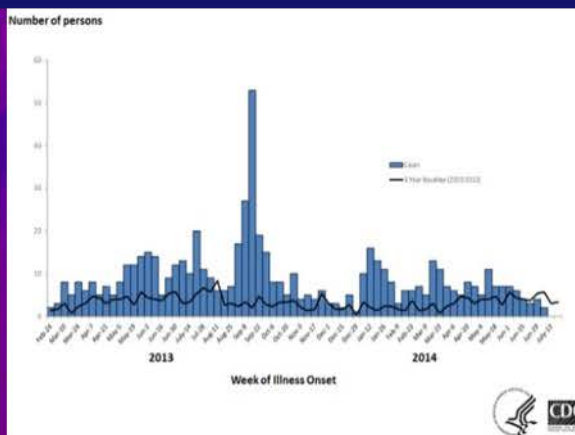
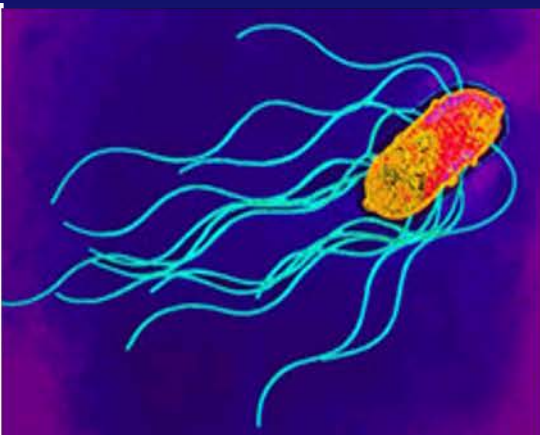
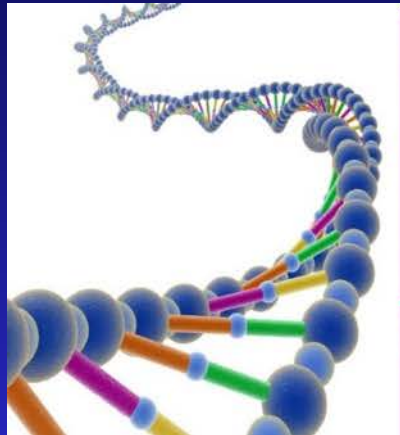


# Whole genome sequencing and the transformation of public health surveillance (for enteric infections)



## Georgia Emerging Infections Program Annual Conference

March 24, 2017

Atlanta, Georgia

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Director,

Division of Foodborne, Waterborne, and Environmental Diseases

National Center for Emerging and Zoonotic Infectious Diseases

Centers for Disease Control and Prevention





1946 Atlanta

2012 Bldg 24



## What does CDC do?

Protect the health of the public with expert science, by:

- Informing with reliable scientific information for decision makers
- Protecting everyone's health by detecting, solving, stopping and preventing outbreaks
- Innovating to improve scientific methods to public health challenges
- Building capacity in local and state health departments and international partners

***Partnership is vital to everything we do***

# Looking forward – a few broad themes

- Bringing WGS into daily practice in public health labs for characterizing and subtyping enteric bacteria
- Increasing investigative capacity in state and local health departments
- New strategies for diagnosis – in clinical laboratories and ultimately in the public health labs as well.
- Expanding partnerships
  - Interagency
  - Public-private
  - International

# Improving information for decision making

- Updating the estimates of health burden of enteric illness
  - Starting the new FoodNet population survey in April
  - 2 year cycle, multimodal surveys
- Use to adjust health burden, trends and food source estimates for changes in
  - Diagnostic tests,
  - Physician behavior
- New attribution estimates with expert elicitation for
  - % of infections coming from different pathways:
  - food, water, animal contact, person-to-person contact

***Result: New general estimates of burden of foodborne illness***

## Making our information more available

- FoodNet Fast
  - Interactive display of graph and tables of FoodNet data
  - Will add more capabilities and mapping
  
- Web reports on major multistate foodborne outbreaks
  - Will add: more investigative details, relevant to industry
  
- CDC Foodborne Outbreak Online Database (FOOD) Tool
  - Interactive search and summary of reported foodborne outbreaks
  - Will add: ability to search waterborne, animal contact and person-to-person outbreaks for enteric pathogens
  
- CDC NARMS NOW
  - Interactive display of resistance by drug and pathogen
  - Will add: ability to display selected groups of resistance

# A surveillance network combines strain subtyping and patient interviews

- Detecting a dispersed outbreak among many sporadic cases
  - Means finding the signal in background noise
  - Depends on the surveillance system in use
  - Identifies food safety gaps early in food production
- Starts with the report of a diagnosed illness, and referral of isolate
  - Interview the patient
  - Subtype the strain in a public health laboratory
- Subtyping methods have been improving over time

# Improved surveillance with subtyping for foodborne bacterial pathogens

- 1940's - present: Routine clinical laboratory cultures
- 1960's - present: Serotyping (*Salmonella*, *Shigella*)
- 1980's - 1990's: Plasmid profiles
- 1996 - Present: PulseNet molecular subtype-based surveillance (based on PFGE)
  - *E. coli* O157/STEC
  - *Salmonella*
  - *Listeria*
  - *Shigella*
  - *Campylobacter*

# PulseNet 1996-2016: National network for molecular surveillance of bacterial enteric infections



Links with:

- PulseNet Canada
- VoluntaryNet (food industry)

Standard PFGE method  
Results in CDC database  
All participants can use

87 labs participate:

