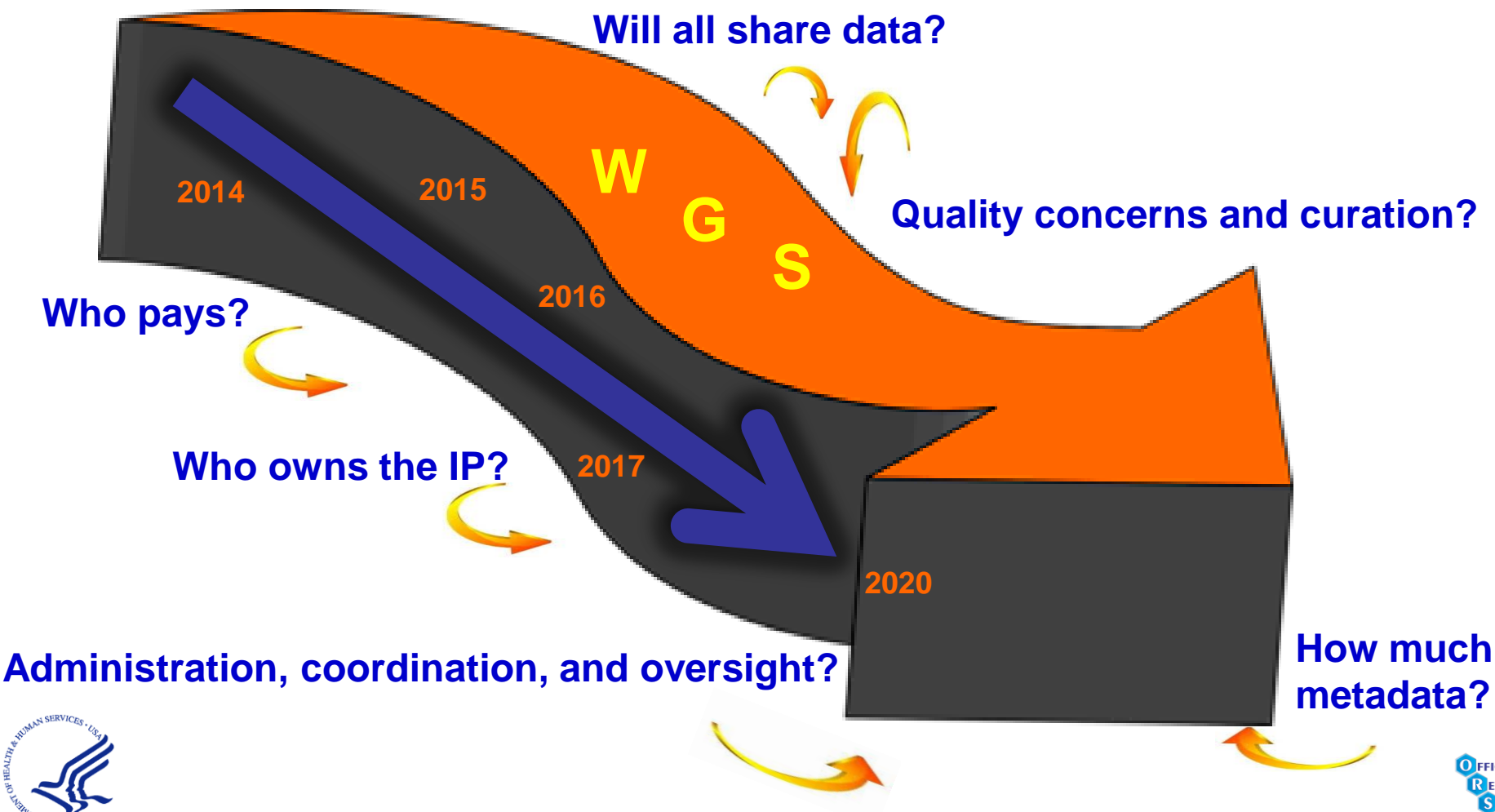
- NGS clearly defines foodborne outbreaks – more than 15 different examples
- NGS network is reliable, efficient and can provide very good location specificity of outbreaks
- GT collaborators have sequenced more than 15,000 *Salmonella*, more than 4,000 *Listeria monocytogenes*, and closed 100 genomes for outbreak mapping. Our current rate is about 600 draft sequences a month or 1 genome per hour.
- The need for increased number of well characterized environmental (food, water, facility, etc.) sequences may outweigh need for extensive clinical isolates
- Highly successful partnership with CDC on real-time tracking of *Listeria* outbreaks but need to expand into other pathogens like *Salmonella* (#1 most devastating foodborne pathogen)