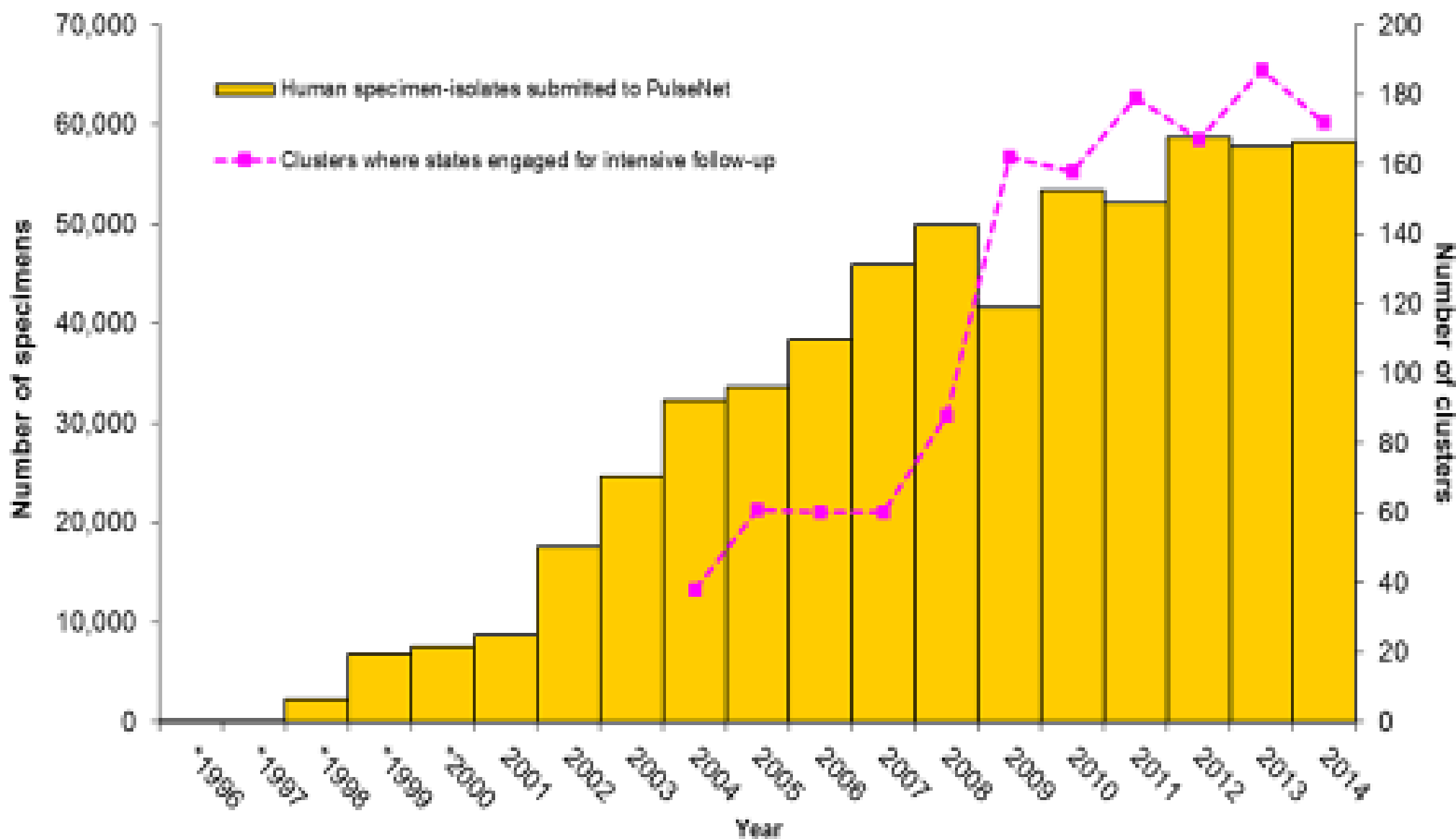
- All state health departments
- City health departments
- FDA laboratories
- FSIS laboratories

50,000 bacteria/year from

- ill people
- foods
- animals



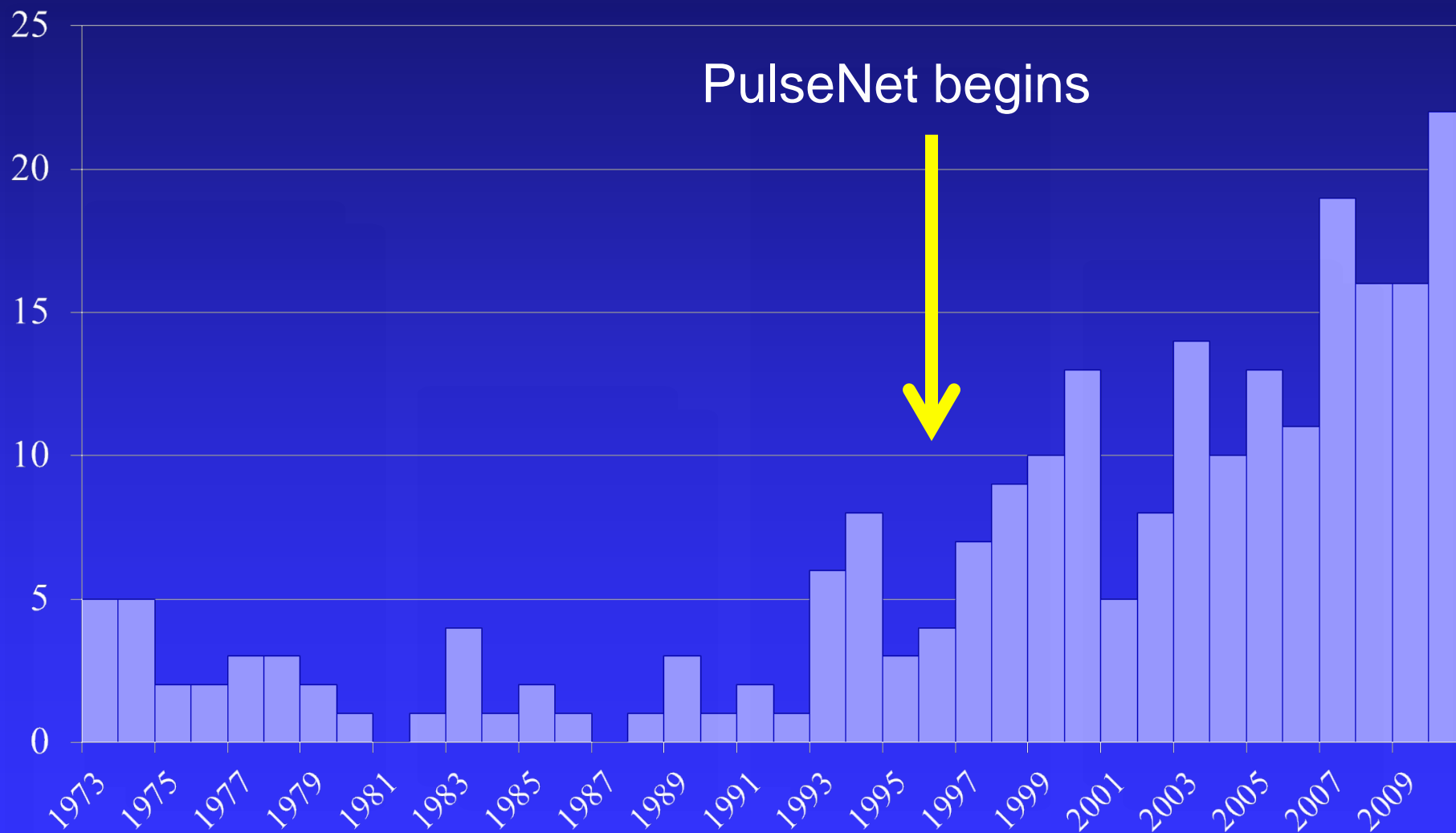
# Human Specimen Isolates Uploaded to PulseNet USA and Identified Clusters, 1996-2014<sup>†</sup>



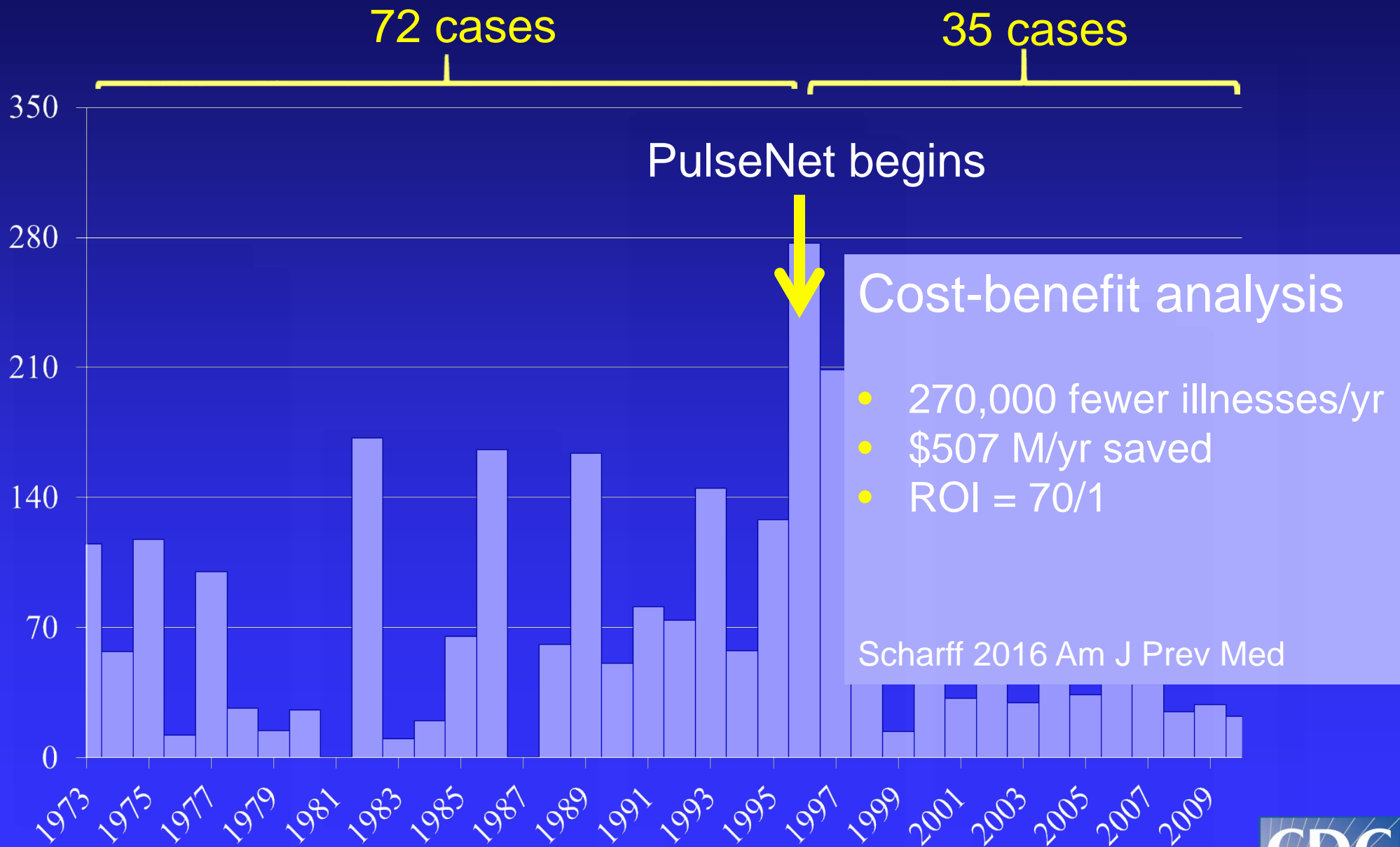
<sup>†</sup> Data are preliminary and subject to change

\* data type information may not be complete for these years

# Multistate foodborne outbreaks reported to CDC 1973-2010



# Median size of multistate foodborne outbreaks reported to CDC 1973-2010



# Novel foods implicated in outbreaks since 2006 in the United States

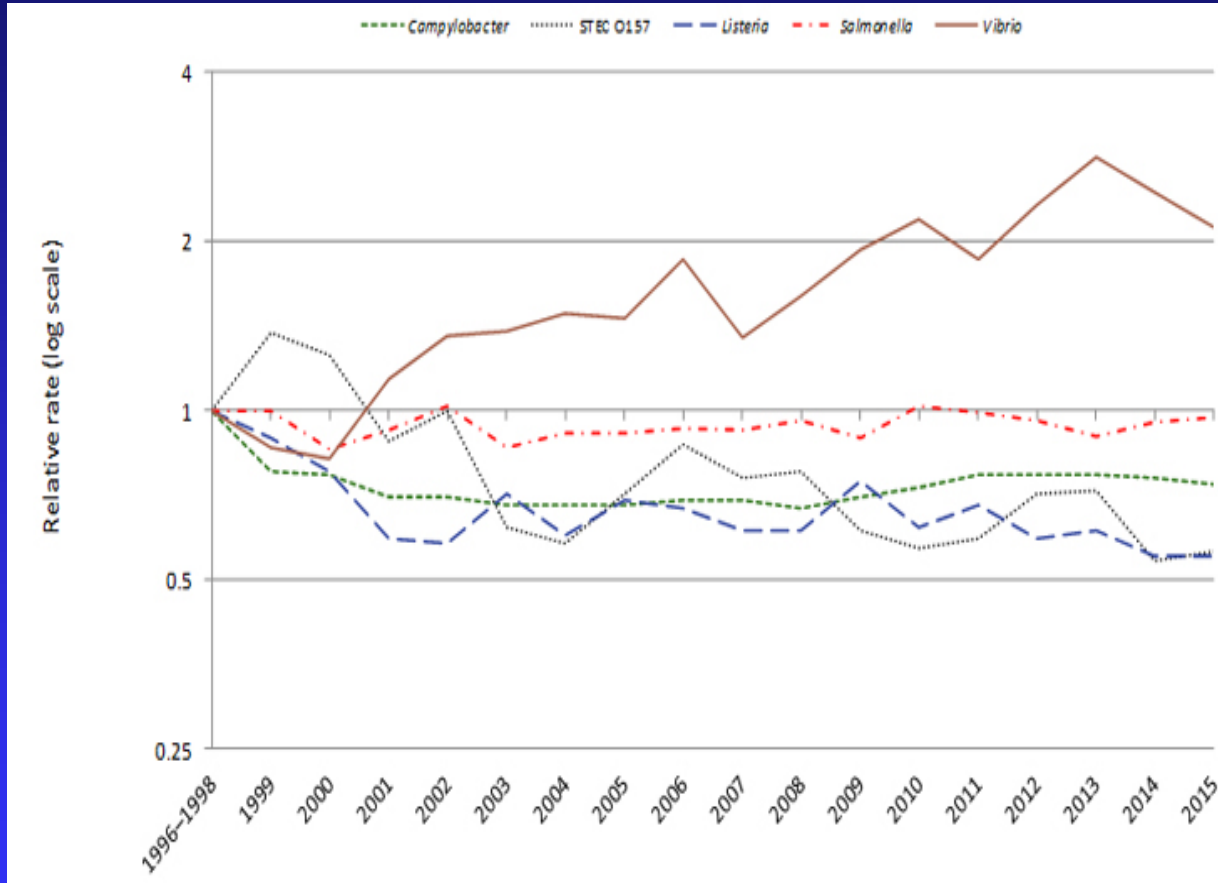
- Bagged spinach
- Carrot juice
- Peanut butter
- Broccoli powder on a snack food
- Dry dog food
- Frozen pot pies
- Canned chili sauce
- Hot peppers
- White and black pepper
- Raw cookie dough (flour?)
- Hazelnuts
- Fenugreek sprouts
- Papayas
- Pine nuts
- Raw scraped tuna
- Pomegranate anils
- Torshi
- Cashew nut cheese
- Cucumbers
- Chia sprout powder
- Cheeses cut on the same cutting board as other cheeses