Industry Potential

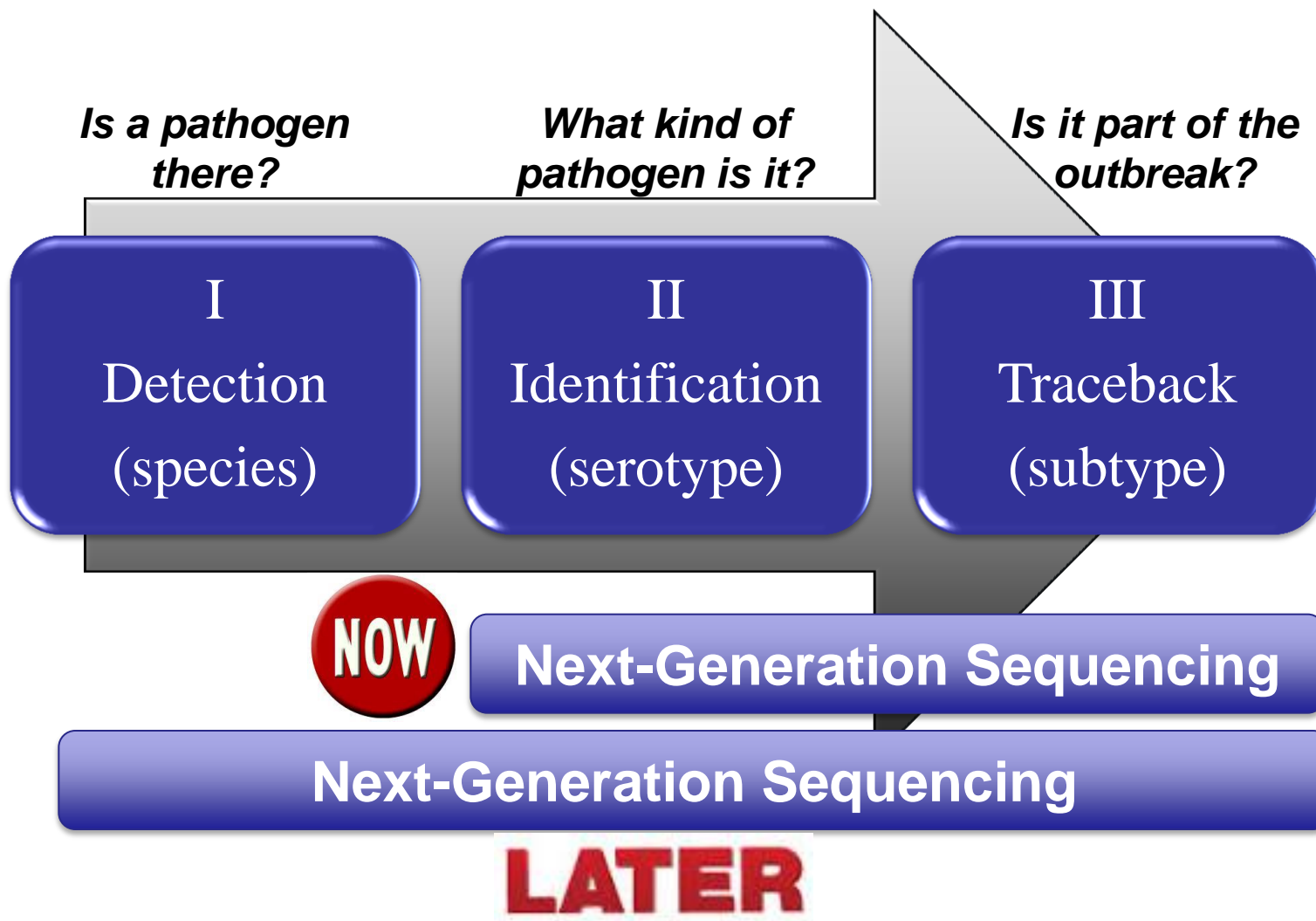
WGS-based monitoring can pinpoint root causes in the Fresh-cut Produce Supply Chain:



Next-Generation sequencing faces several large challenges as it deploys to a global public health tool:



Investigating Food Contamination Events with OMICS Approaches





Acknowledgements

- **FDA**
 - Center for Food Safety and Applied Nutrition
 - Center for Veterinary Medicine
 - Office of Regulatory Affairs
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 - National Center for Biotechnology Information
- **State Health and University Labs**
 - Alaska
 - Arizona
 - California
 - Florida
 - Hawaii
 - Maryland
 - Minnesota
 - New Mexico
 - New York
 - South Dakota
 - Texas
 - Virginia
 - Washington
- **USDA/FSIS**
 - Eastern Laboratory
- **CDC**
 - Enteric Diseases Laboratory
- **INEI-ANLIS “Carlos Malbran Institute,” Argentina**
- **Centre for Food Safety, University College Dublin, Ireland**
- **Food Environmental Research Agency, UK**
- **Public Health England, UK**
- **WHO**
- **Illumina**
- **Pac Bio**
- **CLC Bio**
- **Other independent collaborators**