All found  
as a result of multi-state  
investigations



# Trends in foodborne illness, United States, FoodNet, 1996-2015

Since 1996, accurate data on diagnosed infections from 10 sites, 15 % of population



← **Vibrio – increased**

← **Salmonella - no change**

← **Campylobacter,**

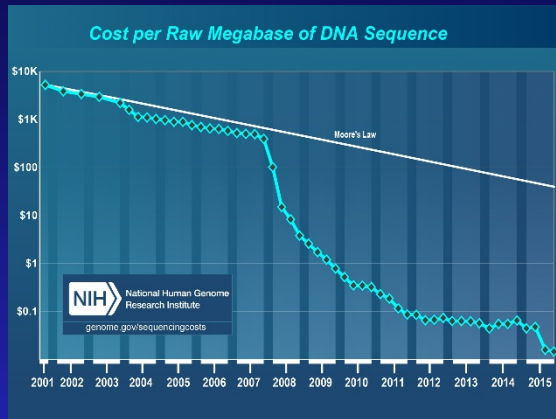
← ***E. coli* O157, and**

← **Listeria decreased significantly**

Since 2006-2008, only *E. coli* O157 has decreased significantly

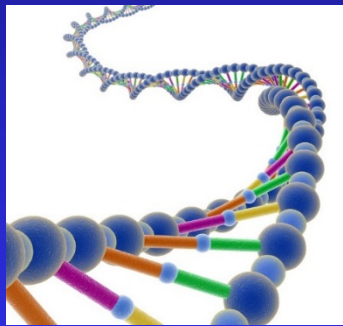
# Reading and comparing bacterial DNA sequences

## Big data meets microbiology



➤ In 15 years, cost and speed of sequencing DNA from a bacterium has dropped from \$100,000s and a year to \$100 and hours

➤ Reading and interpreting the whole genome sequence is faster and more automated



➤ 3M base pairs = 1800 pages of text

➤ Comparing alleles and sequences provides much greater precision than PFGE to say:

- Strains are closely related (and thus may have same source)
- Strains are not closely related, (and can be excluded from investigation)
- Strains from ill people are closely related to strains from suspect foods or environment (a clue to the source)

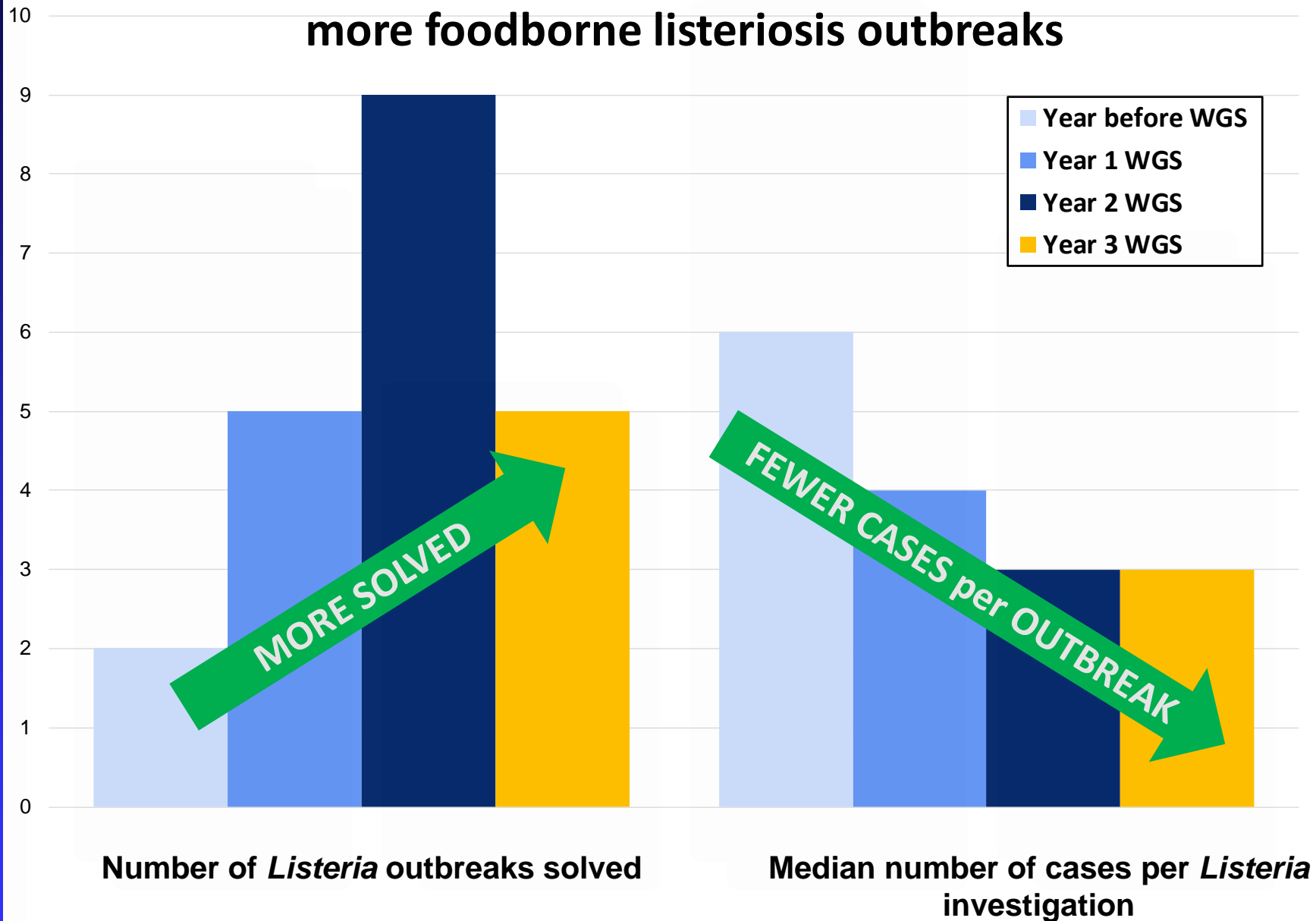
What happens if we use this new technology in PulseNet?

## 2013 Pilot project: Does WGS technology improve listeriosis surveillance?

- Since 1998, State public health laboratories have used PFGE in the PulseNet network for *L. monocytogenes*
- In 2013, collaborative multiagency effort began sequencing isolates of *Listeria monocytogenes* as part of routine surveillance
  - Clinical isolates at CDC (~800/year),
  - Food isolates at FDA, USDA
  - WGS data stored at NIH
- State health departments interviewed all listeriosis cases
- Coordination with Canada, UK, France, Denmark, Australia



## Surveillance based on DNA Sequencing: Solving more foodborne listeriosis outbreaks





# Foods implicated in listeriosis outbreaks since 2013 in the United States (in the WGS era)

## ➤ Expected foods:

- Raw milk
- Soft cheeses
- Mung bean sprouts
- (Not processed meats)

## ➤ Novel foods:

- Caramel-dipped apples
- Ice cream
- Packaged leafy green salads
- Stone fruits (nectarines)
- Frozen raw vegetables

Found as a result of  
multi-state investigations

Contamination often  
occurred at the packing  
shed or processing facility

Most investigations started  
with ill people. A few  
started with finding *Listeria*  
in a food, that matched  
strains from patients who  
ate that food

***New efforts in food industry now to  
reduce contamination with listeriosis***

# Listeria and raw milk, 2014-2016

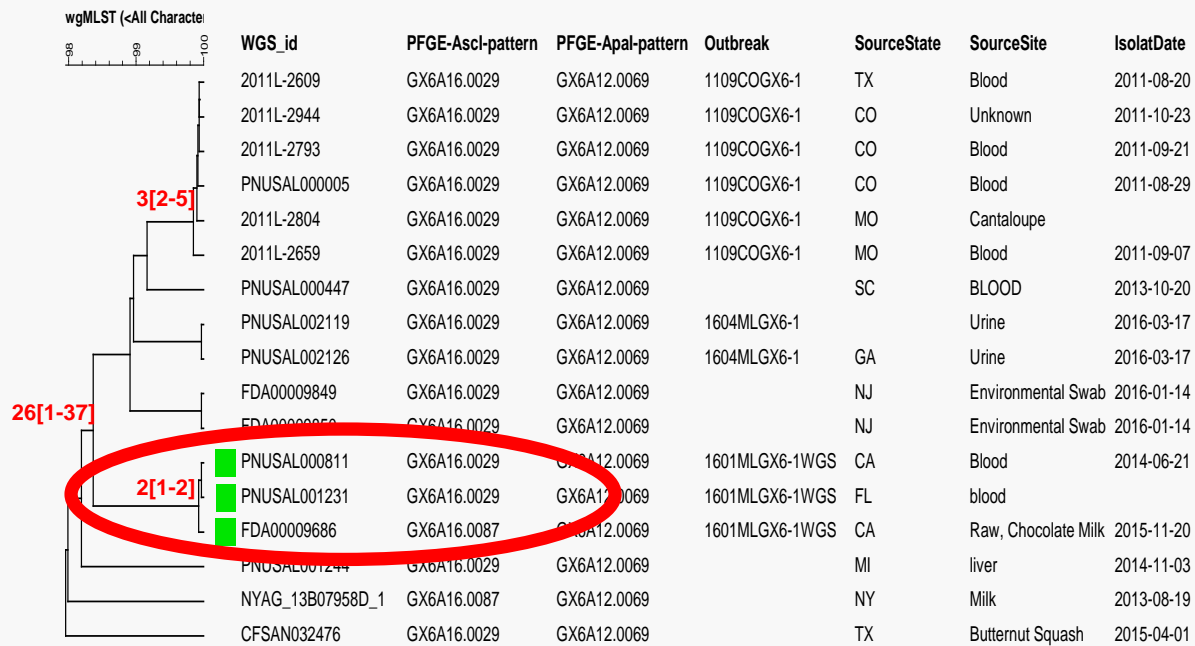
- November 2015: FDA collected raw milk sample at a raw milk conference in CA
- January 2016: *Listeria* isolated from raw milk, WGS matched 2 infections from 2014
- Patients in FL and CA
- Mean age 77: both hospitalized, 1 died
- PFGE: Two different patterns
- WGS: Extremely close: Within 2 SNPs

By PAULA COHEN / CBS NEWS / March 18, 2016, 4:12 PM

## Deadly listeria outbreak linked to raw milk



A 2014 listeria outbreak has been traced to raw milk. / OKSANA BRATANOVA

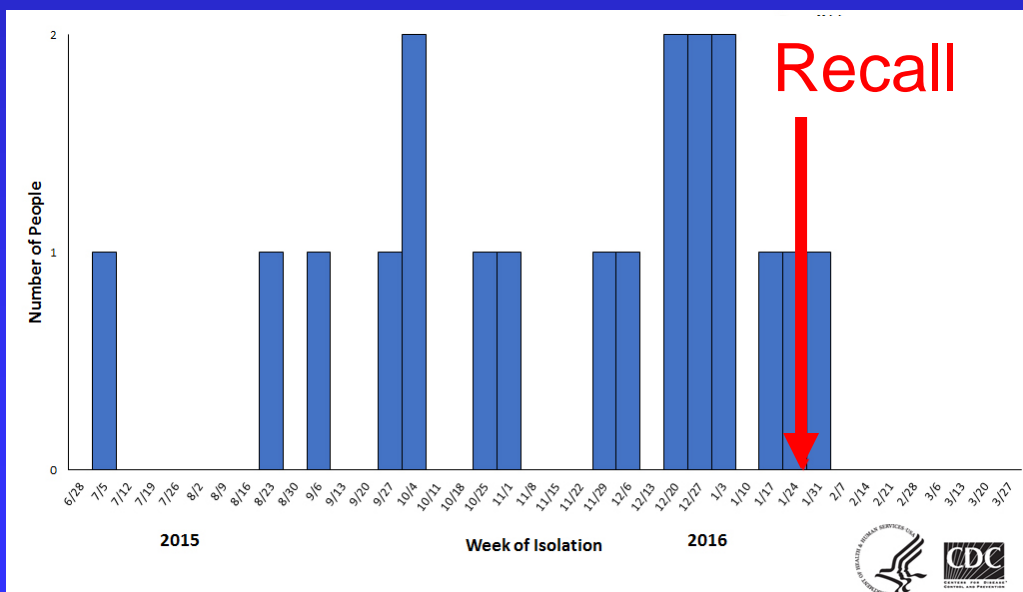
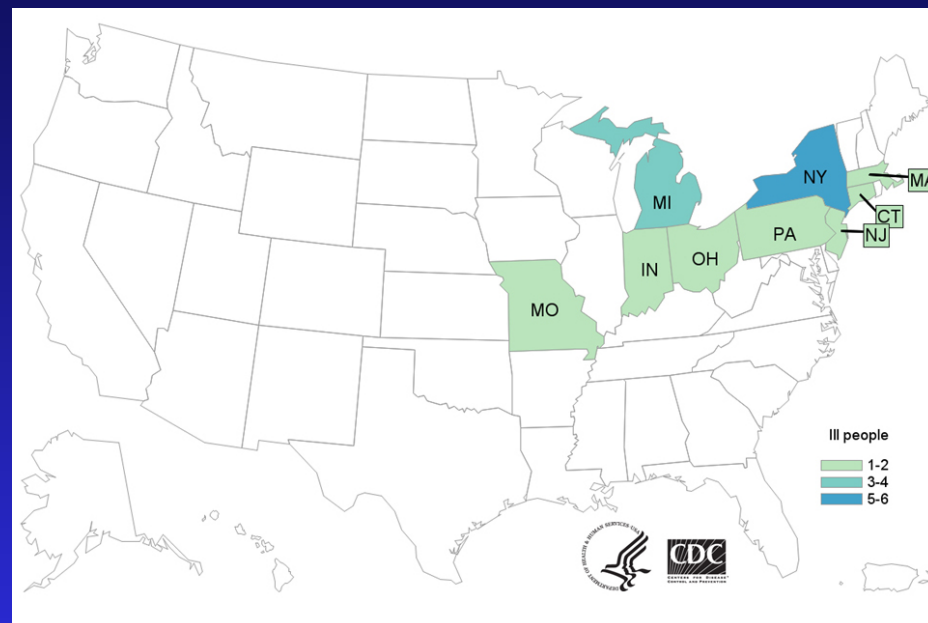


- Both drank raw milk
- One reported to get milk online from same PA farm that FDA had sampled
- Source of other unclear
- PA farm sold milk interstate over the web
- Private membership organization
- March 18: CDC warned public

[www.cdc.gov/listeria/outbreaks/](http://www.cdc.gov/listeria/outbreaks/)

# Listeria and bagged salads, 2015-2016

- July 2015 - Jan 2016
- 19 cases in US, 14 in Canada (33 total)
- Closely related by WGS
- 9 states, 5 provinces
- All hospitalized, 4 died
- Median age 64 years, 74% female
- 13/14 ate bagged salad, 9 named 1 brand
- WGS match to *Listeria* from same brand
  - regulatory salad sample in Ohio
  - bagged salad tested in Canada



- Concern focused on multiple products made at one packaging plant in Ohio
- CDC and FDA shared information with company
- Halted production, and recalled product
- Plant closed for 4 months
- Intensive assessment, sanitation
- New program of in-plant monitoring

# Salmonella Enteritidis (SE) and frozen stuffed breaded raw chicken products – Minnesota, 2015

- Minnesota DH began sequencing SE
- Found 2 clusters in summer of 2015
- Cluster #1: 5 illnesses
- Ate one brand of frozen stuffed breaded raw chicken entrée
- Same strain found in product
- Product distributed to many states
- 2.4 M pounds recalled



www.fsis.usda.gov



- Cluster #2: 15 illnesses (including 7 in other states)
- Ate a different brand of frozen stuffed breaded chicken products
- Same strain found in frozen product
- Product distributed to many states
- 1.7 M pounds recalled

- Most patients knew the product was raw, and followed cooking instructions
- Some even checked the internal temperature
- UDSA now considering further standards for products like this

[www.cdc.gov/salmonella/outbreaks/](http://www.cdc.gov/salmonella/outbreaks/)

and thanks to Carlota Medus

# Value added by using whole genome sequencing

- Close genetic similarity means greater confidence that a group of infections may share a common origin, so more focused investigations
  - Split up common PFGE patterns into more related subgroups
  - Join strains with different PFGE types that are closely related
  - Compare strains from foods, animals, and production environments
  - Better determination of which cases to interview, which to exclude
- Whole genome sequencing as part of public health surveillance can
  - Replace serotyping, toxin typing, resistance testing
  - Provide fine-grained subtyping that is phylogenetically relevant
  - Like serotyping in the 1960's, PFGE in the 1990's, detecting clusters
- Empowers epidemiologists, rather than replacing them
  - Still need to find out what patients ate, that others did not
  - Still need to trace foods to their sources

## Improving our ability to detect, solve and stop outbreaks

- Routine whole genome sequencing is swiftly becoming part of routine public health surveillance
- 3 year collaborative pilot using WGS with *Listeria* 2013 – 2016
- Now placing WGS capacity in state and city health departments
  - Starting with *Listeria*
  - Expanding to STEC, *Salmonella*, *Campylobacter*, *Shigella*...
  - Likely to start finding more clusters
  - Expanding investigative capacity in states as well

***Anticipate using WGS as main subtyping method in 2019***

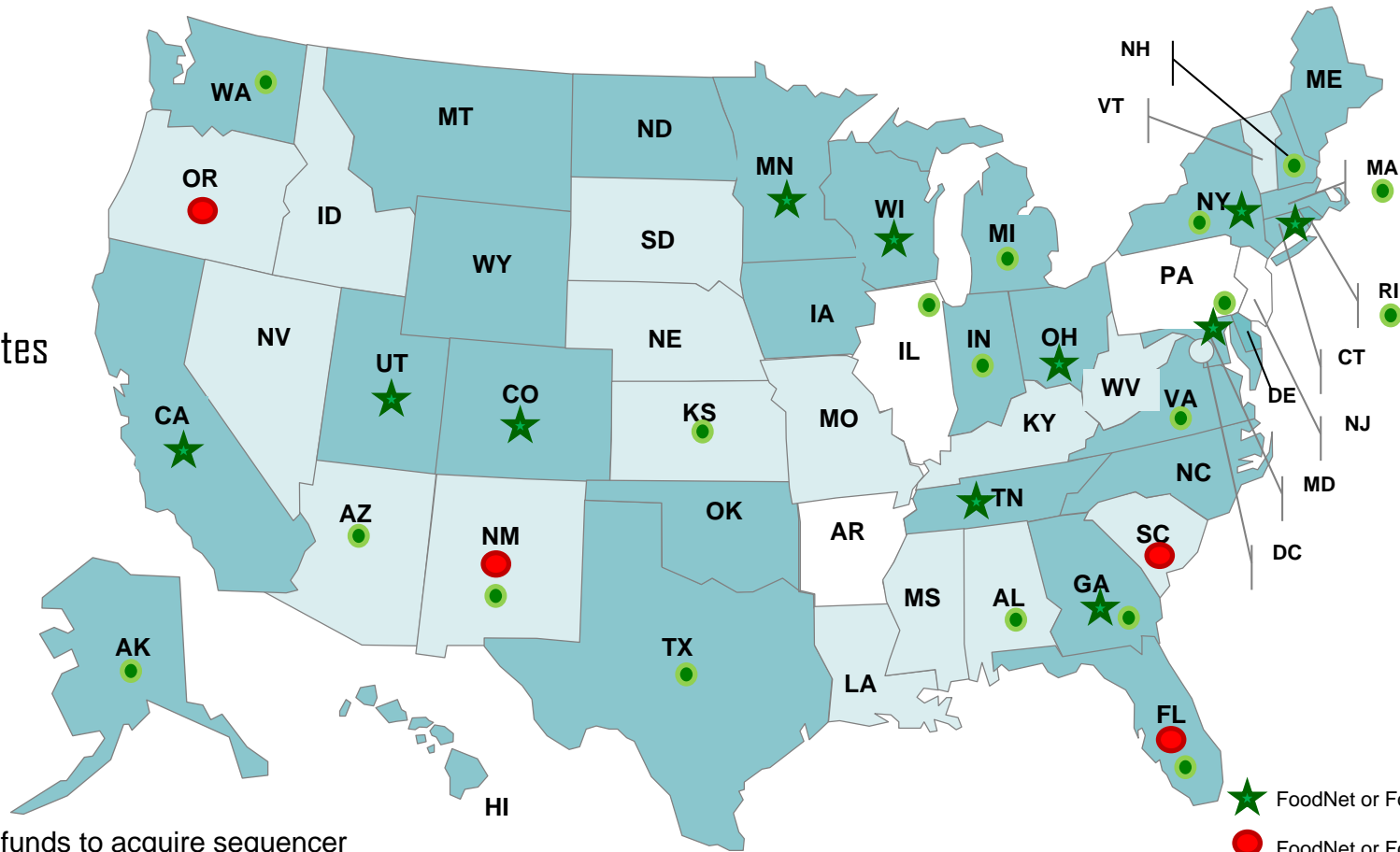
# Accelerating deployment of WGS is part of the plan to Combat Antibiotic Resistant Bacteria

- 2016 Federal Budget included support for CDC to address the threat of antimicrobial resistance in many pathogens, including some foodborne ones (The Combatting Antibiotic Resistant Bacteria plan, or CARB)
- With WGS, resistance is known as soon as an outbreak of *Salmonella* infections is detected
- Outbreaks caused by multi-drug resistant (MDR) strains can be prioritized for investigation and control
- Goal: Reduce MDR *Salmonella* infections by 25% by 2020

# PulseNet Sequencing Capacity – February 2017

33 labs in 30 states certified;

4 states without sequencers



- Awarded ELC funds to acquire sequencer
- Has sequencer but not certified
- PulseNet certified

- FoodNet or FoodCore with WGS capacity
- FoodNet or FoodCore without WGS capacity
- Outbreak Net Enhanced



# Innovation – After Whole Genome Sequencing, what do we do for an encore?

- WGS depends on
  - Isolating of a pure culture
  - Shipping it to the public health laboratory
  - Sequencing and interpreting
  - *Can take a week*
- To make surveillance faster, public health needs more advanced molecular diagnostic tools for use on the clinical specimen that
  - Provide species identification
  - Predict serotype, virulence, antimicrobial resistance, subtype
  - Report results in hours, rather than days
- We and others have begun exploratory work in this area
  - Amplifying around key targets, like Shiga toxin-coding phage genes
  - Metagenomic approaches with long-read sequencing
  - Single cell sequencing

***Will be of great use where cost and complexity prohibit culture***

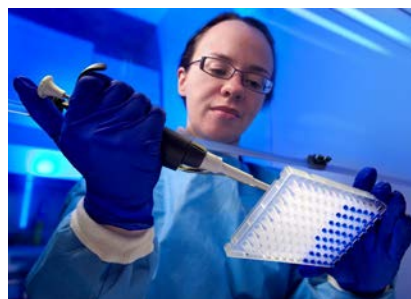
# Diagnostic Methods Through Time



1860s:  
**Culture-based tests**  
Invented by Louis Pasteur, Robert Koch, et al



1980s-90s:  
**Antigen-based tests**  
Detects antigens specific to pathogen type



2000s:  
**Polymerase Chain Reaction (PCR) tests**  
Detects short genetic sequences specific to pathogen type



2010s:  
**Multiplex PCR panels**  
Uses PCR to detect multiple pathogens simultaneously, often designed for disease syndromes

**Culture-independent Diagnostic Tests**

# Innovation – The culture-independent diagnostic tests (CIDTs) are starting to change clinical practice

- The most popular CIDT platform tests for 22 pathogens in an hour
- Physicians can now base immediate treatment decisions on lab diagnosis
- Test routinely for pathogens rarely considered before
  - *Cryptosporidium*
  - Enterotoxigenic *E. coli*
  - Norovirus
  - *Vibrio parahaemolyticus*
  - *Yersinia enterocolitica*
- Laboratory workflow is simplified
- Rapidly increasing in use

# Innovation – CIDTs will likely lead to increases in reported case numbers

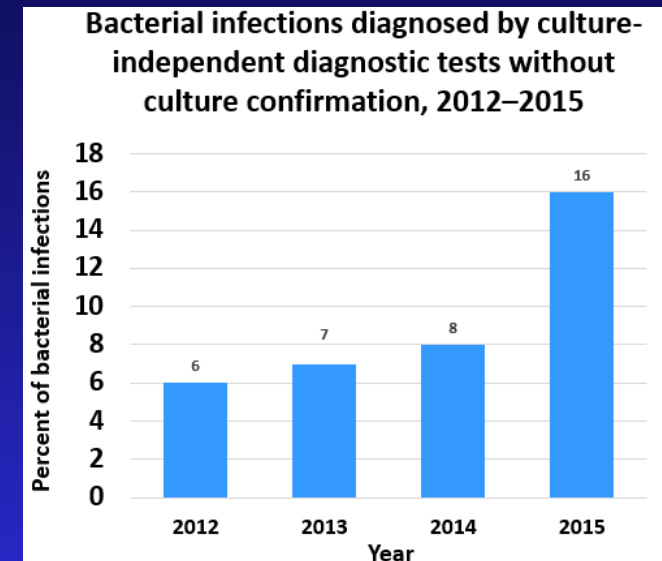
Use of CIDTs in clinical practice may increase

- Likelihood of testing (which drives reported case numbers up)
- Sensitivity of detection, perhaps because the test identifies damaged or dead organisms in the specimen (which drives reported case numbers up)
- Reports of infections that were previously rarely diagnosed (which drives those case numbers up even more)

*We are developing models to account for these effects, so that we can continue to track progress in prevention*

# Innovation – Minding the gap, as culture-independent diagnostic tests (CIDTs) become more common

- FoodNet tracks the uptake of CIDTs
- Between 2012 and 2015, bacterial infections identified only by CIDT, without culture confirmation, went from 6% to 15%
- As CIDTs become more common, we see a gap as fewer cultures are available to public health
- To preserve access to isolates, states are changing their disease reporting requirements to encourage “reflex culture”
- Culture CIDT-positive specimens at clinical lab, or ship specimen to public health laboratory
- Public health surveillance will depend on those isolates for at least the next 5 years



# Culture-independent diagnostic tests: Challenges to public health programs

- Current CIDT platforms do not provide isolates
- Public health currently depends on the isolate to:
  - Detect and investigate outbreaks
  - Track cases and trends accurately
  - Estimate the overall burden from specific sources
  - Track changes in antimicrobial resistance
  - Drive public health prevention

# Meeting the challenge to public health of culture-independent diagnostic tests

- Shorter term: Preserve access to isolates:
  - Work with medical community, state public health labs, FDA and diagnostic testing industry, clinicians
  - Request reflex culture of positive specimens to confirm them, and provide isolates
  - In clinical labs or public health labs
- Longer term: Diagnostic assays that get critical information directly from stool specimen, that are culture-independent
  - Selective amplification at diagnostic regions of genome?
  - Metagenomic shotgun sequencing?
  - Single cell sequencing?

# Evolutionary path of public health surveillance

## Preparing for a culture-independent environment

Surveillance using  
current methods  
(serotype, PFGE, etc.)

1) Need cultured isolates:  
Reflex culture of  
specimens positive in  
multiplex PCR panels

Surveillance using  
whole genome  
sequencing (WGS)

2) Need reflex cultures:  
Develop large genome  
databases

3) New culture-  
independent methods  
that provide public  
health data

Surveillance using  
direct characterization  
of pathogens in  
specimens



# Long track record of success in controlling and preventing foodborne diseases – to be continued

- Identified major problems in outbreak investigations, which triggered extensive applied research, and then multipronged prevention
  - *Salmonella* Enteritidis and shell egg laying flocks
  - *E. coli* O157:H7 and ground beef
  - *Listeria monocytogenes* in processed meats
- More recently:
  - *Listeria monocytogenes* in caramel apples (2013-14)
  - *Salmonella* Heidelberg in chicken parts (2013-14)
- With new approaches, we can solve challenges like
  - STEC in raw flour
  - MDR *Salmonella* in veal calves and roaster pigs

**Can expect more issues to emerge, in need of new solutions**

# Could 2017 be a tipping point for improving foodborne disease prevention?

- USDA/FSIS: Implementing new performance standards for poultry parts, ground poultry, for *Salmonella* and *Campylobacter*
- FDA: New regulations under FSMA for
  - Preventive controls for processed foods, animal feeds
  - Produce safety
  - Foreign supplier verification
- Companies imposing new requirements for suppliers, making food safety part of corporate culture
- Consumers demanding food that is responsibly produced

# Future foodborne outbreaks more likely to be

- Detected by sequence-based surveillance
- Dispersed in space: Multi-state, multi-national
- Dispersed in time: Multi-year
- Detected as contaminated product first
  
- Associated with
  - fresh produce and minimally processed foods
  - imported foods
  - novel food vehicles
  - novel routes and pathways of contamination

# Control of foodborne disease in the 21<sup>st</sup> century: An evolving public health approach

- Whole genome sequence-based surveillance is a major evolutionary step forward
- Better outbreak detection, investigation and attribution
- Requires patient interviews and traceback of suspect foods
- With WGS we can anticipate that
  - more outbreaks are detected and stopped while smaller,
  - new food safety gaps are identified
- New diagnostic tests will be increasing the number of reported cases and driving efforts to preserve access to isolates (for WGS)
- Collaboration with many partners is vital to
  - investigate contamination events throughout food chain
  - focus and improve prevention measures
  - reduce the number of foodborne infections



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# Thank you

*The findings and conclusions in this presentation are those of the author and do not necessarily represent the views of the Centers for Disease Control and Prevention*



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# Our websites

FoodNet:

[www.cdc.gov/foodnet](http://www.cdc.gov/foodnet)

PulseNet:

[www.cdc.gov/pulsenet](http://www.cdc.gov/pulsenet)

Foodborne outbreak surveillance:

[www.cdc.gov/foodsafety/outbreaks/index.html](http://www.cdc.gov/foodsafety/outbreaks/index.html)

General Information About Foodborne Diseases:

[www.cdc.gov/foodsafety/](http://www.cdc.gov/foodsafety/)  
[www.cdc.gov/vitalsigns/foodsafety/](http://www.cdc.gov/vitalsigns/foodsafety/)

FoodNet Fast

[wwwn.cdc.gov/foodnetfast/](http://wwwn.cdc.gov/foodnetfast/)

CDC NARMS NOW

[wwwn.cdc.gov/narmsnow/](http://wwwn.cdc.gov/narmsnow/)

Foodborne Outbreak Online Database (FOOD) Tool

[wwwn.cdc.gov/foodborneoutbreaks/](http://wwwn.cdc.gov/foodborneoutbreaks/)

Foodborne Outbreak Updates

[www.cdc.gov/foodsafety/outbreaks/multistate-outbreaks/index.html](http://www.cdc.gov/foodsafety/outbreaks/multistate-outbreaks/index.html)



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